

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 1.06257 Seconds
(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-1
Perfect score: 185
Sequence: 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	75	40.5	36	2	US-08-933-314-7
5	75	40.5	37	1	US-08-682-485A-6
6	75	40.5	37	2	US-08-933-314-6
7	72.5	39.2	37	4	US-09-894-882-5
8	69	37.3	31	4	US-09-894-882-461
9	69	37.3	39	4	US-09-894-882-497
10	69	37.3	67	4	US-09-894-882-247
11	67	36.2	32	4	US-09-894-882-470
12	67	36.2	40	4	US-09-894-882-498
13	67	36.2	68	4	US-09-894-882-274
14	59	31.9	155	4	US-09-252-991A-28474
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17	59	31.9	2471	1	US-08-083-590A-19
18	59	31.9	2471	3	US-08-532-384-19
19	59	31.9	2471	4	US-08-899-232-1
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21	58.5	31.6	34	1	US-08-117-080-5
22	58.5	31.6	34	1	US-08-471-329-5
23	58.5	31.6	34	2	US-08-915-142-5
24	58.5	31.6	908	4	US-08-714-741-44
25	58	31.4	39	4	US-09-894-882-248
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29	57	30.8	493	4	US-09-252-991A-16925	Sequence 16925, A
30	56.5	30.5	30	4	US-09-894-882-474	Sequence 474, App
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33	56.5	30.5	70	4	US-09-894-882-295	Sequence 295, App
34	56	30.3	642	3	US-08-872-855-10	Sequence 10, Appl
35	56	30.3	2732	4	US-09-086-436-30	Sequence 30, Appl
36	55.5	30.0	291	4	US-09-902-540-15052	Sequence 15052, A
37	55.5	30.0	2211	3	US-09-738-884-1	Sequence 1, Appli
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39	54.5	29.5	30	4	US-09-894-882-471	Sequence 471, App
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41	54.5	29.5	44	4	US-09-894-882-278	Sequence 278, App
42	54.5	29.5	44	4	US-09-894-882-281	Sequence 281, App
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ALIGNMENTS

RESULT 1
US-09-894-882-3
; Sequence 3, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894, 882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-3
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Best Local Similarity 51.5%; Pred. No. 0.0041;
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;
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DB 2 ICTGADRPCAACCCPGTSCQGPESNGVVYCR 34
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US-09-894-882-4
; Sequence 4, Application US/09894882
; Patent No. 6767895

RESULT 3
US-08-682-485A-7
; Sequence 7, Application US/08682485A
; Patent No. 5763568
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996

RESULT 4
US-08-933-314-7
; Sequence 7, Application US/08933314
; Patent No. 5959182
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,314
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PLO722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
;

REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis

US-08-933-314-7

Query Match 40.5%; Score 75; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.027;
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DB 4 CTGADRPCAACCCPGTSCGPEPNGVSYCR 35

RESULT 5

US-08-682-485A-6
Sequence 6, Application US/08682485A
Patent No. 5763568
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
FUNNEL WEB (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
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NAME/KEY: Modified-site
LOCATION: 37
OTHER INFORMATION: /label= a
OTHER INFORMATION: /note= "this site may be amidated without loss
of biological activity"
US-08-682-485A-6

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QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33
DB 4 CTGADRPCAACCCPGTSCGPEPNGVSYCR 35

RESULT 6

US-08-933-314-6
Sequence 6, Application US/08933314
Patent No. 5959182
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
FUNNEL WEB (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
TOPOLOGY: linear


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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
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; OTHER INFORMATION: of biological activity"
US-08-933-314-6

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Best Local Similarity 50.0%; Pred. No. 0.028;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

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RESULT 7
US-09-894-882-5
; Sequence 5, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-5

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Db 2 ICTGADRPCAACCCPGTCKRAESGVSYCR 33

RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
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; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

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Best Local Similarity 44.8%; Pred. No. 0.12;
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US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 3.24047 Seconds
(without alignments)
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Title: US-10-019-823B-1

Perfect score: 185

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Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	44.3	36	9	US-09-894-882-3
2	79	42.7	36	9	US-09-894-882-4
3	73	39.5	35	14	US-10-072-602B-571
4	73	39.5	82	14	US-10-072-602B-140
5	72.5	39.2	37	9	US-09-894-882-5
6	69.5	37.6	30	14	US-10-072-602B-570
7	69.5	37.6	77	14	US-10-072-602B-137
8	69	37.3	31	9	US-09-894-882-461
9	69	37.3	39	9	US-09-894-882-497
10	69	37.3	67	9	US-09-894-882-247
11	67	36.2	32	9	US-09-894-882-470
12	67	36.2	32	14	US-10-072-602B-581
13	67	36.2	40	9	US-09-894-882-498

14	67	36.2	68	9	US-09-894-882-274	Sequence 274, App
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24	64	34.6	3501	14	US-10-123-155-37	Sequence 37, Appl
25	64	34.6	3501	14	US-10-146-731-37	Sequence 37, Appl
26	64	34.6	3501	14	US-10-140-472-37	Sequence 37, Appl
27	64	34.6	3501	14	US-10-141-761-37	Sequence 37, Appl
28	64	34.6	3501	14	US-10-142-885-37	Sequence 37, Appl
29	64	34.6	3501	14	US-10-158-790-37	Sequence 37, Appl
30	64	34.6	3501	15	US-10-137-871-37	Sequence 37, Appl
31	64	34.6	3501	15	US-10-140-923-37	Sequence 37, Appl
32	64	34.6	3501	15	US-10-141-759-37	Sequence 37, Appl
33	64	34.6	3501	15	US-10-141-759-37	Sequence 37, Appl
34	64	34.6	3501	15	US-10-140-805-37	Sequence 37, Appl
35	64	34.6	3501	15	US-10-140-864-37	Sequence 37, Appl
36	64	34.6	3501	15	US-10-142-426-37	Sequence 37, Appl
37	63	34.1	1971	14	US-10-123-155-139	Sequence 139, App
38	63	34.1	1971	14	US-10-146-731-139	Sequence 139, App
39	63	34.1	1971	14	US-10-140-472-139	Sequence 139, App
40	63	34.1	1971	14	US-10-141-761-139	Sequence 139, App
41	63	34.1	1971	14	US-10-142-885-139	Sequence 139, App
42	63	34.1	1971	14	US-10-158-790-139	Sequence 139, App
43	63	34.1	1971	15	US-10-137-871-139	Sequence 139, App
44	63	34.1	1971	15	US-10-140-923-139	Sequence 139, App
45	63	34.1	1971	15	US-10-141-756-139	Sequence 139, App

ALIGNMENTS

RESULT 1

US-09-894-882-3
; Sequence 3, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-3


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; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 571
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-571

Query Match 39.5%; Score 73; DB 14; Length 35;
Best Local Similarity 43.3%; Pred. No. 0.18;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33
Db 2 CGESGGCYSVRPCCPGLICKGTGGGLCR 31

RESULT 4
US-10-072-602B-140
; Sequence 140, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-140

Query Match 39.5%; Score 73; DB 14; Length 82;
Best Local Similarity 43.3%; Pred. No. 0.39;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33
Db 49 CGESGGCYSVRPCCPGLICKGTGGGLCR 78

RESULT 5
US-09-894-882-5
; Sequence 5, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: Jones, Robert M.

```



```

; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-5

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```

Query Match      39.2%; Score 72.5; DB 9; Length 37;
Best Local Similarity 46.9%; Pred. No. 0.22;
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNN-KVCR 33
DB 2 ICTGADRPCAACCCPCPGTSCKAESNGVSYCR 33

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RESULT 6
US-10-072-602B-570
; Sequence 570, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,408
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 570
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-570

```

```

Query Match      37.6%; Score 69.5; DB 14; Length 30;
Best Local Similarity 44.8%; Pred. No. 0.41;
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

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QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
DB 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32

```

```

Db 2 CGHSGAGC-YTRPCCPGLHCSGGAGGLC 29
RESULT 7
US-10-072-602B-137
; Sequence 137, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,408
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 137
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-137

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```

Query Match      37.6%; Score 69.5; DB 14; Length 77;
Best Local Similarity 44.8%; Pred. No. 0.93;
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

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QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
DB 4 CGHSGAGC-YTRPCCPGLHCSGGAGGLC 76

```

```

RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match          37.3%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.48;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNV 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          37.3%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.58;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNV 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          37.3%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.58;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNV 27

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 470
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-470

Query Match          36.2%; Score 67; DB 9; Length 32;
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match          37.3%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.48;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNV 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          37.3%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.58;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNV 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          37.3%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.58;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNV 27

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 470
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-470

Query Match          36.2%; Score 67; DB 9; Length 32;
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Thu Mar 10 14:26:01 2005

```

; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 255
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Conus virgo
US-10-072-602B-255

Query Match      36.2%; Score 67; DB 14; Length 79;
Best Local Similarity 48.4%; Pred. No. 1.8;
Matches 15; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

QY      4 CTPAGVKCPAALPCCPGLRCI-GGVNKKVCR 33
Db      49 CGQGEGC-YTQPCCPGLRCRGGTGGGVCQ 78
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Search completed: March 9, 2005, 18:08:02
Job time : 4.24047 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:50:50 ; Search time 176 Seconds
(without alignments)
96.015 Million cell updates/sec

Title: US-10-019-823B-1
Perfect score: 185
Sequence: 1 XXICTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33

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Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	83	44.9	36	1	TXJA_HADVE	P82227 hadronyche
2	80	43.2	36	1	TXJB_HADVE	P82226 hadronyche
3	73.5	39.7	37	1	TXJC_HADVE	P82228 hadronyche
4	73	39.5	72	2	Q9TVN1	Q9tvn1 conus livid
5	73	39.5	72	2	Q9UAA2	Q9uaa2 conus livid
6	73	39.5	72	2	Q9UAA3	Q9uaa3 conus livid
7	73	39.5	72	2	Q9UAA4	Q9uaa4 conus livid
8	73	39.5	72	2	Q9UAA5	Q9uaa5 conus livid
9	73	39.5	72	2	Q9UAA7	Q9uaa7 conus livid
10	73	39.5	72	2	Q9UAB0	Q9uab0 conus livid
11	73	39.5	72	2	Q9UAB1	Q9uab1 conus livid
12	72	38.9	2524	2	Q9GPA5	Q9gpa5 brachiostoma
13	71.5	38.6	33	1	TXC5_PHONI	P84015 phoneutria
14	71.5	38.6	3775	2	Q7PMF9	Q7pmf9 anopheles g
15	69	37.3	67	1	CKX_CONVR	Q7yze9 conus virgo
16	68	36.8	71	2	Q9UAA9	Q9uaa9 conus livid
17	66	35.7	71	2	Q9UAB3	Q9uab3 conus livid
18	66	35.7	1064	1	FBP1_STRPU	P10079 strongyloce
19	65	35.1	71	2	Q9TW08	Q9tw08 conus livid
20	65	35.1	71	2	Q9UAA0	Q9uaa0 conus livid
21	65	35.1	71	2	Q9UAA1	Q9uaa1 conus livid
22	65	35.1	71	2	Q9UAA6	Q9uaa6 conus livid
23	65	35.1	71	2	Q9UAA8	Q9uaa8 conus livid
24	65	35.1	71	2	Q9UAB2	Q9uab2 conus livid
25	64.5	34.9	76	2	Q9BP93	Q9bp93 conus ventr
26	64	34.6	77	2	Q75WH6	Q75wh6 macrothele
27	63	34.1	233	2	Q946Y8	Q946y8 hordeum vul
28	62.5	33.8	80	2	Q9BP85	Q9bp85 conus arena
29	62	33.5	328	2	Q6TVP0	Q6tvp0 orf virus
30	61.5	33.2	77	2	Q75WH3	Q75wh3 macrothele
31	61.5	33.2	494	2	Q6FNU8	Q6fnu8 candida gla

RESULT 1		TXJA_HADVE		STANDARD;		PRT;		36 AA.	
AC	P82227;								
DT	30-MAY-2000	(Rel. 39, Created)							
DT	30-MAY-2000	(Rel. 39, Last sequence update)							
DT	05-JUL-2004	(Rel. 44, Last annotation update)							
DE	Janus-atracotoxin-Hv1a (J-ActX-Hv1a).								
OS	Hadroryche versuta (Blue mountains funnel-web spider) (Atrax versutus).								
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;								
OC	Eukaryomorphae; Hexathelidae; Hadroryche.								
OX	NCBI_TaxID=6904;								
RP	[1]								
RP	SEQUENCE.								
RC	TISSUE=Venom;								
RX	MEDLINE=20343014; PubMed=10891200; DOI=10.1038/75921;								
RA	Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,								
RA	Nicholson G.M., Christie M.J., King G.F.;								
RT	"Discovery and characterization of a family of insecticidal								
RT	neurotoxins with a rare vicinal disulfide bridge.";								
RL	Nat. Struct. Biol. 7:505-513(2000).								
CC	- - FUNCTION: Insecticidal neurotoxin.								
CC	- - SUBCELLULAR LOCATION: Secreted.								
CC	- - TISSUE SPECIFICITY: Expressed by the venom gland.								
DR	HSSP; P82228; IDL0.								
KW	Direct protein sequencing; Neurotoxin; Toxin.								
FT	DISULFID 3 17	By similarity.							
FT	DISULFID 10 22	By similarity.							
FT	DISULFID 13 14	By similarity.							
FT	DISULFID 16 33	By similarity.							
SQ	SEQUENCE 36 AA; 3685 MW; D1598B2560BFE997 CRC64;								
Query Match 44.9%; Score 83; DB 1; Length 36;									
Best Local Similarity 50.0%; Pred. No. 0.0046;									
Matches 17; Conservative 2; Mismatches 13; Indels 2;									
Qy	2	XICTPAGVKCPAALPCCPGLCIGGVNKKV--CR 33							
Dd	1	TICTGADRPCAACCCPGTSCQGPSNGVVYCR 34							
RESULT 2									
TXJB_HADVE		STANDARD;		PRT;		36 AA.			
AC	P82226;								
DT	30-MAY-2000	(Rel. 39, Created)							
DT	30-MAY-2000	(Rel. 39, Last sequence update)							
DT	05-JUL-2004	(Rel. 44, Last annotation update)							
DE	Janus-atracotoxin-Hv1b (J-ActX-Hv1b).								
OS	Hadroryche versuta (Blue mountains funnel-web spider) (Atrax versutus).								
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;								
OC	Eukaryomorphae; Hexathelidae; Hadroryche.								

OX NCBI_TaxID=6904;
RN (1)
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;
RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
RA Nicholson G.M., Christie M.J., King G.F.;
RT "Discovery and characterization of a family of insecticidal
RL neurotoxins with a rare vicinal disulfide bridge.";
RL Nat. Struct. Biol. 7:505-513(2000).
CC -|- FUNCTION: Insecticidal neurotoxin.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom gland.
DR HSP; P82228; IDL0.
KW Direct protein sequencing; Neurotoxin; Toxin.
FT DISULFID 3 17 By similarity.
FT DISULFID 10 22 By similarity.
FT DISULFID 13 14 By similarity.
FT DISULFID 16 33 By similarity.
SQ SEQUENCE 36 AA; 3651 MW; D23A442560B8997 CRC64;
Query Match 43.2%; Score 80; DB 1; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.011;
Matches 17; Conservative 1; Mismatches 14; Indels 2; Gaps 1;
QY 2 XICTPAGVKCPAALPCCPGLRCIGGVNNKVC-CR 33
DB 1 TICTGADRPCAACCCPCPGTSCQGPENGVSYCR 34
RESULT 3
TXJC_HADVE STANDARD; PRT; 37 AA.
AC P82228;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Janus-atracotoxin-Hv1c (J-Actx-Hv1c).
OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
OS versutus).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Hexathelidae; Hadronyche.
OX NCBI_TaxID=6904;
RN (1)
RP SEQUENCE, FUNCTION, AND STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;
RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
RA Nicholson G.M., Christie M.J., King G.F.;
RT "Discovery and characterization of a family of insecticidal
RT neurotoxins with a rare vicinal disulfide bridge.";
RL Nat. Struct. Biol. 7:505-513(2000).
CC -|- FUNCTION: Insecticidal neurotoxin.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom gland.
DR PDB; IDL0; NMR; A=1-37.
KW 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.
FT DISULFID 3 17
FT DISULFID 10 22
FT DISULFID 13 14
FT DISULFID 16 32
FT TURN 6 7
FT STRAND 9 9
FT TURN 18 19
FT STRAND 20 24
FT TURN 26 27
FT STRAND 30 34
SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;
Query Match 39.7%; Score 73.5; DB 1; Length 37;
Best Local Similarity 45.5%; Pred. No. 0.068;
Matches 15; Conservative 1; Mismatches 16; Indels 1; Gaps 1;

QY 2 XICTPAGVKCPAALPCCPGLRCIGGVNN-KVCR 33
DB 1 AICTGADRPCAACCCPCPGTSCKAESNGVSYCR 33
RESULT 4
O9TVN1
ID Q9TVN1 PRELIMINARY; PRT; 72 AA.
AC Q9TVN1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Four-loop conotoxin LVVIA (Four-loop conotoxin LVVIB
DE (Fragment)).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RT rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089958; AAD48213.1; -
DR EMBL; AF089902; AAD48158.1; -
DR EMBL; AF089906; AAD48162.1; -
DR EMBL; AF089907; AAD48163.1; -
DR EMBL; AF089910; AAD48165.1; -
DR EMBL; AF089913; AAD48168.1; -
DR EMBL; AF089914; AAD48169.1; -
DR EMBL; AF089915; AAD48170.1; -
DR EMBL; AF089916; AAD48171.1; -
DR EMBL; AF089917; AAD48172.1; -
DR EMBL; AF089918; AAD48173.1; -
DR EMBL; AF089919; AAD48174.1; -
DR EMBL; AF089920; AAD48175.1; -
DR EMBL; AF089921; AAD48176.1; -
DR EMBL; AF089922; AAD48177.1; -
DR EMBL; AF089923; AAD48178.1; -
DR EMBL; AF089924; AAD48179.1; -
DR EMBL; AF089925; AAD48180.1; -
DR EMBL; AF089926; AAD48181.1; -
DR EMBL; AF089927; AAD48182.1; -
DR EMBL; AF089928; AAD48183.1; -
DR EMBL; AF089929; AAD48184.1; -
DR EMBL; AF089930; AAD48185.1; -
DR EMBL; AF089931; AAD48186.1; -
DR EMBL; AF089932; AAD48187.1; -
DR EMBL; AF089933; AAD48188.1; -
DR EMBL; AF089941; AAD48196.1; -
DR EMBL; AF089942; AAD48197.1; -
DR EMBL; AF089943; AAD48198.1; -
DR EMBL; AF089944; AAD48199.1; -
DR EMBL; AF089945; AAD48200.1; -
DR EMBL; AF089946; AAD48201.1; -
DR EMBL; AF089947; AAD48202.1; -
DR EMBL; AF089948; AAD48203.1; -
DR EMBL; AF089949; AAD48204.1; -
DR EMBL; AF089950; AAD48205.1; -
DR EMBL; AF089951; AAD48206.1; -
DR EMBL; AF089953; AAD48208.1; -
DR EMBL; AF089954; AAD48209.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
FT Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 72 AA; 7984 MW; B2057DDC87553B8D CRC64;

Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27
Db 41 TRTCSPAGEVCTSKSPCCTGFLCSHIGGM 69

RESULT 5
Q9UAA2
ID Q9UAA2 PRELIMINARY; PRT; 72 AA.
AC Q9UAA2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089959; AAD48214.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 7924 MW; 74762D9C9193EB8B CRC64;

Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27
Db 41 TRTCSPAGEVCTSKSPCCTGFLCSHIGGM 69

RESULT 6
Q9UAA3
ID Q9UAA3 PRELIMINARY; PRT; 72 AA.
AC Q9UAA3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089959; AAD48214.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.

FT NON_TER 1
SQ SEQUENCE 72 AA; 8014 MW; C2757DDC87553EDD CRC64;

Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27
Db 41 TRTCSPAGEVCTSKSPCCTGFLCSHIGGM 69

RESULT 7
Q9UAA4
ID Q9UAA4 PRELIMINARY; PRT; 72 AA.
AC Q9UAA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089955; AAD48210.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 7998 MW; B4DE7DDC87553B8D CRC64;

Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27
Db 41 TRTCSPAGEVCTSKSPCCTGFLCSHIGGM 69

RESULT 8
Q9UAA5
ID Q9UAA5 PRELIMINARY; PRT; 72 AA.
AC Q9UAA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089952; AAD48207.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.

DR EMBL; AF089905; AAD48161.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 8028 MW; B5720DDC87503E8D CRC64;

Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27
::|:|||:|:|||||:
Db 41 TRTCSPAGEVCTSKSPCTGFLCSHIGGM 69

RESULT 11

Q9UAB1 ID Q9UAB1 PRELIMINARY; PRT; 72 AA.
AC Q9UAB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsgastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9928955; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089904; AAD48160.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 7935 MW; 64C72DDC8755282F CRC64;

Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27
::|:|||:|:|||||:
Db 41 TRTCSPAGEVCTSKSPCTGFLCSHIGGM 69

RESULT 12

Q9GPAS ID Q9GPAS PRELIMINARY; PRT; 2524 AA.
AC Q9GPAS;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative notch receptor protein.
GN Name=notch;
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
ON NCBI_TaxID=7739;
OX [1]
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE=Whole larvae;
RA Holland L.Z., Burgtoef C., Holland N.D., Lehrach H., Tamme R.,

ID CXK_CONV STANDARD; PRT; 67 AA.
AC Q7YZS9;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kappa-conotoxin ViTx precursor.
GN Name=ViTx;
OS Conus virgo (Virgin cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89427;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 27-53, SYNTHESIS OF 27-60, AND MASS SPECTROMETRY.
RC TISSUE=Venom, and Venom duct;
RX PubMed=12893060; DOI=10.1016/S0041-0101(03)00099-0;
RA Kaufenstein S., Huys I., Lamthanh H., Stocklin R., Sotro F., Menez A., Tytgat J., Mebs D.;
RT "A novel conotoxin inhibiting vertebrate voltage-sensitive potassium channels.";
RL Toxicon 42:43-52(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RA Kaufenstein S.;
RL Thesis (2001), University of Darmstadt, Germany.
CC -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive potassium channels. This toxin inhibits the vertebrate potassium channels Kv1.1 and Kv1.3, but not Kv1.2. It has no effect on HERG-type channels, sodium hH1 channels and Kir-type channels (IRK1).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- PTM: Contains four disulfide bonds.
CC -!- MASS SPECTROMETRY: MW=3933.3; METHOD=Electrospray; RANGE=27-60; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type family.
CC -----
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CC -----
DR EMBL; AJ560778; CAD90965.1; -.
KW Direct protein sequencing; Signal; Toxin.
FT SIGNAL 1 26
FT CHAIN 27 60 Kappa-conotoxin ViTx.
FT PROPEP 61 67
FT CONFLICT 38 38 P -> S (in Ref. 1).
FT CONFLICT 49 49 G -> S (in Ref. 1).
SQ SEQUENCE 67 AA; 7599 MW; 46671D012446F62D CRC64;
Query Match 37.3%; Score 69; DB 1; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.41;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;
QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db 29 CFPPIYCTPYLPCCWGICC--GTCRNV 55

Search completed: February 14, 2005, 21:04:58
Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:56:55 ; Search time 39 Seconds
(without alignments)
81.414 Million cell updates/sec

Title: US-10-019-823B-1
Perfect score: 185
Sequence: 1 XXICTPAGVKCPAALPCCGLRCIGGVNKKVCR 33
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	35.7	1064	2 A40136	fibropellin Ia - s
2	60	32.4	422	2 S48564	probable membrane
3	60	32.4	570	2 A48836	fibropellin C prec
4	58.5	31.6	34	2 A31043	mu-conotoxin GS -
5	58.5	31.6	1390	2 T30346	insulin receptor -
6	58	31.4	37	2 E44007	apoptoxin III - tr
7	58	31.4	1221	2 T23472	hypothetical prote
8	57	30.8	2531	2 S18188	notch protein homo
9	57	30.8	2531	2 A46019	notch-1 protein -
10	56.5	30.5	4543	1 A53102	alpha-2-macroglobu
11	56	30.3	197	2 T10081	sperm mitochondria
12	56	30.3	585	2 S43572	COSB5.5 protein (c
13	56	30.3	585	2 E88571	protein COSB5.5 [i
14	56	30.3	2352	2 T30201	Notch homolog prot
15	55.5	30.0	768	2 A87722	protein ZC123.1 [i
16	55	29.7	132	2 H75335	hypothetical prote
17	55	29.7	238	2 T04166	thaumatin-like pro
18	55	29.7	2139	2 A35672	crumbs protein - f
19	55	29.7	2318	2 S45306	notch 3 protein -
20	55	29.7	2321	2 S78549	notch3 protein - h
21	54.5	29.5	417	2 T08724	hypothetical prote
22	54.5	29.5	601	2 T22025	hypothetical prote
23	54.5	29.5	601	2 D89711	protein F40E10.4 [
24	54.5	29.5	4544	1 S02392	alpha-2-macroglobu
25	54.5	29.5	4545	1 S25111	platelet aggregati
26	54	29.2	73	2 H43019	hypothetical prote
27	54	29.2	269	2 T26957	hypothetical prote
28	54	29.2	283	2 E88597	protein Y47D3B.6 [
29	54	29.2	596	2 T26950	hypothetical prote

30	54	29.2	1203	2 A49175	Notch B protein -
31	54	29.2	1449	2 S47423	E2 glycoprotein pr
32	54	29.2	2437	2 S42612	transmembrane prot
33	54	29.2	2524	2 A35844	Notch protein - Af
34	53	28.6	456	1 KXBO	protein C (activat
35	53	28.6	1447	1 VGIHE3	E2 glycoprotein pr
36	53	28.6	1447	1 VGIHE2	E2 glycoprotein pr
37	53	28.6	1449	1 A43573	E2 glycoprotein pr
38	53	28.6	1449	1 VGIHFS	E2 glycoprotein pr
39	53	28.6	1451	1 JQ1719	E2 glycoprotein pr
40	53	28.6	1453	2 S41453	spike protein - ca
41	52	28.1	64	2 A25775	metallothionein A
42	52	28.1	64	2 A33825	metallothionein A
43	52	28.1	71	2 G43019	platelet aggregati
44	52	28.1	134	2 AD0652	conserved hypothet
45	52	28.1	249	2 T32060	hypothetical prote

ALIGNMENTS

RESULT 1

A40136
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
N:Alternate names: epidermal growth factor homolog precursor
N:Contains: alternatively spliced fibropellin Ib (EGFI)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A40136; B40136; C40136; A29316; A43131
R:Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A:Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpuratus
A:Reference number: A40136; MUID:90112459; PMID:2514273
A:Accession: A40136
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114
A:Cross-references: UNIPROT:P10079; GB:X17530; NID:G10225; PID:G667061
A:Accession: B40136
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
A:Accession: C40136
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'K',747-821,898-978 <DE3>
R:Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A:Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A:Reference number: A29316; MUID:87319677; PMID:3498216
A:Accession: A29316
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 'S',280-481,786-1064 <HUR>
A:Cross-references: GB:M17421; NID:G161474; PIDN:AAA30050.1; PID:G552260
R:Hunt, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A:Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
A:Reference number: A43131; MUID:89196806; PMID:2784773
A:Contents: annotation
C:Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
F:1-19/Domains: signal sequence #status predicted <SIG>
F:20-1064/Product: fibropellin I #status predicted <FIB>
F:23-54/Domains: EGF homology <EG01>
F:57-175/Domains: Ctr/Cls repeat homology <Clr>
F:180-211/Domains: EGF homology <EG02>
F:218-249/Domains: EGF homology <EG03>
F:256-287/Domains: EGF homology <EG04>
F:294-325/Domains: EGF homology <EG05>
F:332-363/Domains: EGF homology <EG06>
F:370-401/Domains: EGF homology <EG07>
F:408-439/Domains: EGF homology <EG08>
F:446-477/Domains: EGF homology <EG09>

Query Match 31.6%; Score 58.5; DB 2; Length 1390;
Best Local Similarity 34.9%; Pred. No. 33;
Matches 15; Conservative 4; Mismatches 11; Indels 13; Gaps 3;

QY 1 XXICTPAGVKCPAALP-----CCPGLRCIGGVN-----NKVCR 33
Db 226 QTCICPP---ECPKACSKTGVCCDAESCLGCGNLPNTSSGVSVC 265

RESULT 6
E44007
aptoxin III - trap-door spider (Aptostichus schlingeri)
N:Alternate names: insecticidal peptide Aps III
C:Species: Aptostichus schlingeri
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E44007
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Quistad, G.B.
Toxinon 30, 1043-1050, 1992
A:Title: Identification of insecticidal peptides from venom of the trap-door spider, Aptostichus schlingeri
A:Reference number: A44007; MUID:93069259; PMID:1440641
A:Accession: E44007
A:Molecule type: protein
A:Residues: 1-37 <SKI>
A:Cross-references: UNIPROT:P49268; PIDN:AAB24051.1; PID:G259281
A:Note: sequence extracted from NCBI backbone (NCBIP:119526)
C:Keywords: disulfide bond; toxin; venom

Query Match 31.4%; Score 58; DB 2; Length 37;
Best Local Similarity 37.1%; Pred. No. 2.2;
Matches 13; Conservative 1; Mismatches 15; Indels 6; Gaps 1;

QY 4 CTPAGVKCPAALPCCPG-----LRICGGVNNKVC 32
Db 1 CNSKGTPTCTNADECCKGKCAVNVNVCIGGCKTC 35

RESULT 7
T23472
hypothetical protein K08E7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23472
R:Smyle, R.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19745
A:Accession: T23472
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1221 <WIL>
A:Cross-references: UNIPROT:Q21344; EMBL:Z77666; PIDN:CAB01228.1; GSPDB:GN00022; CESP:K08E7
A:Experimental source: clone K08E7
C:Genetics:
A:Gene: CESP:K08E7.5
A:Map position: 4
A:Introns: 26/1; 103/1; 170/1; 640/1; 802/2; 831/1; 864/3; 891/3; 908/1; 938/2; 980/1; 1000/1;

Query Match 31.4%; Score 58; DB 2; Length 1221;
Best Local Similarity 31.2%; Pred. No. 34;
Matches 10; Conservative 5; Mismatches 15; Indels 2; Gaps 1;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db 968 QNCCAPPAPCCLFTIPCCPPICC--PQPKIC 997

RESULT 8
S18188
notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991

A:Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Cross-references: EMBL:X57405; NID:G57634; PID:G57635
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF2>
F:1233-1264/Domain: EGF homology <EGF2>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 30.8%; Score 57; DB 2; Length 2531;
Best Local Similarity 34.1%; Pred. No. 79;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 2;

QY 1 XXICTP--AGVKCPAALPCCPGLR-----CIGGVNNKVC 33
Db 242 ECACLPGFAGQNCENVDPCGNCKNGGACVDGVNTYNCR 282

RESULT 9
A46019
notch-1 protein - mouse
N:Alternate names: notch protein
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C:Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109
R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gridj Genomics 15, 259-264, 1993
A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch, suggested by its expression pattern.
A:Reference number: A46019; MUID:93194170; PMID:8449489
A:Accession: A46019
A>Status: not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-2531
A:Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:G288502; PIDN:CAA77941.1; R:Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; submitted to the EMBL Data Library, April 1992
A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggested by its expression pattern.
A:Reference number: S25144
A:Accession: S25144
A:Molecule type: mRNA
A:Residues: 1551-2108, 'O', 2110-2114, 'ALP', 2118-2170 <FRA>
A:Cross-references: EMBL:Z11886
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of tissues.
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: C49175
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1161-1547 <LAR>
A:Cross-references: EMBL:X68278; NID:G287987; PIDN:CAA48339.1; PID:G287988
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126159)
R:Xopan, R.; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A:Title: Mouse notch: expression in hair follicles correlates with cell fate determination.
A:Reference number: A46438; MUID:93252998; PMID:8486742
A:Accession: B46438
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054-2055, 'S', 2056-2057, 'S', 2058-2059, 'S', 2060-2061, 'S', 2062-2063, 'S', 2064-2065, 'S', 2066-2067, 'S', 2068-2069, 'S', 2070-2071, 'S', 2072-2073, 'S', 2074-2075, 'S', 2076-2077, 'S', 2078-2079, 'S', 2080-2081, 'S', 2082-2083, 'S', 2084-2085, 'S', 2086-2087, 'S', 2088-2089, 'S', 2090-2091, 'S', 2092-2093, 'S', 2094-2095, 'S', 2096-2097, 'S', 2098-2099, 'S', 2100-2101, 'S', 2102-2103, 'S', 2104-2105, 'S', 2106-2107, 'S', 2108-2109, 'S', 2110-2111, 'S', 2112-2113, 'S', 2114-2115, 'S', 2116-2117, 'S', 2118-2119, 'S', 2120-2121, 'S', 2122-2123, 'S', 2124-2125, 'S', 2126-2127, 'S', 2128-2129, 'S', 2130-2131, 'S', 2132-2133, 'S', 2134-2135, 'S', 2136-2137, 'S', 2138-2139, 'S', 2140-2141, 'S', 2142-2143, 'S', 2144-2145, 'S', 2146-2147, 'S', 2148-2149, 'S', 2150-2151, 'S', 2152-2153, 'S', 2154-2155, 'S', 2156-2157, 'S', 2158-2159, 'S', 2160-2161, 'S', 2162-2163, 'S', 2164-2165, 'S', 2166-2167, 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C;Genetics:
 A;Gene: notch-1
 A;Map position: 2
 A;Note: proximal region of chromosome 2

C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology

F;106-138/Domain: EGF homology <EGF1>
 F;144-175/Domain: EGF homology <EG01>
 F;222-254/Domain: EGF homology <EGF2>
 F;261-292/Domain: EGF homology <EG02>
 F;339-370/Domain: EGF homology <EG03>
 F;416-449/Domain: EGF homology <EGF3>
 F;456-487/Domain: EGF homology <EG04>
 F;494-525/Domain: EGF homology <EG05>
 F;532-563/Domain: EGF homology <EG06>
 F;607-638/Domain: EGF homology <EG07>
 F;682-713/Domain: EGF homology <EG08>
 F;757-788/Domain: EGF homology <EG09>
 F;795-826/Domain: EGF homology <EG10>
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 F;987-1018/Domain: EGF homology <EG14>
 F;1025-1056/Domain: EGF homology <EG15>
 F;1063-1094/Domain: EGF homology <EG16>
 F;1149-1180/Domain: EGF homology <EG17>
 F;1187-1218/Domain: EGF homology <EG18>
 F;1233-1264/Domain: EGF homology <EGF4>
 F;1352-1383/Domain: EGF homology <EG19>
 F;1391-1425/Domain: EGF homology <EGF>
 F;1917-1948/Domain: ankyrin repeat homology <AN1>
 F;1949-1981/Domain: ankyrin repeat homology <AN2>
 F;1983-2015/Domain: ankyrin repeat homology <AN3>
 F;2016-2048/Domain: ankyrin repeat homology <AN4>
 F;2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 30.8%; Score 57; DB 2; Length 2531;

Best Local Similarity 34.1%; Pred. No. 79;

Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 2;

QY 1 XXICTP--AGVKCPAALPCPCGLR-----CIGGVNKNKVC 33

DB 242 ECACLPFGAGQNCENVDPCGNCKNGGACVDGVNTYNCR 282

RESULT 10

A53102

alpha-2-macroglobulin receptor precursor - chicken
 N;Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor
 C;Species: Gallus gallus (chicken)

C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004

C;Accession: A53102

R;Nimble, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.

J. Biol. Chem. 269, 212-219, 1994

A;Title: The somatic cell-specific low density lipoprotein receptor-related protein of t

A;Reference number: A53102; MUID:94103212; PMID:7506255

A;Accession: A53102

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-4543 <NIM>

A;Cross-references: UNIPROT:P98157; GB:X74904; NID:G438006; PIDN:CAAS2870.1; PID:G438007

C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated protein.

C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

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F;18-3942, 3943-4543/Product: alpha-2-macroglobulin receptor #status predicted <MAT>

F;29-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F;74-110/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F;117-190/Domain: EGF homology <EG1>

F;150-190/Domain: EGF homology <EG2>

F;200-241/Domain: LDL receptor YWTD-containing repeat homology <YW01>

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 F;381-422/Domain: LDL receptor YWTD-containing repeat homology <YW05>
 F;423-470/Domain: LDL receptor YWTD-containing repeat homology <YW06>
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 F;713-754/Domain: LDL receptor YWTD-containing repeat homology <YW10>
 F;755-797/Domain: LDL receptor YWTD-containing repeat homology <YW11>
 F;805-840/Domain: EGF homology <EG4>
 F;852-888/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F;893-929/Domain: LDL receptor ligand-binding repeat homology <LDL4>
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 F;1143-1180/Domain: LDL receptor ligand-binding repeat homology <LDLA>
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 F;1795-1842/Domain: LDL receptor YWTD-containing repeat homology <YW23>
 F;1846-1882/Domain: EGF homology <EG8>
 F;1930-1972/Domain: LDL receptor YWTD-containing repeat homology <YW24>
 F;1973-2015/Domain: LDL receptor YWTD-containing repeat homology <YW25>
 F;2016-2059/Domain: LDL receptor YWTD-containing repeat homology <YW26>
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 F;2155-2190/Domain: EGF homology <EG9>
 F;2195-2237/Domain: LDL receptor YWTD-containing repeat homology <YW29>
 F;2247-2288/Domain: LDL receptor YWTD-containing repeat homology <YW30>
 F;2338-2382/Domain: LDL receptor YWTD-containing repeat homology <YW31>
 F;2383-2423/Domain: LDL receptor YWTD-containing repeat homology <YW32>
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F:3826-3858/Domain: EGF homology <EG15>
F:3866-3909/Domain: LDL receptor WYTD-containing repeat homology <YW40>
F:3910-3968/Domain: LDL receptor WYTD-containing repeat homology <YW41>
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F:3969-4011/Domain: 85K chain extracellular #status predicted <EXT>
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F:4056-4098/Domain: LDL receptor WYTD-containing repeat homology <YW43>
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F:116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643
3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carboxylate (Asn) (covalent)
F:168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 30.5%; Score 56.5; DB 1; Length 4543;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 13; Conservative 6; Mismatches 13; Indels 7; Gaps 2;

QY 1 XXICTPAGVKCPAALPCCPGL-RCIG-----GVNNKVC 32
Db 3407 IHVCLPSQFKCTNTRCIPGIFRCNGQDNCDEKDC 3445

RESULT 11

Tl0081
sperm mitochondrial capsule selenoprotein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C:Accession: Tl0081; A37199
R:Kleene, K.C.; Smith, J.; Bozorgadeh, A.; Harris, M.; Hahn, L.; Karimpour, I.; Gerstel
Dev. Biol. 137, 395-402, 1990
A:Title: Sequence and developmental expression of the mRNA encoding the seleno-protein c
A:Reference number: A37199; MUID:90152148; PMID:2303168
A:Accession: Tl0081
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-6, 'X', 8-16, 'X', 18-33, 'X', 35-197 <KLE1>
A:Cross-references: UNIPROT:P15265; EMBL:M29603; NID:g199088; PIDN:AAA53045.1; PID:g5672
A:Experimental source: strain CD-1
A>Note: in Genbank entry MUSMCS, release 113.0, PIDN:AAA53045.1, the selenocysteine UGA
A:Accession: A37199
A:Molecule type: mRNA
A:Residues: 55-197 <KLE2>
A:Cross-references: GB:M29603; NID:g199088
A>Note: the authors translated the codon TGT for residue 112 as Pro

C:Genetics:
A:Gene: MCS
A:Genome: nuclear
C:Keywords: mitochondrion; selenocysteine; sperm
F:7,17,34/Modified site: selenocysteine #status predicted

Query Match 30.3%; Score 56; DB 2; Length 197;
Best Local Similarity 45.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGLRC 23

Db 87 CCPKSPCCPKSPCCPKPK 106

RESULT 12

S43572
C05B5.5 protein (clone C05B5) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S43572
R:Mortimore, B.
submitted to the EMBL Data Library, April 1994
A:Reference number: S43570
A:Accession: S43572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <MOR>
A:Cross-references: EMBL:Z32679
C:Genetics:
A:Introns: 35/2; 218/3; 292/2; 328/1; 442/2

Query Match 30.3%; Score 56; DB 2; Length 585;
Best Local Similarity 33.3%; Pred. No. 33;
Matches 12; Conservative 1; Mismatches 9; Indels 14; Gaps 1;

QY 6 PAGVKC-----PAALPCCPGLRCIGGV 27
Db 541 PTGYQCIDGKCKTKRHFLAPPCVAECPPGTRCINGV 576

RESULT 13

E88571
protein C05B5.5 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E88571
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: E88571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <STO>
A:Cross-references: UNIPROT:P34293; GB:chr_III; PIDN:CAAB3593.1; PID:g3873993; GSPDB:GN01
C:Genetics:
A:Gene: C05B5.5
A:Map position: 3

Query Match 30.3%; Score 56; DB 2; Length 585;
Best Local Similarity 33.3%; Pred. No. 33;
Matches 12; Conservative 1; Mismatches 9; Indels 14; Gaps 1;

QY 6 PAGVKC-----PAALPCCPGLRCIGGV 27
Db 541 PTGYQCIDGKCKTKRHFLAPPCVAECPPGTRCINGV 576

RESULT 14

T30201
Notch homolog protein - sea squirt (Halocynthia roretzi)
C:Species: Halocynthia roretzi
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2002
C:Accession: T30201
R:Hori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A:Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cent
A:Reference number: Z20775
A:Accession: T30201
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2352 <HOR>
A:Cross-references: EMBL:AB001327; NID:dl026501; PID:dl026501; PIDN:BAA25571.1
C:Genetics:

A;Gene: Notch
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 30.3%; Score 56; DB 2; Length 2352;
Best Local Similarity 36.8%; Pred. No. 98;
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;

QY 4 CTP--AGVKCPAAL-----PCCPGLRCIGGVNKKVCR 33
||| | | | : || | | ||| | |
Db 593 CTGTYGTHCDTIDNECDSPNCPMNGATCQNEVNFVCQ 630

RESULT 15
A87722
protein ZC123.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A87722
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A87722
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-768 <STO>
A;Cross-references: UNIPROT:O45021; GB:chr_I; PIDN:AAB97604.1; PID:g2804500; GSPDB:GN000
A;Note: contains similarity to granulins
C;Genetics:
A;Gene: ZC123.1
A;Map position: 1

Query Match 30.0%; Score 55.5; DB 2; Length 768;
Best Local Similarity 37.5%; Pred. No. 47;
Matches 12; Conservative 4; Mismatches 11; Indels 5; Gaps 2;

QY 1 XXICTPAGVK--CPAALPCCPGLR---CIGGV 27
: : | | | | | | | : |
Db 227 NPTCCNQGQKACCPPEQPCPELKLDNCLASV 258

Search completed: February 14, 2005, 21:05:43
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 21:01:05 ; Search time 129 Seconds
(without alignments)
83.587 Million cell updates/sec

Title: US-10-019-823B-1
Perfect score: 185
Sequence: 1 XXICTPAGVKCPAALPCCPLRCIGGVNKKVCR 33

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	44.9	36	9	US-09-894-882-3
2	80	43.2	36	9	US-09-894-882-4
3	73.5	39.7	37	9	US-09-894-882-5
4	73	39.5	35	14	US-10-072-602B-571
5	73	39.5	32	14	US-10-072-602B-140
6	69.5	37.6	30	14	US-10-072-602B-570
7	69.5	37.6	77	14	US-10-072-602B-137
8	69	37.3	31	9	US-09-894-882-461
9	69	37.3	39	9	US-09-894-882-497
10	69	37.3	67	9	US-09-894-882-247
11	67	36.2	32	9	US-09-894-882-470
12	67	36.2	32	14	US-10-072-602B-581
13	67	36.2	40	9	US-09-894-882-498

14	67	36.2	68	9	US-09-894-882-274	Sequence 274, App
15	67	36.2	79	14	US-10-072-602B-255	Sequence 255, App
16	66	35.7	566	10	US-09-900-449A-6	Sequence 6, Appli
17	66	35.7	572	10	US-09-900-449A-7	Sequence 7, Appli
18	66	35.7	601	10	US-09-900-449A-5	Sequence 5, Appli
19	66	35.7	639	10	US-09-900-449A-4	Sequence 4, Appli
20	66	35.7	1064	14	US-10-173-461-5	Sequence 5, Appli
21	65	35.1	77	14	US-10-072-602B-191	Sequence 191, App
22	65	35.1	3501	14	US-10-123-155-37	Sequence 37, Appl
23	65	35.1	3501	14	US-10-146-731-37	Sequence 37, Appl
24	65	35.1	3501	14	US-10-140-472-37	Sequence 37, Appl
25	65	35.1	3501	14	US-10-141-761-37	Sequence 37, Appl
26	65	35.1	3501	14	US-10-142-885-37	Sequence 37, Appl
27	65	35.1	3501	14	US-10-158-790-37	Sequence 37, Appl
28	65	35.1	3501	15	US-10-137-871-37	Sequence 37, Appl
29	65	35.1	3501	15	US-10-140-923-37	Sequence 37, Appl
30	65	35.1	3501	15	US-10-141-756-37	Sequence 37, Appl
31	65	35.1	3501	15	US-10-141-759-37	Sequence 37, Appl
32	65	35.1	3501	15	US-10-140-805-37	Sequence 37, Appl
33	65	35.1	3501	15	US-10-140-864-37	Sequence 37, Appl
34	65	35.1	3501	15	US-10-142-426-37	Sequence 37, Appl
35	64.5	34.9	86	15	US-10-424-599-240605	Sequence 240605,
36	64	34.6	30	14	US-10-072-602B-576	Sequence 576, App
37	64	34.6	1971	14	US-10-123-155-139	Sequence 139, App
38	64	34.6	1971	14	US-10-146-731-139	Sequence 139, App
39	64	34.6	1971	14	US-10-140-472-139	Sequence 139, App
40	64	34.6	1971	14	US-10-141-761-139	Sequence 139, App
41	64	34.6	1971	14	US-10-142-885-139	Sequence 139, App
42	64	34.6	1971	14	US-10-158-790-139	Sequence 139, App
43	64	34.6	1971	15	US-10-137-871-139	Sequence 139, App
44	64	34.6	1971	15	US-10-140-923-139	Sequence 139, App
45	64	34.6	1971	15	US-10-141-756-139	Sequence 139, App

ALIGNMENTS

RESULT 1
US-09-894-882-3
; Sequence 3, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-3

Query Match	44.9%	Score 83	DB 9	Length 36
Best Local Similarity	50.0%	Pred. No. 0.018		
Matches	17	Conservative	2	Gaps 1
QY	2	XICTPAGVKCPAALPCCPGLCIGGVNNKV--CR	33	
Db	1	TICTGADRPCCAAACCCPGTSCQGPESNGVVYCR	34	
RESULT 2				
US-09-894-882-4				
Sequence 4, Application US/09894882				
Patent No. US20020102607A1				
GENERAL INFORMATION:				
APPLICANT: University of Utah Research Foundation				
APPLICANT: Cognetix, Inc.				
APPLICANT: Walker, Craig S.				
APPLICANT: Shetty, Reshma				
APPLICANT: Jimenez, Elsie C.				
APPLICANT: McIntosh, J. Michael				
APPLICANT: Olivera, Baldomero M.				
APPLICANT: Watkins, Maren				
APPLICANT: Jones, Robert M.				
APPLICANT: Shen, Greg S.				
TITLE OF INVENTION: I-Superfamily Conotoxins				
FILE REFERENCE: 2314-238				
CURRENT APPLICATION NUMBER: US/09/894,882				
CURRENT FILING DATE: 2001-06-29				
PRIOR APPLICATION NUMBER: US 60/				
PRIOR FILING DATE: 2000-06-30				
PRIOR APPLICATION NUMBER: US 60/243,410				
PRIOR FILING DATE: 2000-10-27				
PRIOR APPLICATION NUMBER: US 60/246,581				
PRIOR FILING DATE: 2000-11-08				
PRIOR APPLICATION NUMBER: US 60/247,714				
PRIOR FILING DATE: 2000-11-14				
PRIOR APPLICATION NUMBER: US 60/264,256				
PRIOR FILING DATE: 2001-01-29				
NUMBER OF SEQ ID NOS: 506				
SOFTWARE: Patent in version 3.0				
SEQ ID NO 4				
LENGTH: 36				
TYPE: PRT				
ORGANISM: Hadronyche versuta				
US-09-894-882-4				
Query Match	43.2%	Score 80	DB 9	Length 36
Best Local Similarity	50.0%	Pred. No. 0.038		
Matches	17	Conservative	1	Mismatches 14; Indels 2; Gaps 1
QY	2	XICTPAGVKCPAALPCCPGLCIGGVNNKV--CR	33	
Db	1	TICTGADRPCCAAACCCPGTSCQGPENGVYCR	34	
RESULT 3				
US-09-894-882-5				
Sequence 5, Application US/09894882				
Patent No. US20020102607A1				
GENERAL INFORMATION:				
APPLICANT: University of Utah Research Foundation				
APPLICANT: Cognetix, Inc.				
APPLICANT: Walker, Craig S.				
APPLICANT: Shetty, Reshma				
APPLICANT: Jimenez, Elsie C.				
APPLICANT: McIntosh, J. Michael				
APPLICANT: Olivera, Baldomero M.				
APPLICANT: Watkins, Maren				
APPLICANT: Jones, Robert M.				
APPLICANT: Shen, Greg S.				
TITLE OF INVENTION: I-Superfamily Conotoxins				
FILE REFERENCE: 2314-238				

GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-140

Query Match 39.5%; Score 73; DB 14; Length 82;
Best Local Similarity 43.3%; Pred. No. 0.5;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
Db 49 CGESGGGCVSRPCCPGLICKGTGGGLCR 78

RESULT 6
US-10-072-602B-570
; Sequence 570, Application US/10072602B
; Publication No. US20030109670A1
GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 570
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-570

Query Match 37.6%; Score 69.5; DB 14; Length 30;
Best Local Similarity 44.8%; Pred. No. 0.5;
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db 49 CGESGGGCVSRPCCPGLICKGTGGGLCR 78

Db 2 CGHSGAGC-YTRPCCPGLHCSGGQAGGLC 29

RESULT 7
US-10-072-602B-137
; Sequence 137, Application US/10072602B
; Publication No. US20030109670A1
GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 137
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-137

Query Match 37.6%; Score 69.5; DB 14; Length 77;
Best Local Similarity 44.8%; Pred. No. 1.2;
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db 49 CGHSGAGC-YTRPCCPGLHCSGGQAGGLC 76

RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. US20020102607A1
GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: 1-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506

Best Local Similarity 50.0%; Pred. No. 1;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRCIG 25
Db 1 CFPLGTFCRSRYLPCCSGMCCSG 22

RESULT 12

US-10-072-602B-581
; Sequence 581, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grille, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 581
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-10-072-602B-581

Query Match 36.2%; Score 67; DB 14; Length 32;
Best Local Similarity 48.4%; Pred. No. 1;
Matches 15; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

Qy 4 CTPAGVKCPAALPCCPGLRCI-GGVNKKVC 33
Db 2 CGGQGGEC-YTPCCPGLRCRGGTGGGVQC 31

RESULT 13

US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match 36.2%; Score 67; DB 9; Length 40;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRCIG 25
Db 1 CFPLGTFCRSRYLPCCSGMCCSG 22

RESULT 14

US-09-894-882-274
; Sequence 274, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 274
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-274

Query Match 36.2%; Score 67; DB 9; Length 68;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRCIG 25
Db 29 CFPLGTFCRSRYLPCCSGMCCSG 50

RESULT 15

US-10-072-602B-255
; Sequence 255, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation


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; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Balomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 255
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Conus virgo
US-10-072-602B-255

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Query Match      36.2%; Score 67; DB 14; Length 79;
Best Local Similarity 48.4%; Pred. No. 2.3;
Matches 15; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

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QY      4 CTPAGVKCPAALPCCPLRCI-GGWNKVC 33
      | | | | | | | | | | | | | | | |
Db      49 CGGQEGC-YTPCCPLRCRGGGTGGVCQ 78

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Search completed: February 14, 2005, 21:08:47
Job time : 129 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	83	44.9		36	4	US-09-894-882-3	Sequence 3, Appli
2	80	43.2		36	4	US-09-894-882-4	Sequence 4, Appli
3	76	41.1		36	1	US-08-682-485A-7	Sequence 7, Appli
4	76	41.1		36	2	US-08-933-314-7	Sequence 7, Appli
5	76	41.1		37	1	US-08-682-485A-6	Sequence 6, Appli
6	76	41.1		37	2	US-08-933-314-6	Sequence 6, Appli
7	73.5	39.7		37	4	US-09-894-882-5	Sequence 5, Appli
8	69	37.3		31	4	US-09-894-882-461	Sequence 461, App
9	69	37.3		39	4	US-09-894-882-497	Sequence 497, App
10	69	37.3		67	4	US-09-894-882-247	Sequence 247, App
11	67	36.2		32	4	US-09-894-882-470	Sequence 470, App
12	67	36.2		40	4	US-09-894-882-498	Sequence 498, App
13	67	36.2		68	4	US-09-894-882-274	Sequence 274, App
14	61	33.0		211	4	US-09-902-540-15694	Sequence 15694, A
15	61	33.0		2471	1	US-08-185-432-16	Sequence 16, Appl
16	61	33.0		2471	1	US-08-083-590A-19	Sequence 19, Appl
17	61	33.0		2471	3	US-08-532-384-19	Sequence 19, Appl
18	61	33.0		2471	3	US-08-899-232-1	Sequence 1, Appli
19	61	33.0		2471	4	US-09-121-457-1	Sequence 1, Appli
20	59	31.9		155	4	US-09-252-991A-28474	Sequence 28474, A
21	59	31.9		259	3	US-09-161-241-11	Sequence 11, Appl
22	58.5	31.6		34	1	US-08-117-080-5	Sequence 5, Appli
23	58.5	31.6		34	1	US-08-471-323-5	Sequence 5, Appli
24	58.5	31.6		34	2	US-08-915-142-5	Sequence 5, Appli
25	58.5	31.6		180	4	US-09-510-238A-286	Sequence 286, App
26	58.5	31.6		908	4	US-08-714-741-44	Sequence 44, Appl
27	57.5	31.1		70	4	US-09-894-882-295	Sequence 295, App

GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 36
TYPE: PRT
ORGANISM: Hadronyche versuta
US-09-894-882-4

Query Match 43.2%; Score 80; DB 4; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.009;
Matches 17; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 2 XICTPAGVKCPAALPCCGRLRCIGGVNKKV--CR 33
Db 1 TICTGADRPCAACCCPCGTSCQGPENGVSYCR 34
RESULT 3
US-08-682-485A-7
Sequence 7, Application US/08682485A
Patent No. 5763568
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996

APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
US-08-682-485A-7

Query Match 41.1%; Score 76; DB 1; Length 36;
Best Local Similarity 45.7%; Pred. No. 0.026;
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

QY 1 XXICTPAGVKCPAALPCCGRLRCIGGVNKKV--CR 33
Db 1 SPTCTGADRPCAACCCPCGTSCQGPENGVSYCR 35

RESULT 4
US-08-933-314-7
Sequence 7, Application US/08933314
Patent No. 5959182
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.

REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
US-08-933-314-7

Query Match 41.1%; Score 76; DB 2; Length 36;
Best Local Similarity 45.7%; Pred. No. 0.026;
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;
Qy 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKV--CR 33
Db 1 SPTCTGADRPCAACCCPCPGTSCCKGPEPNGVSYCR 35

RESULT 5
US-08-682-485A-6
Sequence 6, Application US/08682485A
Patent No. 5763568
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
FEATURE:
NAME/KEY: Modified-site
LOCATION: 37
OTHER INFORMATION: /label= a
OTHER INFORMATION: /note= "this site may be amidated without loss
OTHER INFORMATION: of biological activity"
US-08-682-485A-6

Query Match 41.1%; Score 76; DB 1; Length 37;
Best Local Similarity 45.7%; Pred. No. 0.027;
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;
Qy 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKV--CR 33
Db 1 SPTCTGADRPCAACCCPCPGTSCCKGPEPNGVSYCR 35

RESULT 6
US-08-933-314-6
Sequence 6, Application US/08933314
Patent No. 5959182
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
TOPOLOGY: linear


```

; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Acrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
; OTHER INFORMATION: /note= "this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
US-08-933-314-6

```

```

Query Match 41.1%; Score 76; DB 2; Length 37;
Best Local Similarity 45.7%; Pred. No. 0.027;
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

```

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QY 1 XXICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33
      :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 SPTCTGADRCACACCPCCPGTCKGPGNGVSYCR 35

```

RESULT 7

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US-09-894-882-5
; Sequence 5, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.

```

```

; TITLE OF INVENTION: I-Superfamily Conotoxins

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; FILE REFERENCE: 2314-238

```

```

; CURRENT APPLICATION NUMBER: US/09/894,882

```

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; PRIOR FILING DATE: 2001-06-29

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; PRIOR FILING DATE: 2000-06-30

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; PRIOR FILING DATE: 2000-10-27

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; PRIOR FILING DATE: 2000-11-08

```

```

; PRIOR FILING DATE: 2000-11-14

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```

; PRIOR FILING DATE: 2001-01-29

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```

; NUMBER OF SEQ ID NOS: 506

```

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; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 5

```

```

; LENGTH: 37

```

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; TYPE: PRT

```

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; ORGANISM: Hadronyche versuta

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US-09-894-882-5

```

```

Query Match 39.7%; Score 73.5; DB 4; Length 37;
Best Local Similarity 45.5%; Pred. No. 0.052;
Matches 15; Conservative 1; Mismatches 16; Indels 1; Gaps 1;

```

```

QY 2 XICTPAGVKCPAALPCCPGLRCIGGVNN-KVCR 33
      :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 AICTGADRCACACCPCCPGTCKAESNGVSYCR 33

```

RESULT 8

```

US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:

```

```

; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.

```

```

; TITLE OF INVENTION: I-Superfamily Conotoxins

```

```

; FILE REFERENCE: 2314-238

```

```

; CURRENT APPLICATION NUMBER: US/09/894,882

```

```

; PRIOR FILING DATE: 2001-06-29

```

```

; PRIOR FILING DATE: 2000-06-30

```

```

; PRIOR FILING DATE: 2000-10-27

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```

; PRIOR FILING DATE: 2000-11-08

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; PRIOR FILING DATE: 2000-11-14

```

```

; PRIOR FILING DATE: 2001-01-29

```

```

; NUMBER OF SEQ ID NOS: 506

```

```

; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 461

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```

; LENGTH: 31

```

```

; TYPE: PRT

```

```

; ORGANISM: Conus emaciatus

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US-09-894-882-461

```

```

Query Match 37.3%; Score 69; DB 4; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

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QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
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Db 1 CFPPIGYCTPYLPCCWGICC--GTCRNVC 27

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RESULT 9

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US-09-894-882-497

```

```

; Sequence 497, Application US/09894882

```

```

; Patent No. 6767895

```

```

; GENERAL INFORMATION:

```

```

; APPLICANT: University of Utah Research Foundation

```

```

; APPLICANT: Cognetix, Inc.

```

```

; APPLICANT: Walker, Craig S.

```

```

; APPLICANT: Shetty, Reshma

```

```

; APPLICANT: Jimenez, Elsie C.

```

```

; APPLICANT: McIntosh, J. Michael

```

```

; APPLICANT: Olivera, Baldomero M.

```

```

; APPLICANT: Watkins, Maren

```

```

; APPLICANT: Jones, Robert M.

```

```

; APPLICANT: Shen, Greg S.

```

```

; TITLE OF INVENTION: I-Superfamily Conotoxins

```

```

; FILE REFERENCE: 2314-238

```

```

; CURRENT APPLICATION NUMBER: US/09/894,882

```

```

; PRIOR FILING DATE: 2001-06-29

```

```

; PRIOR FILING DATE: 2000-06-30

```

```

; PRIOR FILING DATE: 2000-10-27

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```

; PRIOR FILING DATE: 2000-11-08

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```

; PRIOR FILING DATE: 2000-11-14

```

```

; PRIOR FILING DATE: 2001-01-29

```

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; NUMBER OF SEQ ID NOS: 506

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; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 497

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; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          37.3%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.18;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db 1 CFPPIGYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 2000-11-08
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 470
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-470

Query Match          36.2%; Score 67; DB 4; Length 32;
Best Local Similarity 50.0%; Pred. No. 0.25;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRCIG 25
Db 1 CFPPLGTCGRYLPCCSGMCCSG 22

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 2000-11-08
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match          36.2%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.31;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```


US-09-902-540-15694

ORGANISM: *Myxococcus xanthus*

Db 667 SCVCSPGFTGQRCNIDIDECASNPCRKGATCINGVNGFRC 70

Search completed: February 14, 2005, 21:06:32
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:40:40 ; Search time 69 Seconds

(without alignments)
184.972 Million cell updates/sec

Title: US-10-019-823B-1

Perfect score: 185

Sequence: 1 XXICTPAGVKCPAALPCCPLRCIGGVNKNVCR 33

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	100.0	33	4 AAB66899	Aab66899 Insectici
2	185	100.0	33	4 AAB66900	Aab66900 Insectici
3	185	100.0	33	6 AAE36283	Aae36283 Paecilomy
4	185	100.0	34	6 AAE36261	Aae36261 Insectici
5	185	100.0	34	6 AAE36295	Aae36295 Insectici
6	185	100.0	34	6 AAE36260	Aae36260 Insectici
7	185	100.0	34	6 AAE36294	Aae36294 Insectici
8	185	100.0	34	6 AAE36259	Aae36259 Insectici
9	185	100.0	34	6 AAE36290	Aae36290 Insectici
10	185	100.0	34	6 AAE36292	Aae36292 Insectici
11	185	100.0	34	6 AAE36287	Aae36287 Insectici
12	185	100.0	34	6 AAE36289	Aae36289 Insectici
13	185	100.0	34	6 AAE36263	Aae36263 Insectici
14	185	100.0	34	6 AAE36284	Aae36284 Insectici
15	185	100.0	34	6 AAE36288	Aae36288 Insectici
16	185	100.0	34	6 AAE36296	Aae36296 Insectici
17	185	100.0	34	6 AAE36286	Aae36286 Insectici
18	185	100.0	34	6 AAE36291	Aae36291 Insectici
19	185	100.0	34	6 AAE36264	Aae36264 Insectici
20	185	100.0	34	6 AAE36285	Aae36285 Insectici
21	185	100.0	34	6 AAE36262	Aae36262 Insectici
22	185	100.0	34	6 AAE36297	Aae36297 Insectici
23	185	100.0	34	6 AAE36298	Aae36298 Insectici
24	185	100.0	34	6 AAE36293	Aae36293 Insectici
25	185	100.0	35	4 AAB66901	Aab66901 Insectici

Search of Seq 1 was run using "BLOSUM62DX" matrix - this allows an X in the query sequence to match any amino acid in the database sequence.

ALIGNMENTS

RESULT 1

AAB66899 ID AAB66899 standard; peptide; 33 AA.

XX AAB66899;

AC AAB66899;

XX 12-APR-2001 (first entry)

DT Insecticidal protein #1.

DE Insecticidal protein #1.

XX Insecticide; transgenic plant; insect-resistance.

KW Paecilomyces sp.

OS WO200100841-A1.

XX 04-JAN-2001.

PF 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE) ZENECA LTD.

PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

XX production.

XX Claim 1; Page 30; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained

CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The

CC insecticidal proteins can be used to produce transgenic plants, which are

CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed

XX Sequence 33 AA;

SQ Query Match 100.0%; Score 185; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 9.2e-14;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

26	185	100.0	35	6 AAE36281	Aae36281 Insectici
27	185	100.0	35	6 AAE36265	Aae36265 Insectici
28	185	100.0	35	6 AAE36282	Aae36282 Insectici
29	83	44.9	36	5 ABB88548	Abb88548 Janus fac
30	80	43.2	36	5 ABB88549	Abb88549 Janus fac
31	76	41.1	36	2 AAR39319	Aar39319 Fla toxin
32	76	41.1	37	2 AAR39318	Aar39318 Fla toxin
33	73.5	39.7	37	5 ABB88550	Abb88550 Janus fac
34	73.5	39.7	37	7 ADL11907	Adl11907 Atracotox
35	73	39.5	35	5 ABG99786	Abg99786 Conus sp
36	73	39.5	82	5 ABG99454	Abg99454 Conus sp
37	72	38.9	33	7 ADL11905	Adl11905 Raventoxi
38	69.5	37.6	30	5 ABG99785	Abg99785 Conus sp
39	69.5	37.6	77	5 ABG99452	Abg99452 Conus sp
40	69	37.3	31	5 ABB88889	Abb88889 Conus ema
41	69	37.3	39	5 ABB88925	Abb88925 Conus ema
42	69	37.3	67	5 ABB88713	Abb88713 Conus ema
43	67	36.2	32	5 ABB88898	Abb88898 Conus vir
44	67	36.2	32	5 ABG99796	Abg99796 Conus sp
45	67	36.2	40	5 ABB88926	Abb88926 Conus vir

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33

RESULT 2
ID AAB66900 standard; peptide; 33 AA.
AC AAB66900;

DT 12-APR-2001 (first entry)
XX Insecticidal protein #2.
DE Insecticide; transgenic plant; insect-resistance.
XX Paecilomyces sp.

OS WO200100841-A1.
PN 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
PF 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.

PS Claim 3; Page 30; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed

SQ Sequence 33 AA;

Query Match 100.0%; Score 185; DB 4; Length 33;
Best Local Similarity 93.9%; Pred. No. 9.2e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33

RESULT 3
ID AAE36283 standard; peptide; 33 AA.
AC AAE36283;

DT 26-JUN-2003 (first entry)

XX Paecilomyces farinosus insecticidal protein.
DE Insecticidal protein; pesticide.
XX Paecilomyces farinosus.

OS WO200298911-A2.
PN

XX 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN) SYNGENTA LTD.

XX Vincent JL, Viner R;

PI WPI; 2003-175137/17.

DR New insecticidal protein comprising an X-glycine motif at the amino-
XX terminus, useful as an active ingredient of a pesticide.

PS Example 2; Page 62; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC Paecilomyces farinosus insecticidal protein

XX Sequence 33 AA;

Query Match 100.0%; Score 185; DB 6; Length 33;
Best Local Similarity 93.9%; Pred. No. 9.2e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33

RESULT 4

ID AAE36261 standard; peptide; 34 AA.

XX AAE36261;

XX 26-JUN-2003 (first entry)

DE Insecticidal protein #3.

XX Insecticidal protein; pesticide.

OS Unidentified.

XX WO200298911-A2.

PN 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN) SYNGENTA LTD.

XX Vincent JL, Viner R;

PI WPI; 2003-175137/17.

DR New insecticidal protein comprising an X-glycine motif at the amino-
XX terminus, useful as an active ingredient of a pesticide.
XX Claim 6; Page 23; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the


```
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
XX
SQ Sequence 34 AA;

Query Match      100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 5
AAE36295
ID AAE36295 standard; peptide; 34 AA.
AC
AC AAE36295;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #25.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
DR New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 66; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
XX
SQ Sequence 34 AA;

Query Match      100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 6
AAE36260
ID AAE36260 standard; peptide; 34 AA.
AC
AC AAE36260;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #2.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
DR New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 5; Page 23; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
XX
SQ Sequence 34 AA;

Query Match      100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 7
AAE36294
ID AAE36294 standard; peptide; 34 AA.
AC
AC AAE36294;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #24.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
```



```
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
XX
PS Example 1; Page 66; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db ::::::::::::::::::::::::::::::::::
2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 9
AAE36290
ID AAE36290 standard; peptide; 34 AA.
XX
AC AAE36290;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #20.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 64; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db ::::::::::::::::::::::::::::::::::
2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 8
AAE36259
ID AAE36259 standard; peptide; 34 AA.
XX
AC AAE36259;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #1.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Xaa = any amino acid"
FT
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 1; Page 23; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
CC
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```
CC Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db ::::::::::::::::::::::::::::::::::
2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 9
AAE36290
ID AAE36290 standard; peptide; 34 AA.
XX
AC AAE36290;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #20.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 64; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db ::::::::::::::::::::::::::::::::::
2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 10
AAE36292
ID AAE36292 standard; peptide; 34 AA.
XX
AC AAE36292;
```



```
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
   :|||||
Db 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 34

RESULT 13
AAE36263
ID AAE36263 standard; peptide; 34 AA.
XX
AC AAE36263;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #5.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 62; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
   :|||||
Db 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 34

RESULT 15
AAE36288
ID AAE36288 standard; peptide; 34 AA.
XX
AC AAE36288;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #18.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 64; 67pp; English.
```


XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXICTPAGVKCPAALPCCPGLCIGGVNNKVC 33
Db :::::::::::::::::::::::::::::::::::::
2 GKICTPAGVKCPAALPCCPGLCIGGVNNKVC 34

Search completed: February 14, 2005, 21:01:56
Job time : 70 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 1.06257 Seconds
(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNKNKVC 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	42.3	36	4	US-09-894-882-3
2	79	40.7	36	4	US-09-894-882-4
3	75	38.7	36	1	US-08-682-485A-7
4	75	38.7	36	2	US-08-933-314-7
5	75	38.7	37	1	US-08-682-485A-6
6	75	38.7	37	2	US-08-933-314-6
7	72.5	37.4	37	4	US-09-894-882-5
8	69	35.6	31	4	US-09-894-882-461
9	69	35.6	39	4	US-09-894-882-497
10	69	35.6	67	4	US-09-894-882-247
11	67	34.5	32	4	US-09-894-882-470
12	67	34.5	40	4	US-09-894-882-498
13	67	34.5	68	4	US-09-894-882-274
14	59	30.4	155	4	US-09-252-991A-28474
15	59	30.4	211	4	US-09-902-540-15694
16	59	30.4	2471	1	US-08-185-432-16
17	59	30.4	2471	1	US-08-083-590A-19
18	59	30.4	2471	3	US-08-532-384-19
19	59	30.4	2471	4	US-08-899-232-1
20	59	30.4	2471	4	US-09-121-457-1
21	58.5	30.2	34	1	US-08-117-080-5
22	58.5	30.2	34	1	US-08-471-329-5
23	58.5	30.2	34	2	US-08-915-142-5
24	58.5	30.2	908	4	US-08-714-741-44
25	58	29.9	39	4	US-09-894-882-248
26	57.5	29.6	180	4	US-09-510-238A-286
27	57.5	29.6	281	4	US-09-252-991A-23962

28	57.5	29.6	420	4	US-09-907-794A-109	Sequence 109, App
29	57.5	29.6	420	4	US-09-905-125A-109	Sequence 109, App
30	57.5	29.6	420	4	US-09-902-775A-109	Sequence 109, App
31	57.5	29.6	420	4	US-09-906-700-109	Sequence 109, App
32	57.5	29.6	420	4	US-09-903-603A-109	Sequence 109, App
33	57.5	29.6	420	4	US-09-904-920A-109	Sequence 109, App
34	57.5	29.6	420	4	US-09-909-064-109	Sequence 109, App
35	57.5	29.6	420	4	US-09-905-381A-109	Sequence 109, App
36	57.5	29.6	420	4	US-09-906-618-109	Sequence 109, App
37	57	29.4	259	3	US-09-161-241-11	Sequence 11, Appl
38	57	29.4	493	4	US-09-252-991A-16925	Sequence 16925, A
39	56.5	29.1	30	4	US-09-894-882-474	Sequence 474, App
40	56.5	29.1	44	4	US-09-894-882-296	Sequence 296, App
41	56.5	29.1	44	4	US-09-894-882-502	Sequence 502, App
42	56.5	29.1	70	4	US-09-894-882-295	Sequence 295, App
43	56	28.9	642	3	US-08-872-855-10	Sequence 10, Appl
44	56	28.9	2732	4	US-09-086-436-30	Sequence 30, Appl
45	55.5	28.6	161	4	US-10-293-622-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-894-882-3
; Sequence 3, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
; US-09-894-882-3

Query Match 42.3%; Score 82; DB 4; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.0044;
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVNKNV--CR 33
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Db 2 ICTGADRPCAACCCPGTSCQGPESNGVYCR 34

RESULT 2
US-09-894-882-4
; Sequence 4, Application US/09894882
; Patent No. 6767895


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; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
; US-09-894-882-4

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Query Match 40.7%; Score 79; DB 4; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.0098;
Matches 17; Conservative 0; Mismatches 14; Indels

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D6	3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

RESULT 3
US-08-682-485A-7
; Sequence 7, Application US/08682485A
; Patent No. 5763568
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Attrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996

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/ APPLICATION NUMBER: US/08/256,933
/ FILING DATE: 27-JULY-1994
/ APPLICATION NUMBER: WO 93/15108
/ FILING DATE: 29-JAN-1993
/ APPLICATION NUMBER: AU PL0722
/ FILING DATE: 31-JAN-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Shaw, Melissa A.
/ REGISTRATION NUMBER: 38,301
/ REFERENCE/DOCKET NUMBER: PPD 5099/D1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 510-231-1542
/ TELEFAX: 510-231-1112
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEetical: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Atrax formidabilis
/
/ US-08-682-485A-7
/
Query Match 38.7%; Score 75; DB 1; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 14; Indels
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QY 4 CTGAGVKCPAALPCCPGRLRCIGGVNNKV-CR 33
/ / / / / / / / / / / / / / / /
Db 4 CTGADRPCAACCCPGTCKGPEPNGVSYCR 35
/ / / / / / / / / / / / / / / /
RESULT 4
US-08-933-314-7
/ Sequence 7, Application US/08933314
/ Patent No. 5959182
/ GENERAL INFORMATION:
/ APPLICANT: ATKINSON, RONALD K
/ APPLICANT: HOWDEN, MERLIN E.H.
/ APPLICANT: TYLER, MARGARET I
/ APPLICANT: VONARX, EDWARD J
/ TITLE OF INVENTION: Insecticidal Toxins Derived From
/ TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Zeneca, Inc.
/ STREET: 1200 South 47th Street
/ CITY: Richmond
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,314
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/682,485
/ FILING DATE: 17-JULY-1996
/ APPLICATION NUMBER: US/08/256,933
/ FILING DATE: 27-JULY-1994
/ APPLICATION NUMBER: WO 93/15108
/ FILING DATE: 29-JAN-1993
/ APPLICATION NUMBER: AU PL0722
/ FILING DATE: 31-JAN-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Shaw, Melissa A.
/

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RESULT 4
US-08-933-314-7
; Sequence 7, Application US/08933314
; Patent No. 5959182
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,314
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PL0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.

REGISTRATION NUMBER: 36,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
TOPOLOGY: linear


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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label=a
; OTHER INFORMATION: /notes="this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
; US-08-933-314-6

Query Match      38.7%; Score 75; DB 2; Length 37;
Best Local Similarity 50.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

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Db      4 CTGADRPCAACCCPCPGTSGCKGPEPNGVSYCR 35

RESULT 7
US-09-894-882-5
; Sequence 5, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Hadronyche versuta
; US-09-894-882-5

Query Match      37.4%; Score 72.5; DB 4; Length 37;
Best Local Similarity 46.9%; Pred. No. 0.057;
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
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; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
; US-09-894-882-461

Query Match      35.6%; Score 69; DB 4; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.12;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

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RESULT 9
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; Sequence 497, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
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RESULT 14
US-09-991A-28474
; Sequence 28474, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28474
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28474

Search completed: March 9, 2005, 17:27:35
Job time : 2.06257 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 3.24047 Seconds
(without alignments)
3350.901 Million cell updates/sec

Title: US-10-019-823B-2
Perfect score: 194
Sequence: 1 GKICTPAGVKCPAALPCCPLRCIGGVNKNVCR 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	42.3	36	9 US-09-894-882-3	Sequence 3, Appli
2	79	40.7	36	9 US-09-894-882-4	Sequence 4, Appli
3	73	37.6	35	14 US-10-072-602B-571	Sequence 571, App
4	73	37.6	82	14 US-10-072-602B-140	Sequence 140, App
5	72.5	37.4	37	9 US-09-894-882-5	Sequence 5, Appli
6	69.5	35.8	30	14 US-10-072-602B-570	Sequence 570, App
7	69.5	35.8	77	14 US-10-072-602B-137	Sequence 137, App
8	69	35.6	31	9 US-09-894-882-461	Sequence 461, App
9	69	35.6	39	9 US-09-894-882-497	Sequence 497, App
10	69	35.6	67	9 US-09-894-882-247	Sequence 247, App
11	68	35.1	3501	14 US-10-123-155-37	Sequence 37, Appl
12	68	35.1	3501	14 US-10-146-731-37	Sequence 37, Appl
13	68	35.1	3501	14 US-10-140-472-37	Sequence 37, Appl

14	68	35.1	3501	14	US-10-141-761-37	Sequence 37, Appl
15	68	35.1	3501	14	US-10-142-885-37	Sequence 37, Appl
16	68	35.1	3501	14	US-10-158-790-37	Sequence 37, Appl
17	68	35.1	3501	15	US-10-137-871-37	Sequence 37, Appl
18	68	35.1	3501	15	US-10-140-923-37	Sequence 37, Appl
19	68	35.1	3501	15	US-10-141-756-37	Sequence 37, Appl
20	68	35.1	3501	15	US-10-141-759-37	Sequence 37, Appl
21	68	35.1	3501	15	US-10-140-805-37	Sequence 37, Appl
22	68	35.1	3501	15	US-10-140-864-37	Sequence 37, Appl
23	68	35.1	3501	15	US-10-142-426-37	Sequence 37, Appl
24	67	34.5	32	9	US-09-894-882-470	Sequence 470, App
25	67	34.5	32	14	US-10-072-602B-581	Sequence 581, App
26	67	34.5	40	9	US-09-894-882-498	Sequence 498, App
27	67	34.5	68	9	US-09-894-882-274	Sequence 274, App
28	67	34.5	79	14	US-10-072-602B-255	Sequence 255, App
29	65	33.5	77	14	US-10-072-602B-191	Sequence 191, App
30	65	33.5	2292	14	US-10-184-644-493	Sequence 493, App
31	65	33.5	2292	14	US-10-184-634-493	Sequence 493, App
32	64.5	33.2	86	15	US-10-424-539-240605	Sequence 240605,
33	64	33.0	30	14	US-10-072-602B-576	Sequence 576, App
34	64	33.0	566	10	US-09-900-449A-6	Sequence 6, Appli
35	64	33.0	572	10	US-09-900-449A-7	Sequence 7, Appli
36	64	33.0	601	10	US-09-900-449A-5	Sequence 5, Appli
37	64	33.0	639	10	US-09-900-449A-4	Sequence 4, Appli
38	64	33.0	1064	14	US-10-173-461-5	Sequence 5, Appli
39	63	32.5	1971	14	US-10-123-155-139	Sequence 139, App
40	63	32.5	1971	14	US-10-146-731-139	Sequence 139, App
41	63	32.5	1971	14	US-10-140-472-139	Sequence 139, App
42	63	32.5	1971	14	US-10-141-761-139	Sequence 139, App
43	63	32.5	1971	14	US-10-142-885-139	Sequence 139, App
44	63	32.5	1971	14	US-10-158-790-139	Sequence 139, App
45	63	32.5	1971	15	US-10-137-871-139	Sequence 139, App

ALIGNMENTS

RESULT 1
US-09-894-882-3
; Sequence 3, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-3


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Query Match      42.3%; Score 82; DB 9; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.022;
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

QY      3 ICTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
      ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2 ICTGADRPAAACCCPGTSCQGPESNGVVYCR 34

RESULT 2
US-09-894-882-4
; Sequence 4, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-4

Query Match      40.7%; Score 79; DB 9; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.049;
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY      3 ICTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
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DB      2 ICTGADRPAAACCCPGTSCQGPENGVSYCR 34

RESULT 3
US-10-072-602B-571
; Sequence 571, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.

```


RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506


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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match      35.6%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.58;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      35.6%; Score 69; DB 9; Length 67;
Best Local Similarity 44.8%; Pred. No. 1.2;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 2;

Qy      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 11
US-10-123-155-37
; Sequence 37, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-123-155-37

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Best Local Similarity 46.2%; Pred. No. 51;
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGG 26
Db 888 GACCAAGTACCAAGCCTGTGCTGG 913

RESULT 15
US-10-142-885-37
; Sequence 37, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-142-885-37

Query Match 35.1%; Score 68; DB 14; Length 3501;
Best Local Similarity 46.2%; Pred. No. 51;
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGG 26
Db 888 GACCAAGTACCAAGCCTGTGCTGG 913

Search completed: March 9, 2005, 18:08:03
Job time : 4.24047 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 0.761133 Seconds
(without alignments)
4171.616 Million cell updates/sec

Title: US-10-019-823B-2
Perfect score: 194
Sequence: 1 GKICTPAGVKCPAALPCCPLRCIGGVNKKVCR 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	33.0	1064	2 A40136	fibropellin Ia - s
2	60	30.9	422	2 S48564	probable membrane
3	60	30.9	570	2 A48836	fibropellin C prec
4	58.5	30.2	34	2 A31043	mu-conotoxin GS -
5	58	29.9	37	2 E44007	apoptoxin III - tr
6	57.5	29.6	417	2 T08724	hypothetical prote
7	57	29.4	1221	2 T23472	hypothetical prote
8	56.5	29.1	585	2 S43572	C05B5.5 protein (c
9	56.5	29.1	585	2 E88571	protein C05B5.5 [i
10	56.5	29.1	1390	2 T30346	insulin receptor -
11	56	28.9	197	2 T10081	sperm mitochondria
12	56	28.9	238	2 T04166	thauartin-like pro
13	56	28.9	2352	2 T30201	Notch homolog prot
14	56	28.9	2531	2 S18188	notch protein homo
15	56	28.9	2531	2 A46019	notch-1 protein -
16	55	28.4	132	2 H75335	hypothetical prote
17	54.5	28.1	218	2 T03287	osmotin protein ho
18	54.5	28.1	601	2 T22025	hypothetical prote
19	54.5	28.1	601	2 D89711	protein F40E10.4 [
20	54.5	28.1	768	2 A87722	protein ZC123.1 [i
21	54.5	28.1	1207	1 EGHU	epidermal growth f
22	54.5	28.1	4543	1 A53102	alpha-2-macroglobu
23	54	27.8	73	2 H43019	platelet aggregati
24	54	27.8	74	2 S25773	testis-specific pr
25	54	27.8	269	2 T26957	hypothetical prote
26	54	27.8	283	2 E88597	protein Y47D3B.6 [
27	54	27.8	2318	2 S45306	notch 3 protein -
28	54	27.8	2321	2 S78549	notch3 protein - h
29	53	27.3	375	2 A41428	CEF-10 protein pre

30 53 27.3 456 1 KXBO
31 53 27.3 686 2 JC7569
32 53 27.3 2139 2 A35672
33 53 27.3 2524 2 A35844
34 52.5 27.1 596 2 T26950
35 52.5 27.1 4544 1 S02392
36 52.5 27.1 4545 1 S25111
37 52 26.8 64 2 A25775
38 52 26.8 71 2 G43019
39 52 26.8 134 2 AD0652
40 52 26.8 1203 2 A49175
41 52 26.8 1449 2 S47423
42 52 26.8 2437 2 S42612
43 51.5 26.5 233 2 S31829
44 51.5 26.5 238 2 S28001
45 51.5 26.5 246 2 S30144

ALIGNMENTS

RESULT 1

A40136
Fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
N;Alternate names: epidermal growth factor homolog precursor
N;Contains: alternatively spliced fibropellin Ib (EGFI)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: A40136; B40136; C40136; A29316; A43131
R;Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpuratus
A;Reference number: A40136; MUID:90112459; PMID:2514273
A;Accession: A40136
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-114
A;Cross-references: UNIPROT:P10079; GB:X17530; NID:gl0225; PID:g667061
A;Accession: B40136
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
A;Accession: C40136
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 'K',747-821,898-978 <DE3>
R;Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A;Reference number: A29316; MUID:87319677; PMID:3498216
A;Accession: A29316
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'S',280-481,786-1064 <HUR>
A;Cross-references: GB:M17421; NID:gl161474; PIDN:AAA30050.1; PID:g552260
R;Hunt, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A;Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
A;Reference number: A43131; MUID:89196806; PMID:2784773
A;Contents: annotation
C;Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1064/Product: fibropellin I #status predicted <FIB>
F;23-54/Domain: EGF homology <EG01>
F;57-175/Domain: C1r/C1s repeat homology <C1r>
F;180-211/Domain: EGF homology <EG02>
F;218-249/Domain: EGF homology <EG03>
F;256-287/Domain: EGF homology <EG04>
F;294-325/Domain: EGF homology <EG05>
F;332-363/Domain: EGF homology <EG06>
F;370-401/Domain: EGF homology <EG07>
F;408-439/Domain: EGF homology <EG08>
F;446-477/Domain: EGF homology <EG09>

Query Match 29.9%; Score 58; DB 2; Length 37;
Best Local Similarity 37.1%; Pred. No. 2.3;
Matches 13; Conservative 1; Mismatches 15; Indels 6; Gaps 1;

QY 4 CTPAGVKCPAALPCCPG-----LRGIGGVNNKVC 32
Db 1 CNSKGTPTCTNADECCGKCAYNVWNCIGGGCKTC 35

RESULT 6
T08724
hypothetical protein DKFp566D213.1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08724
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16468
A:Accession: T08724
A:Molecule type: mRNA
A:Residues: 1-417 <KOE>
A:Cross-references: UNIPROT:Q9Y409; EMBL:AL050275
A:Experimental source: fetal kidney; clone DKFp566D213
C:Genetics:
A>Note: DKFp566D213.1

Query Match 29.6%; Score 57.5; DB 2; Length 417;
Best Local Similarity 31.1%; Pred. No. 18;
Matches 14; Conservative 4; Mismatches 14; Indels 13; Gaps 1;

QY 2 KJCTPAGVKCPAALPC-----CPGLRCIGGVNNKVC 33
Db 140 KLCCPAGTFGPSCLPCGGTERPCGGYGQCEGEGTRGGSHGDCQ 184

RESULT 7
T23472
hypothetical protein K08E7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23472
R:Smye, R.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19745
A:Accession: T23472
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1221 <WIL>
A:Cross-references: UNIPROT:Q21344; EMBL:Z77666; PIDN:CAB01228.1; GSPDB:GN00022; CESP:K0
A:Experimental source: clone K08E7
C:Genetics:
A:Gene: CESP:K08E7.5
A:Map position: 4
A:Introns: 26/1; 103/1; 170/1; 640/1; 802/2; 831/1; 864/3; 891/3; 908/1; 938/2; 980/1; 1

Query Match 29.4%; Score 57; DB 2; Length 1221;
Best Local Similarity 34.5%; Pred. No. 49;
Matches 10; Conservative 3; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db 971 CAPPAPCCLPTIPCCPIPCC--POPKIC 997

RESULT 8
S43572
C05B5.5 protein (clone C05B5) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S43572
R:Mortimore, B.
submitted to the EMBL Data Library, April 1994

A:Reference number: S43570
A:Accession: S43572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <MOR>
A:Cross-references: EMBL:Z32679
C:Genetics:
A:Introns: 35/2; 218/3; 292/2; 328/1; 442/2

Query Match 29.1%; Score 56.5; DB 2; Length 585;
Best Local Similarity 30.4%; Pred. No. 31;
Matches 14; Conservative 2; Mismatches 11; Indels 19; Gaps 2;

QY 1 GKICT-----PAGVKC-----PAALPCCPGRLRCIGGV 27
Db 531 GGYCSTSTQCPTGYQCIDGKCKTKRHLAPPVCAECPPGTRCINGV 576

RESULT 9
E88571
protein C05B5.5 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E88571
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: E88571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <STO>
A:Cross-references: UNIPROT:P34293; GB:chr_III; PIDN:CAAB3593.1; PID:G3873993; GSPDB:GN0
C:Genetics:
A:Gene: C05B5.5
A:Map position: 3

Query Match 29.1%; Score 56.5; DB 2; Length 585;
Best Local Similarity 30.4%; Pred. No. 31;
Matches 14; Conservative 2; Mismatches 11; Indels 19; Gaps 2;

QY 1 GKICT-----PAGVKC-----PAALPCCPGRLRCIGGV 27
Db 531 GGYCSTSTQCPTGYQCIDGKCKTKRHLAPPVCAECPPGTRCINGV 576

RESULT 10
T30346
insulin receptor - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30346
R:Graf, R.; Neuenschwander, S.; Brown, M.R.; Ackermann, U.
Insect Mol. Biol. 6, 151-163, 1996
A:Title: Insulin mediated secretion of ecdysteroids from mosquito ovaries and molecular
A:Reference number: Z20834
A:Accession: T30346
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-1390 <GRA>
A:Cross-references: UNIPROT:Q93105; EMBL:U72939; NID:g1620749; PID:g1620750; PIDN:AAB170;
C:Superfamily: insulin receptor; protein kinase homology

Query Match 29.1%; Score 56.5; DB 2; Length 1390;
Best Local Similarity 36.6%; Pred. No. 62;
Matches 15; Conservative 2; Mismatches 11; Indels 13; Gaps 3;

QY 3 ICTPAGVKCPAALP-----CCPGLRCIGGVN-----NKVCR 33
Db 228 ICPP-----ECPKACSKTGVCCDAESCLGGCNLPNTSSCSVCR 265

RESULT 11
T10081
sperm mitochondrial capsule selenoprotein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C;Accession: T10081; A37199
R;Kleene, K.C.; Smith, J.; Bozorgzadeh, A.; Harris, M.; Hahn, L.; Karimpour, I.; Gerstel
Dev. Biol. 137, 395-402, 1990
A;Title: Sequence and developmental expression of the mRNA encoding the seleno-protein c
A;Reference number: A37199; MUID:90152148; PMID:2303168
A;Accession: T10081
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-6, 'X', 8-16, 'X', 18-33, 'X', 35-197 <KLE1>
A;Cross-references: UNIPROT:P15265; EMBL:M29603; NID:g199089; PIDN:AAA53045.1; PID:g5672
A;Experimental source: strain CD-1
A;Note: in Genbank entry MUSMCS, release 113.0, PIDN:AAA53045.1, the selenocysteine UGA
A;Accession: A37199
A;Molecule type: mRNA
A;Residues: 55-197 <KLE2>
A;Cross-references: GB:M29603; NID:g199088
A;Note: the authors translated the codon TGT for residue 112 as Pro
C;Genetics:
A;Genome: MCS
A;Keywords: mitochondrion; selenocysteine; sperm
F;7,17,34/Modified site: selenocysteine #status predicted
Query Match 28.9%; Score 56; DB 2; Length 197;
Best Local Similarity 45.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 4 CTPAGVKCPAALPCCPGLRC 23
Db 87 CCKPSPPKPPKPPKPPK 106
RESULT 12
T04166
thaumatin-like protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04166
R;Cole, K.C.; Velazhahan, R.; Anuratha, C.S.; Muthukrishnan, S.
submitted to the EMBL Data Library, November 1996
A;Description: Induction of thaumatin-like proteins (TLPs) in Rhizoctonia solani- infect
A;Reference number: Z15250
A;Accession: T04166
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-238 <COL>
A;Cross-references: UNIPROT:O04364; EMBL:U77657; NID:g2062388; PIDN:AAB53368.1; PID:g206
C;Superfamily: thaumatin I
Query Match 28.9%; Score 56; DB 2; Length 238;
Best Local Similarity 45.2%; Pred. No. 17;
Matches 14; Conservative 2; Mismatches 13; Indels 2; Gaps 2;
Qy 1 GKICTPAGVKCPAAL-PCCPG-LRCIGGVNN 29
Db 146 GAGCPKGGPRCATATPQCPSELAPGGCNN 176
RESULT 13
T30201
Notch homolog protein - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2002
C;Accession: T30201
R;Hori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cen

A;Reference number: Z20775
A;Accession: T30201
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2352 <HOR>
A;Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1
C;Genetics:
A;Gene: Notch
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
Query Match 28.9%; Score 56; DB 2; Length 2352;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;
Qy 4 CTP--AGVKCPAAL-----PCCPGLRCIGGVNNKVC 33
Db 593 CTPGYTGEHCTDINECDSPNCPMGATCQNEVNVFCQ 630
RESULT 14
S18188
notch protein homolog - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S18188
R;Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A;Title: A homolog of Drosophila Notch expressed during mammalian development.
A;Reference number: S18188; MUID:92111383; PMID:1764995
A;Accession: S18188
A;Molecule type: mRNA
A;Residues: 1-2531 <WEI>
A;Cross-references: EMBL:X57405; NID:g57634; PID:g57635
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;987-1018/Domain: EGF homology <EGF1>
F;1025-1056/Domain: EGF homology <EGF>
F;1233-1264/Domain: EGF homology <EGF2>
F;1917-1949/Domain: ankyrin repeat homology <AN1>
F;1950-1982/Domain: ankyrin repeat homology <AN2>
F;1984-2016/Domain: ankyrin repeat homology <AN3>
F;2017-2049/Domain: ankyrin repeat homology <AN4>
F;2050-2082/Domain: ankyrin repeat homology <AN5>
Query Match 28.9%; Score 56; DB 2; Length 2531;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;
Qy 4 CTP--AGVKCPAALPCCPGLR-----CIGGVNNKVC 33
Db 245 CLPGFAGQNCENVDPCGNNCKNGGACVDGVTYNCR 282
RESULT 15
A46019
notch-1 protein - mouse
N;Alternate names: notch protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gridl
Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
A;Reference number: A46019; MUID:93194170; PMID:8449489
A;Accession: A46019
A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2531
A;Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1; I
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; N
submitted to the EMBL Data Library, April 1992
A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggeste
A;Reference number: S25144

A:Accession: S25144
 A:Molecule type: mRNA
 A:Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <FRA>
 A:Cross-references: EMBL:Z11886
 R:Lardelli, M.; Lendahl, U.
 Exp. Cell Res. 204, 364-372, 1993
 A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of
 A:Reference number: A49175; MUID:93178563; PMID:8440332
 A:Accession: C49175
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1161-1547 <LAR>
 A:Cross-references: EMBL:X68278; NID:G287987; PIDN:CAA48339.1; PID:G287988
 A:Experimental source: embryo
 A:Note: sequence extracted from NCBI backbone (NCBIP:126159)
 R:Kopan, R.; Weintraub, H.
 J. Cell Biol. 121, 631-641, 1993
 A:Title: Mouse notch: expression in hair follicles correlates with cell fate determination
 A:Reference number: A46438; MUID:93252998; PMID:8486742
 A:Accession: B46438
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054
 A:Experimental source: embryo
 A:Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
 C:Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
 C:Comment: This protein is one of the neurogenic proteins controlling the decision between
 C:Genetics:
 A:Gene: notch-1
 A:Map position: 2
 A:Note: proximal region of chromosome 2
 C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
 F:106-138/Domain: EGF homology <EGF1>
 F:144-175/Domain: EGF homology <EGF1>
 F:222-254/Domain: EGF homology <EGF2>
 F:261-292/Domain: EGF homology <EGF2>
 F:339-370/Domain: EGF homology <EGF3>
 F:416-449/Domain: EGF homology <EGF3>
 F:456-487/Domain: EGF homology <EGF4>
 F:494-525/Domain: EGF homology <EGF5>
 F:532-563/Domain: EGF homology <EGF6>
 F:607-638/Domain: EGF homology <EGF7>
 F:682-713/Domain: EGF homology <EGF8>
 F:757-788/Domain: EGF homology <EGF9>
 F:795-826/Domain: EGF homology <EGF10>
 F:873-904/Domain: EGF homology <EGF11>
 F:911-942/Domain: EGF homology <EGF12>
 F:949-980/Domain: EGF homology <EGF13>
 F:987-1018/Domain: EGF homology <EGF14>
 F:1025-1056/Domain: EGF homology <EGF15>
 F:1063-1094/Domain: EGF homology <EGF16>
 F:1149-1180/Domain: EGF homology <EGF17>
 F:1187-1218/Domain: EGF homology <EGF18>
 F:1233-1264/Domain: EGF homology <EGF19>
 F:1352-1383/Domain: EGF homology <EGF19>
 F:1391-1425/Domain: EGF homology <EGF>
 F:1917-1948/Domain: ankyrin repeat homology <AN1>
 F:1949-1981/Domain: ankyrin repeat homology <AN2>
 F:1983-2015/Domain: ankyrin repeat homology <AN3>
 F:2016-2048/Domain: ankyrin repeat homology <AN4>
 F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 28.9%; Score 56; DB 2; Length 2531;
 Best Local Similarity 36.8%; Pred. No. 1.1e+02;
 Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;
 QY 4 CTP--AGVKCPAALPCFGLR-----CIGGVNKKVCR 33
 Db 245 CLPGFAGQNCENVDPCGNNCKNGGACVDGVNTYNCR 282

Search completed: February 14, 2005, 21:00:42
 Job time : 0.761133 secs

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OX NCBI_TaxID=6904;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;
RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
RA Nicholson G.M., Christie M.J., King G.F.;
RA "Discovery and characterization of a family of insecticidal
RT neurotoxins with a rare vicinal disulfide bridge";
RL Nat. Struct. Biol. 7:505-513 (2000).
CC - FUNCTION: Insecticidal neurotoxin.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Expressed by the venom gland.
DR HSSP; P82228; IDL0.
KW Direct protein sequencing; Neurotoxin; Toxin.
FT DISULFID 3 17 By similarity.
FT DISULFID 10 22 By similarity.
FT DISULFID 13 14 By similarity.
FT DISULFID 16 33 By similarity.
SQ SEQUENCE 36 AA; 3651 MW; D23A442560B89997 CRC64;
Query Match 40.7%; Score 79; DB 1; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.018;
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33
DB 2 ICTGADRPCAACCCPCPGTSCQPEPVGYSYCR 34
RESULT 3
Q9TVN1 ID Q9TVN1 PRELIMINARY; PRT; 72 AA.
AC Q9TVN1
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Four-loop conotoxin LVVIA (Four-loop conotoxin LVVIB
DE (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RT rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).
DR EMBL; AF089958; AAD4813.1; -
DR EMBL; AF089902; AAD48158.1; -
DR EMBL; AF089906; AAD48162.1; -
DR EMBL; AF089907; AAD48163.1; -
DR EMBL; AF089910; AAD48165.1; -
DR EMBL; AF089913; AAD48168.1; -
DR EMBL; AF089914; AAD48169.1; -
DR EMBL; AF089915; AAD48170.1; -
DR EMBL; AF089916; AAD48171.1; -
DR EMBL; AF089917; AAD48172.1; -
DR EMBL; AF089918; AAD48173.1; -
DR EMBL; AF089919; AAD48174.1; -
DR EMBL; AF089920; AAD48175.1; -
DR EMBL; AF089921; AAD48176.1; -
DR EMBL; AF089922; AAD48177.1; -
DR EMBL; AF089923; AAD48178.1; -
DR EMBL; AF089924; AAD48179.1; -
DR EMBL; AF089925; AAD48180.1; -
DR EMBL; AF089926; AAD48181.1; -
DR EMBL; AF089927; AAD48182.1; -
DR EMBL; AF089928; AAD48183.1; -
DR EMBL; AF089929; AAD48184.1; -

DR EMBL; AF089930; AAD48185.1; -
DR EMBL; AF089931; AAD48186.1; -
DR EMBL; AF089932; AAD48187.1; -
DR EMBL; AF089933; AAD48188.1; -
DR EMBL; AF089941; AAD48196.1; -
DR EMBL; AF089942; AAD48197.1; -
DR EMBL; AF089943; AAD48198.1; -
DR EMBL; AF089944; AAD48199.1; -
DR EMBL; AF089945; AAD48200.1; -
DR EMBL; AF089946; AAD48201.1; -
DR EMBL; AF089947; AAD48202.1; -
DR EMBL; AF089948; AAD48203.1; -
DR EMBL; AF089949; AAD48204.1; -
DR EMBL; AF089950; AAD48205.1; -
DR EMBL; AF089951; AAD48206.1; -
DR EMBL; AF089953; AAD48208.1; -
DR EMBL; AF089954; AAD48209.1; -
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008200; P:ion channel inhibitor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
NON TER 1
SQ SEQUENCE 72 AA; 7984 MW; B2057DDC87553B8D CRC64;
Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.18;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
DB 42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69
RESULT 4
Q9UAA2 ID Q9UAA2 PRELIMINARY; PRT; 72 AA.
AC Q9UAA2
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RT rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).
DR EMBL; AF089959; AAD48214.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; P:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
NON TER 1
SQ SEQUENCE 72 AA; 7924 MW; 74762D9C9193EB8B CRC64;
Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.18;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
DB 42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69
RESULT 5

11

Tue Feb 15 10:07:48 2005

QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
 DB 42 RTGSPAGEVCTSKSPCTGFLCSHIGGM 69

RESULT 9
 TXJC HADVE STANDARD; PRT; 37 AA.
 AC P82228;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Janus-atracotoxin-Hv1c (J-ActTx-Hv1c).
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_TaxID=6904;
 RN [1]
 RP SEQUENCE, FUNCTION, AND STRUCTURE BY NMR.
 RC TISSUE=Venom;
 RX MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
 RA Nicholson G.M., Christie M.J., King G.F.;
 RT "Discovery and characterization of a family of insecticidal
 neurotoxins with a rare vicinal disulfide bridge."
 RL Nat. Struct. Biol. 7:505-513 (2000).
 CC -1- FUNCTION: Insecticidal neurotoxin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 DR PDB; 1DLO; NMR; A=1-37.
 KW 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.
 FT DISULFID 3 17
 FT DISULFID 10 22
 FT DISULFID 13 14
 FT DISULFID 16 32
 FT TURN 6 7
 FT STRAND 9 9
 FT TURN 18 19
 FT STRAND 20 24
 FT TURN 26 27
 FT STRAND 30 34
 SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;

Query Match 37.4%; Score 72.5; DB 1; Length 37;
 Best Local Similarity 46.9%; Pred. No. 0.11;
 Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNN-KVCR 33
 DB 2 ICTGADRPCAACCCPCPGTSCKAESNGVSYCR 33

RESULT 10
 Q9UAA3 PRELIMINARY; PRT; 72 AA.
 AC Q9UAA3;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Four-loop conotoxin LVVIA (Fragment).
 OS Conus lividus.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89426;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
 RA Duda T.F. Jr., Palumbi S.R.;
 RT "Molecular genetics of ecological diversification: duplication and
 rapid evolution of toxin genes of the venomous gastropod Conus.";
 Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).

DR EMBL; AF089956; AAD48211.1; -;
 DR GO:0005576; C:extracellular; IEA.
 DR GO:0008200; F:ion channel inhibitor activity; IEA.
 DR GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR004214; Conotoxin.
 DR Pfam; PF02950; Conotoxin; 1.
 FT NON TER 1
 SQ SEQUENCE 72 AA; 8014 MW; C2757DDC87553EDD CRC64;

Query Match 37.1%; Score 72; DB 2; Length 72;
 Best Local Similarity 50.0%; Pred. No. 0.24;
 Matches 13; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRC--IGGV 27
 DB 44 CSPAGEVCTSKSPCTGFLCSHIGGM 69

RESULT 11
 Q9UAA5 PRELIMINARY; PRT; 72 AA.
 AC Q9UAA5;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Four-loop conotoxin LVVIA (Fragment).
 OS Conus lividus.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89426;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
 RA Duda T.F. Jr., Palumbi S.R.;
 RT "Molecular genetics of ecological diversification: duplication and
 rapid evolution of toxin genes of the venomous gastropod Conus.";
 Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).

DR EMBL; AF089952; AAD48207.1; -;
 DR GO:0005576; C:extracellular; IEA.
 DR GO:0008200; F:ion channel inhibitor activity; IEA.
 DR GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR004214; Conotoxin.
 DR Pfam; PF02950; Conotoxin; 1.
 FT NON TER 1
 SQ SEQUENCE 72 AA; 7915 MW; D9757DCD87553EDC CRC64;

Query Match 37.1%; Score 72; DB 2; Length 72;
 Best Local Similarity 50.0%; Pred. No. 0.24;
 Matches 13; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRC--IGGV 27
 DB 44 CSPAGEVCTSKSPCTGFLCSHIGGM 69

RESULT 12
 Q9GPA5 PRELIMINARY; PRT; 2524 AA.
 AC Q9GPA5;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Putative notch receptor protein.
 OS Name=notch;
 OC Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TaxID=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Whole larvae;
 RA Holland L.Z., Burgdorf C., Holland N.D., Lehrach H., Tamme R.,

RA Abi-Rached L., Pontarotti P., Lardelli M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole larvae;
RA Lardelli M.T.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12539; CAC19873.1; -.
DR HSSP; P07207; I0T8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008000; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 34.
DR Pfam; PF07645; EGF_Ca; 2.
DR Pfam; PF00066; Notch; 3.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR001010; EGFLOOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_Ca; 21.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS02097; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 23.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 34.
DR PROSITE; PS01186; EGF_2; 28.
DR PROSITE; PS00026; EGF_3; 36.
DR PROSITE; PS01187; EGF_Ca; 22.
KW ANK repeat; EGF-like domain; Receptor.
SQ SEQUENCE 2524 AA; 270970 MW; C2CA57E306D23EC9 CRC64;

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Best Local Similarity 45.9%; Pred. No. 5.4;
Matches 17; Conservative 2; Mismatches 10; Indels 8; Gaps 2;

QY 4 CTPA--GVKCP-----AALPCCPGILRCIGGVNNKVC 32
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DB 768 CLPGYGVNCDINTDECASNPQNGRCGLDGVNNVVC 804

RESULT 13

ID TXC5_PHONI STANDARD; PRT; 33 AA.
AC P84015;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Venom protein PN10C5.
OS Phoneutria nigriventer (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI_TaxID=6918;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RC SPECTROMETRY.
RC TISSUE=Venom;
RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,
RA Figueiredo S.G., Cordeiro M.N.;
RT "New peptide PN10C5 from venom of Brazilian armed spider Phoneutria
RT nigriventer has sequence similarities with snake disintegrins,
RT vasotocin-neurophysins and other spider toxins.";

RL Submitted (JUN-2004) to Swiss-Prot.
CC -!- FUNCTION: Non-toxic to mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=3672.7; METHOD=Electrospray; RANGE=1-33;
CC NOTE=Ref.1.
KW Direct protein sequencing.
SQ SEQUENCE 33 AA; 3679 MW; 77F1127D4785D6E1 CRC64;

Query Match 36.3%; Score 70.5; DB 1; Length 33;
Best Local Similarity 40.0%; Pred. No. 0.18;
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QY 4 CTPAGVKCPAALPCCPGILRCIGGVNNKVC 33
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DB 3 CAQGIKIC-HDIHCCTNLKCVREGSNRVCR 31

RESULT 14

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AC Q7PMF9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000011881 (Fragment).
GN Name=ENSANGG00000009392;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008980; EAA13897.2; -.
DR HSSP; P16109; 1FSB.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF07645; EGF_Ca; 16.
DR PROSITE; PS00010; ASX_HYDROXYL; 17.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 25.
DR PROSITE; PS00026; EGF_3; 25.
DR PROSITE; PS01187; EGF_Ca; 16.
KW EGF-like domain.
FT NON_TER 1 1
FT NON_TER 3775 3775
SQ SEQUENCE 3775 AA; 396198 MW; 51C4106F6E9908F4 CRC64;

Query Match 35.8%; Score 69.5; DB 2; Length 3775;
Best Local Similarity 41.9%; Pred. No. 16;
Matches 13; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 3 ICT-PAGVKCPAALPCCPGILRCIGGVNNKVC 32
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DB 1353 VCTNPRQCQGANMQCPPPGYGVGVGVNNLC 1383

RESULT 15

CXK_CONVR


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ID  CXK  CONVR  STANDARD;  PRT;  67 AA.
AC  Q7YZ59;
DT  29-MAR-2004 (Rel. 43, Created)
DT  29-MAR-2004 (Rel. 43, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Kappa-conotoxin ViTx precursor.
GN  Name=ViTx;
OS  Conus virgo (Virgin cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=89427;
RN  [1]
RP  SEQUENCE FROM N.A., SEQUENCE OF 27-53, SYNTHESIS OF 27-60, AND MASS
RP  SPECTROMETRY.
RC  TISSUE=Venom, and Venom duct;
RX  PubMed=12893060; DOI=10.1016/S0041-0101(03)00099-0;
RA  Kaufenstein S., Huys I., Lamthanh H., Stocklin R., Sotto F., Menez A.,
RA  Tytgat J., Mebs D.;
RT  "A novel conotoxin inhibiting vertebrate voltage-sensitive potassium
RT  channels."
RL  Toxicon 42:43-52(2003).
RN  [2]
RP  SEQUENCE FROM N.A.
RP  TISSUE=Venom duct;
RA  Kaufenstein S.;
RA  Thesis (2001), University of Darmstadt, Germany.
CC  -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC  potassium channels. This toxin inhibits the vertebrate potassium
CC  channels Kv1.1 and Kv1.3, but not Kv1.2. It has no effect on HERG-
CC  type channels, sodium hH1 channels and Kir-type channels (IRK1).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- PTM: Contains four disulfide bonds.
CC  -!- MASS SPECTROMETRY: MW=3933.3; METHOD=Electrospray; RANGE=27-60;
CC  NOTE=Ref.1.
CC  -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC  family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AJ560778; CAD90965.1; -.
KW  Direct protein sequencing; Signal; Toxin.
FT  SIGNAL 1 26
FT  CHAIN 27 60 Kappa-conotoxin ViTx.
FT  PROPEP 61 67
FT  CONFLICT 38 38 P -> S (in Ref. 1).
FT  CONFLICT 49 49 G -> S (in Ref. 1).
SQ  SEQUENCE 67 AA; 7599 MW; 46671D012446F62D CRC64;

Query Match 35.6%; Score 69; DB 1; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.51;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCFGLRCIGGVNKKVC 32
Db 29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55
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GenCore version 5.1.6
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Title: US-10-019-823B-2
Perfect score: 194
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Scoring table: BLOSUM62
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Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	42.3	36	9	US-09-894-882-3
2	79	40.7	36	9	US-09-894-882-4
3	73	37.6	35	14	US-10-072-602B-571
4	73	37.6	82	14	US-10-072-602B-140
5	72.5	37.4	37	9	US-09-894-882-5
6	69.5	35.8	30	14	US-10-072-602B-570
7	69.5	35.8	77	14	US-10-072-602B-137
8	69	35.6	31	9	US-09-894-882-461
9	69	35.6	39	9	US-09-894-882-497
10	69	35.6	67	9	US-09-894-882-247
11	68	35.1	3501	14	US-10-123-155-37
12	68	35.1	3501	14	US-10-146-731-37
13	68	35.1	3501	14	US-10-140-472-37

14	68	35.1	3501	14	US-10-141-761-37	Sequence 37, Appl
15	68	35.1	3501	14	US-10-142-885-37	Sequence 37, Appl
16	68	35.1	3501	14	US-10-158-790-37	Sequence 37, Appl
17	68	35.1	3501	15	US-10-137-871-37	Sequence 37, Appl
18	68	35.1	3501	15	US-10-140-923-37	Sequence 37, Appl
19	68	35.1	3501	15	US-10-141-756-37	Sequence 37, Appl
20	68	35.1	3501	15	US-10-141-759-37	Sequence 37, Appl
21	68	35.1	3501	15	US-10-140-805-37	Sequence 37, Appl
22	68	35.1	3501	15	US-10-140-864-37	Sequence 37, Appl
23	68	35.1	3501	15	US-10-142-426-37	Sequence 37, Appl
24	67	34.5	32	9	US-09-894-882-470	Sequence 470, App
25	67	34.5	32	14	US-10-072-602B-581	Sequence 581, App
26	67	34.5	40	9	US-09-894-882-498	Sequence 498, App
27	67	34.5	68	9	US-09-894-882-274	Sequence 274, App
28	67	34.5	79	14	US-10-072-602B-255	Sequence 255, App
29	65	33.5	77	14	US-10-072-602B-191	Sequence 191, App
30	65	33.5	2292	14	US-10-184-644-493	Sequence 493, App
31	65	33.5	2292	14	US-10-184-634-493	Sequence 493, App
32	64.5	33.2	86	15	US-10-424-599-240605	Sequence 240605,
33	64	33.0	30	14	US-10-072-602B-576	Sequence 576, App
34	64	33.0	566	10	US-09-900-449A-6	Sequence 6, Appli
35	64	33.0	572	10	US-09-900-449A-7	Sequence 7, Appli
36	64	33.0	601	10	US-09-900-449A-5	Sequence 5, Appli
37	64	33.0	639	10	US-09-900-449A-4	Sequence 4, Appli
38	64	33.0	1064	14	US-10-173-461-5	Sequence 5, Appli
39	63	32.5	1971	14	US-10-123-155-139	Sequence 139, App
40	63	32.5	1971	14	US-10-146-731-139	Sequence 139, App
41	63	32.5	1971	14	US-10-140-472-139	Sequence 139, App
42	63	32.5	1971	14	US-10-141-761-139	Sequence 139, App
43	63	32.5	1971	14	US-10-142-885-139	Sequence 139, App
44	63	32.5	1971	14	US-10-158-790-139	Sequence 139, App
45	63	32.5	1971	15	US-10-137-871-139	Sequence 139, App

ALIGNMENTS

RESULT 1
US-09-894-882-3
; Sequence 3, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-3

Query Match 42.3%; Score 82; DB 9; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.022;
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVNNKV--CR 33
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RESULT 2

US-09-894-882-4
; Sequence 4, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.

; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238

; CURRENT APPLICATION NUMBER: US/09/894,882

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 60/243,410

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/246,581

; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 60/264,256

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 506

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Hadronyche versuta

US-09-894-882-4

Query Match 40.7%; Score 79; DB 9; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.048;
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QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVNNKV--CR 33
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Db 2 ICTGADRPAAACCCPCCPOTSCQGPENGVSYCR 34

RESULT 3

US-10-072-602B-571
; Sequence 571, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Grilley, Michelle

; APPLICANT: Schoenfeld, Robert M.

; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma

; APPLICANT: Jones, Robert M.

; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 571
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-571

Query Match 37.6%; Score 73; DB 14; Length 35;
Best Local Similarity 43.3%; Pred. No. 0.22;
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RESULT 4

US-10-072-602B-140

; Sequence 140, Application US/10072602B

; Publication No. US20030109670A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Grilley, Michelle

; APPLICANT: Schoenfeld, Robert M.

; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma

; APPLICANT: Jones, Robert M.

; TITLE OF INVENTION: Cone Snail Peptides

; FILE REFERENCE: 2314-249

; CURRENT APPLICATION NUMBER: US/10/072,602B

; CURRENT FILING DATE: 2002-02-11

; PRIOR APPLICATION NUMBER: US 60/267,408

; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 638

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 140

; LENGTH: 82

; TYPE: PRT

; ORGANISM: Conus lividus

US-10-072-602B-140

Query Match 37.6%; Score 73; DB 14; Length 82;
Best Local Similarity 43.3%; Pred. No. 0.48;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
| | | | | | | | | | | | | | | | | | | |
Db 49 CGESGGQGCYSVRPCCPGLICKGTGGGLCR 78

RESULT 5

US-09-894-882-5

; Sequence 5, Application US/09894882

; Patent No. US20020102607A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Walker, Craig S.

; APPLICANT: Shetty, Reshma

; APPLICANT: Jimenez, Elsie C.

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
; US-09-894-882-461

Query Match 35.6%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.57;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
| | | | | | | | | | | | | | | | | | | | | |
DB 1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: 1-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
; US-09-894-882-497

Query Match 35.6%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.7;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
| | | | | | | | | | | | | | | | | | | | | |
DB 1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael

; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: 1-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
; US-09-894-882-247

Query Match 35.6%; Score 69; DB 9; Length 67;
Best Local Similarity 44.8%; Pred. No. 1.1;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
| | | | | | | | | | | | | | | | | | | | | |
DB 29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 11
US-10-123-155-37
; Sequence 37, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
; US-10-123-155-37

Query Match 35.1%; Score 68; DB 14; Length 3501;
Best Local Similarity 46.2%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGLCIGG 26
Db 888 GACCAAAGTACCAAGCCTGTGCTGG 913

RESULT 12

US-10-146-731-37

; Sequence 37, Application US/10146731

; Publication No. US20030129692A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C198

; CURRENT APPLICATION NUMBER: US/10/146,731

; CURRENT FILING DATE: 2002-05-15

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 37

; LENGTH: 3501

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 2762, 2778

; OTHER INFORMATION: unknown base

US-10-146-731-37

Query Match 35.1%; Score 68; DB 14; Length 3501;
Best Local Similarity 46.2%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGLCIGG 26
Db 888 GACCAAAGTACCAAGCCTGTGCTGG 913

RESULT 13

US-10-140-472-37

; Sequence 37, Application US/10140472

; Publication No. US2003013888A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198
; CURRENT APPLICATION NUMBER: US/10/140,472
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-140-472-37

Query Match 35.1%; Score 68; DB 14; Length 3501;
Best Local Similarity 46.2%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGLCIGG 26
Db 888 GACCAAAGTACCAAGCCTGTGCTGG 913

RESULT 14

US-10-141-761-37

; Sequence 37, Application US/10141761

; Publication No. US20030148432A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198

; CURRENT APPLICATION NUMBER: US/10/141,761

; CURRENT FILING DATE: 2002-05-08

; Prior Application removed - See File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 37

; LENGTH: 3501

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 2762, 2778

; OTHER INFORMATION: unknown base
US-10-141-761-37

Query Match 35.1%; Score 68; DB 14; Length 3501;

Best Local Similarity 46.2%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGG 26
DB 888 GACCAAGTACCAAGCCTGTGCTGG 913

RESULT 15

US-10-142-885-37
; Sequence 37, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762..2778
; OTHER INFORMATION: unknown base
US-10-142-885-37

Query Match 35.1%; Score 68; DB 14; Length 3501;
Best Local Similarity 46.2%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGG 26
DB 888 GACCAAGTACCAAGCCTGTGCTGG 913

Search completed: February 14, 2005, 20:56:33
Job time : 3.75816 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 1.02489 Seconds
(without alignments)
2403.590 Million cell updates/sec

Title: US-10-019-823B-2
Perfect score: 194
Sequence: 1 GKICTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	42.3	36	4	US-09-894-882-3
2	79	40.7	36	4	US-09-894-882-4
3	75	38.7	36	1	US-08-682-485A-7
4	75	38.7	36	2	US-08-933-314-7
5	75	38.7	37	1	US-08-682-485A-6
6	75	38.7	37	2	US-08-933-314-6
7	72.5	37.4	37	4	US-09-894-882-5
8	69	35.6	31	4	US-09-894-882-461
9	69	35.6	39	4	US-09-894-882-497
10	69	35.6	67	4	US-09-894-882-247
11	67	34.5	32	4	US-09-894-882-470
12	67	34.5	40	4	US-09-894-882-498
13	67	34.5	68	4	US-09-894-882-274
14	59	30.4	155	4	US-09-252-991A-28474
15	59	30.4	211	4	US-09-902-540-15694
16	59	30.4	2471	1	US-08-185-432-16
17	59	30.4	2471	1	US-08-083-590A-19
18	59	30.4	2471	3	US-08-532-384-19
19	59	30.4	2471	4	US-08-899-232-1
20	59	30.4	2471	4	US-09-121-457-1
21	58.5	30.2	34	1	US-08-117-080-5
22	58.5	30.2	34	1	US-08-471-329-5
23	58.5	30.2	34	2	US-08-915-142-5
24	58.5	30.2	908	4	US-08-714-741-44
25	58	29.9	39	4	US-09-894-882-248
26	57.5	29.6	180	4	US-09-510-238A-286
27	57.5	29.6	281	4	US-09-252-991A-23962

28	57.5	29.6	420	4	US-09-907-794A-109	Sequence 109, App
29	57.5	29.6	420	4	US-09-905-125A-109	Sequence 109, App
30	57.5	29.6	420	4	US-09-902-775A-109	Sequence 109, App
31	57.5	29.6	420	4	US-09-906-700-109	Sequence 109, App
32	57.5	29.6	420	4	US-09-903-603A-109	Sequence 109, App
33	57.5	29.6	420	4	US-09-904-920A-109	Sequence 109, App
34	57.5	29.6	420	4	US-09-909-064-109	Sequence 109, App
35	57.5	29.6	420	4	US-09-905-381A-109	Sequence 109, App
36	57.5	29.6	420	4	US-09-906-618-109	Sequence 109, App
37	57	29.4	259	3	US-09-161-241-11	Sequence 11, Appl
38	57	29.4	493	4	US-09-252-991A-16925	Sequence 16925, A
39	56.5	29.1	30	4	US-09-894-882-474	Sequence 474, App
40	56.5	29.1	44	4	US-09-894-882-296	Sequence 296, App
41	56.5	29.1	44	4	US-09-894-882-502	Sequence 502, App
42	56.5	29.1	70	4	US-09-894-882-295	Sequence 295, App
43	56	28.9	642	3	US-08-872-855-10	Sequence 10, Appl
44	56	28.9	2732	4	US-09-086-436-30	Sequence 30, Appl
45	55.5	28.6	161	4	US-10-293-622-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-894-882-3
; Sequence 3, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894, 882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-3

Query Match 42.3%; Score 82; DB 4; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.0044;
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

Oy 3 ICTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
Db 2 ICTGADRPCAACCCPCPGTSCQGPESNGVYCR 34

RESULT 2
US-09-894-882-4
; Sequence 4, Application US/09894882
; Patent No. 6767895

GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 36
TYPE: PRT
ORGANISM: Hadronyche versuta
US-09-894-882-4

Query Match 40.7%; Score 79; DB 4; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.0098;
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLCIGGVNKKV--CR 33
DB 2 ICTGADRPCAACCCPGTSCQGPENGVSYCR 34

RESULT 3
US-08-682-485A-7
Sequence 7, Application US/08682485A
Patent No. 5763568
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996

APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
US-08-682-485A-7

Query Match 38.7%; Score 75; DB 1; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLCIGGVNKKV--CR 33
DB 4 CTGADRPCAACCCPGTSCQGPENGVSYCR 35

RESULT 4
US-08-933-314-7
Sequence 7, Application US/08933314
Patent No. 5959182
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.


```

; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; US-08-933-314-7

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Query Match 38.7%; Score 75; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
Db 4 CTGADRPCAACCCPCPGTSCCKGPEPNGVSYCR 35

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RESULT 5
US-08-682-485A-6
; Sequence 6, Application US/08682485A
; Patent No. 5763568
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; FUNNEL WEB (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PL0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids

```

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
; OTHER INFORMATION: /note= "this site may be amidated without loss
; of biological activity"
; US-08-682-485A-6

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Query Match 38.7%; Score 75; DB 1; Length 37;
Best Local Similarity 50.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
Db 4 CTGADRPCAACCCPCPGTSCCKGPEPNGVSYCR 35

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RESULT 6
US-08-933-314-6
; Sequence 6, Application US/08933314
; Patent No. 5959182
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; FUNNEL WEB (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,314
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PL0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
FEATURE:
NAME/KEY: Modified-site
LOCATION: 37
OTHER INFORMATION: /label= a
OTHER INFORMATION: /note= "this site may be amidated without loss
OTHER INFORMATION: of biological activity"
US-08-933-314-6
Query Match 38.7%; Score 75; DB 2; Length 37;
Best Local Similarity 50.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
DB 4 CTGADRPCAACCCPCPGTCKGPEPNGVSYCR 35
RESULT 7
US-09-894-882-5
Sequence 5, Application US/09894882
Patent No. 6767895
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 37
TYPE: PRT
ORGANISM: Hadronyche versuta
US-09-894-882-5
Query Match 37.4%; Score 72.5; DB 4; Length 37;
Best Local Similarity 46.9%; Pred. No. 0.057;
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
QY 3 ICTPAGVKCPAALPCCPGLRCIGGVN-KVCR 33
DB 2 ICTGADRPCAACCCPCPGTCKAESNGVSYCR 33
RESULT 8
US-09-894-882-461
Sequence 461, Application US/09894882
Patent No. 6767895
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 37
TYPE: PRT
ORGANISM: Hadronyche versuta
US-09-894-882-5

APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 461
LENGTH: 31
TYPE: PRT
ORGANISM: Conus emaciatus
US-09-894-882-461
Query Match 35.6%; Score 69; DB 4; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.12;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;
QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKVC 32
DB 1 CFFPGIYCTPYLPCCWGICC--GTCRNVC 27
RESULT 9
US-09-894-882-497
Sequence 497, Application US/09894882
Patent No. 6767895
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 497


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; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          35.6%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.15;
Matches 13; Conservative 2; Mismatches 12; Indels 0; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKNVC 32
Db 1 CFPFGYCTPYLPCCWGICC--GTCRNV 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match          35.6%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.25;
Matches 13; Conservative 2; Mismatches 12; Indels 0; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKNVC 32
Db 29 CFPFGYCTPYLPCCWGICC--GTCRNV 55

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
```

```
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 470
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-470

Query Match          34.5%; Score 67; DB 4; Length 32;
Best Local Similarity 50.0%; Pred. No. 0.22;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGLRCIG 25
Db 1 CFPGLTFCSTRYLPCSCGCCSG 22

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match          34.5%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.27;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 4.51404 Seconds
(without alignments)
2827.419 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPAALPCCPGLRCIGGVNKNKVC 33

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	194	100.0	34	6	AAB66900 Insectici
4	194	100.0	34	6	AAB66900 Insectici
5	194	100.0	34	6	AAB66900 Insectici
6	194	100.0	34	6	AAB66900 Insectici
7	194	100.0	34	6	AAB66900 Insectici
8	194	100.0	34	6	AAB66900 Insectici
9	194	100.0	34	6	AAB66900 Insectici
10	194	100.0	34	6	AAB66900 Insectici
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13	194	100.0	34	6	AAB66900 Insectici
14	194	100.0	34	6	AAB66900 Insectici
15	194	100.0	34	6	AAB66900 Insectici
16	194	100.0	34	6	AAB66900 Insectici
17	194	100.0	34	6	AAB66900 Insectici
18	194	100.0	34	6	AAB66900 Insectici
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20	194	100.0	34	6	AAB66900 Insectici
21	194	100.0	34	6	AAB66900 Insectici
22	194	100.0	34	6	AAB66900 Insectici
23	194	100.0	34	6	AAB66900 Insectici
24	194	100.0	35	4	AAB66901 Insectici
25	194	100.0	35	6	AAB66901 Insectici

26	194	100.0	35	6	AAE36265	AAE36265 Insectici
27	194	100.0	35	6	AAE36282	AAE36282 Insectici
28	183	94.3	33	4	AAB66899	AAB66899 Insectici
29	82	42.3	36	5	ABB88548	ABB88548 Janus fac
30	79	40.7	36	5	ABB88549	ABB88549 Janus fac
31	75	38.7	36	2	AAR39319	AAR39319 Fla toxin
32	75	38.7	37	2	AAR39318	AAR39318 Fla toxin
33	73	37.6	35	5	ABG99786	ABG99786 Conus sp
34	73	37.6	82	5	ABG99454	ABG99454 Conus sp
35	72.5	37.4	37	5	ABB88550	ABB88550 Janus fac
36	72.5	37.4	37	7	ADL11907	ADL11907 Attractox
37	72	37.1	33	7	ADL11905	ADL11905 Raventoxi
38	69.5	35.8	30	5	ABG99785	ABG99785 Conus sp
39	69.5	35.8	77	5	ABG99452	ABG99452 Conus sp
40	69	35.6	31	5	ABB88889	ABB88889 Conus ema
41	69	35.6	39	5	ABB88925	ABB88925 Conus ema
42	69	35.6	67	5	ABB88713	ABB88713 Conus ema
43	69	35.6	2020	8	ADP31056	ADP31056 Human sec
44	67	34.5	32	5	ABB88898	ABB88898 Conus vir
45	67	34.5	32	5	ABG99796	ABG99796 Conus sp

ALIGNMENTS

RESULT 1
AAB66900
ID AAB66900 standard; peptide; 33 AA.
XX
AC AAB66900;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein #2.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
(ZENE) ZENECA LTD.
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
XX
PS Claim 3; Page 30; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 194; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33

RESULT 2
AAE36283
ID AAE36283 standard; peptide; 33 AA.
XX
AC AAE36283;
XX
DT 26-JUN-2003 (first entry)
XX
DE Paecilomyces farinosus insecticidal protein.
XX
KW Insecticidal protein; pesticide.
XX
OS Paecilomyces farinosus.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 6; Page 23; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 4
AAE36295
ID AAE36295 standard; peptide; 34 AA.
XX
AC AAE36295;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #25.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 66; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 194; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33

RESULT 3
AAE36261
ID AAE36261 standard; peptide; 34 AA.
XX
AC AAE36261;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #3.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
FN WO200298911-A2.
```


CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
Db 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 5
AAE36260
ID AAE36260 standard; peptide; 34 AA.
AC AAE36260;
XX
XX 26-JUN-2003 (first entry)
XX Insecticidal protein #2.
XX Insecticidal protein; pesticide.
XX Unidentified.
OS WO200298911-A2.
FN 12-DEC-2002.
PD 30-MAY-2002; 2002WO-GB002666.
XX 07-JUN-2001; 2001GB-00013900.
XX (SYGN) SYNGENTA LTD.
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Claim 5; Page 23; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
Db 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 6
AAE36294
ID AAE36294 standard; peptide; 34 AA.
AC AAE36294;
XX
XX 26-JUN-2003 (first entry)
XX Insecticidal protein #24.
XX Insecticidal protein; pesticide.
XX Unidentified.
OS WO200298911-A2.
FN 12-DEC-2002.
PD 30-MAY-2002; 2002WO-GB002666.
XX 07-JUN-2001; 2001GB-00013900.
XX (SYGN) SYNGENTA LTD.
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Example 1; Page 66; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
Db 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 7
AAE36259
ID AAE36259 standard; peptide; 34 AA.
AC AAE36259;
XX
XX 26-JUN-2003 (first entry)
XX Insecticidal protein #1.
XX Insecticidal protein; pesticide.
XX Unidentified.
OS
XX Key Location/Qualifiers
XX Misc-difference 1 /note= "Xaa = any amino acid"
XX WO200298911-A2.
XX 12-DEC-2002.
XX


```
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
XX (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
XX New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
XX Claim 1; Page 23; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db |||||
2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 8
AAE36290
ID AAE36290 standard; peptide; 34 AA.
XX
AC AAE36290;
XX
XX 26-JUN-2003 (first entry)
DE Insecticidal protein; pesticide.
XX
XX Unidentified.
XX
XX WO200298911-A2.
XX
XX 12-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-GB002666.
XX
XX 07-JUN-2001; 2001GB-00013900.
XX
XX (SYGN ) SYNGENTA LTD.
XX
XX Vincent JL, Viner R;
XX
XX WPI; 2003-175137/17.
XX
XX New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
XX Example 1; Page 64; 67pp; English.
XX
XX The invention relates to insecticidal protein comprising an X-glycine
XX motif at the amino-terminus. Polynucleotide or DNA constructs of the
XX invention are useful for producing plants or plant parts that are
XX resistant to insects. The protein or synergistic combination is useful as
XX an active ingredient of a pesticide or for controlling insects.
XX Antibodies raised to the insecticidal proteins can be used to identify
XX other proteins with insecticidal activity. The present sequence is
XX insecticidal protein
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db |||||
2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 9
AAE36292
ID AAE36292 standard; peptide; 34 AA.
XX
XX AAE36292;
XX
XX 26-JUN-2003 (first entry)
DT Insecticidal protein #22.
XX
XX Insecticidal protein; pesticide.
XX
XX Unidentified.
XX
XX WO200298911-A2.
XX
XX 12-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-GB002666.
XX
XX 07-JUN-2001; 2001GB-00013900.
XX
XX (SYGN ) SYNGENTA LTD.
XX
XX Vincent JL, Viner R;
XX
XX WPI; 2003-175137/17.
XX
XX New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
XX Example 1; Page 65; 67pp; English.
XX
XX The invention relates to insecticidal protein comprising an X-glycine
XX motif at the amino-terminus. Polynucleotide or DNA constructs of the
XX invention are useful for producing plants or plant parts that are
XX resistant to insects. The protein or synergistic combination is useful as
XX an active ingredient of a pesticide or for controlling insects.
XX Antibodies raised to the insecticidal proteins can be used to identify
XX other proteins with insecticidal activity. The present sequence is
XX insecticidal protein
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
Db |||||
2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34

RESULT 10
AAE36287
ID AAE36287 standard; peptide; 34 AA.
XX
XX AAE36287;
```



```
XX DT 26-JUN-2003 (first entry)
XX DE Insecticidal protein #17.
XX KW Insecticidal protein; pesticide.
XX OS Unidentified.
XX PN WO200298911-A2.
XX PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-GB002666.
XX PR 07-JUN-2001; 2001GB-00013900.
XX PA (SYGN ) SYNGENTA LTD.
XX PI Vincent JL, Viner R;
XX KW WPI; 2003-175137/17.
XX PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX PS Example 1; Page 63; 67pp; English.
XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
XX SQ Sequence 34 AA;
XX Query Match 100.0%; Score 194; DB 6; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 1e-14;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
XX DB |||||
XX 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34
XX RESULT 12
XX AAE36263
XX ID AAE36263 standard; peptide; 34 AA.
XX AC AAE36263;
XX DT 26-JUN-2003 (first entry)
XX DE Insecticidal protein #5.
XX KW Insecticidal protein; pesticide.
XX OS Unidentified.
XX PN WO200298911-A2.
XX PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-GB002666.
XX PR 07-JUN-2001; 2001GB-00013900.
XX PA (SYGN ) SYNGENTA LTD.
XX PI Vincent JL, Viner R;
XX KW WPI; 2003-175137/17.
XX PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX PS Claim 40; Page 35; 67pp; English.
XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
XX SQ Sequence 34 AA;
XX Query Match 100.0%; Score 194; DB 6; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 1e-14;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33
XX DB |||||
XX 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34
XX RESULT 11
XX AAE36289
XX ID AAE36289 standard; peptide; 34 AA.
XX AC AAE36289;
XX DT 26-JUN-2003 (first entry)
XX DE Insecticidal protein #19.
XX KW Insecticidal protein; pesticide.
XX OS Unidentified.
XX PN WO200298911-A2.
XX PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-GB002666.
XX PR 07-JUN-2001; 2001GB-00013900.
XX PA (SYGN ) SYNGENTA LTD.
XX PI Vincent JL, Viner R;
```


XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
Db 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

Search completed: February 14, 2005, 20:50:20
Job time : 4.51404 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 80.9984 Seconds
(without alignments)
4539.261 Million cell updates/sec

Title: US-10-019-823B-54
Perfect score: 3749
Sequence: 1. MKLKNQDKHQSFSSNAKVDK.....KRELPEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3722.5	99.3	719	1 C1IA_BACTK	Q45752 bacillus th
2	3722.5	99.3	719	2 O6X181	Q6x181 bacillus th
3	3717.5	99.2	719	2 Q93NJS	Q93nj5 bacillus th
4	3716.5	99.1	719	2 O85796	O85796 bacillus th
5	3587.5	95.7	719	2 O8KY61	O8ky61 bacillus th
6	3513.5	93.7	719	2 Q9F0P8	Q9f0p8 bacillus th
7	3482.5	92.9	719	1 C1IB_BACTE	Q45709 bacillus th
8	3359.5	89.6	719	1 C1ID_BACTU	O9xd11 bacillus th
9	3358.5	89.6	719	1 C1IC_BACTU	O87404 bacillus th
10	2415	64.4	1229	1 C1BB_BACTU	Q45739 bacillus th
11	2415	64.4	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2249	60.0	1228	2 Q93T75	Q93t75 bacillus th
13	2248	60.0	1228	1 C1BA_BACTK	P05517 bacillus th
14	2240	59.7	1228	2 Q93NM5	Q93nm5 bacillus th
15	2165	57.7	849	2 Q6PYW8	Q6pyw8 bacillus th
16	2165	57.7	1227	1 C1BE_BACTU	O85805 bacillus th
17	2089	55.7	1231	2 O8KNY2	O8kny2 bacillus th
18	2084	55.6	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
19	1974	52.7	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1895	50.5	381	2 Q45740	Q45740 bacillus th
21	1652	44.1	1157	1 C8AA_BACUK	Q45704 bacillus th
22	1643.5	43.8	1144	2 O8KZL7	O8kzl7 bacillus th
23	1480.5	39.5	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1473	39.3	1169	1 C8BA_BACUK	Q45705 bacillus th
25	1462	39.0	1166	1 C1GA_BACTU	Q45746 bacillus th
26	1461.5	39.0	1169	1 C1FB_BACTM	O66377 bacillus th
27	1456.5	38.9	1167	1 C1JA_BACTU	Q45738 bacillus th
28	1455.5	38.8	1174	2 Q45749	Q45749 bacillus th
29	1445.5	38.6	1118	2 Q9AM83	O9am83 bacillus th
30	1441.5	38.5	1155	1 C1AB_BACTK	P06578 bacillus th
31	1441.5	38.5	1155	2 Q7BE98	Q7be98 bacillus th

RESULT 1				
C1IA_BACTK				
ID	C1IA_BACTK	STANDARD;	PRT;	719 AA.
AC	Q45752; P71092; Q45750; Q45751; Q45756;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin			
DE	CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
GN	Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryV1;			
OS	Bacillus thuringiensis (subsp. kurstaki).			
OC	Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=29339;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSIR732;			
RX	MEDLINE=93298009; PubMed=8517758;			
RA	Gleave A.P., Williams R., Hedges R.J.;			
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis			
RT	serotypes for the presence of cryV-like insecticidal protein genes and			
RT	characterization of a cryV gene cloned from B. thuringiensis subsp.			
RT	kurstaki.";			
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=JHCC4835;			
RX	MEDLINE=92269582; PubMed=1588820;			
RA	Taylor R., Tippett J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RT	"Identification and characterization of a novel Bacillus thuringiensis			
RT	delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";			
RL	Mol. Microbiol. 6:1211-1217(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HD-1;			
RX	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus			
RT	thuringiensis and cloning of cryV-type genes from Bacillus			
RT	thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.			
RT	entomocidus.";			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AB88;			
RX	MEDLINE=96178985; PubMed=8606196;			
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,			
RA	Craig J.A., Koziel M.G., Estruch J.J.;			
RT	"Cloning of a cryV-type insecticidal protein gene from Bacillus			
RT	thuringiensis: the cryV-encoded protein is expressed early in			
RT	stationary phase.";			
RL	J. Bacteriol. 178:2141-2144 (1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=61;			

32	1441.5	38.5	1155	2	Q9F296	Q9f296 bacillus th
33	1436.5	38.3	1156	2	Q6GUA7	Q6gua7 bacillus th
34	1433	38.2	1180	2	Q9SV58	Q9sv58 bacillus th
35	1432	38.2	1176	2	Q7WZT9	Q7wzt9 bacillus th
36	1431.5	38.2	1177	2	Q6EIX3	Q6eix3 bacillus th
37	1430	38.1	793	2	Q6PYW7	Q6pyw7 bacillus th
38	1429.5	38.1	1155	2	Q93T21	Q93t21 bacillus th
39	1426	38.0	1176	2	Q45736	Q45736 bacillus th
40	1424	38.0	1169	2	Q8GHE8	Q8ghe8 bacillus th
41	1424	38.0	1181	1	C1AE_BACTL	Q03748 bacillus th
42	1422	37.9	1176	1	C1AA_BACTK	P02965 bacillus th
43	1422	37.9	1176	2	Q9RC30	Q9rc30 bacillus th
44	1417	37.8	1169	1	C1GB_BACTZ	Q9zaz6 bacillus th
45	1400	37.3	1179	1	C1AD_BACTA	Q03744 bacillus th

ALIGNMENTS

QY 241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPFSYDTQMPYPIKTTAQLTREVTDAI 300
 Db 241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPFSYDTQMPYPIKTTAQLTREVTDAI 300
 QY 301 GTVHPHPSFTSTTWNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
 Db 301 GTVHPHPSFTSTTWNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
 QY 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFTOPVN-VPR 419
 Db 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFTOPVNGVPR 420
 QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQODSENELPPEATQPNYESYSHRLSHIGLIS 479
 Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQODSENELPPEATQPNYESYSHRLSHIGLIS 480
 QY 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
 QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
 Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
 QY 600 TFXTVGFTTTPFSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 659
 Db 601 TFXTVGFTTTPFSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 660
 QY 660 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718
 Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
 Q93NJ5 PRELIMINARY; PRT; 719 AA.
 AC Q93NJ5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Crylia.
 GN Name=crylia;
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song F., Zhang J., Gu A., Huang D., Li G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF373207; AAK66742.1; -.
 DR HSSP; P02965; 1CIY.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal_bind_like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.2%; Score 3717.5; DB 2; Length 719;
 Best Local Similarity 99.3%; Pred. No. 5.5e-251;
 Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCIKMSEYENVEFVSASTI 60
 Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCIKMSEYENVEFVSASTI 60
 QY 61 QTGIGIAGKILGTGVFPAGQVASYLFGELWPKGNQWEIPMEHVEEIIINQKISTYA 120

Db 61 QTGIGIAGKILGTGVFPAGQVASYLFGELWPKGNQWEIPMEHVEEIIINQKISTYA 120
 QY 121 RNKALTDLKGLGDALAVYHDSLESWVGNNRNRTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
 Db 121 RNKALTDLKGLGDALAVYHDSLESWVGNNRNRTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
 QY 181 BEVPLLPYQAQANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSVHCVKWYS 240
 Db 181 BEVPLLPYQAQANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSVHCVKWYS 240
 QY 241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPFSYDTQMPYPIKTTAQLTREVTDAI 300
 Db 241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPFSYDTQMPYPIKTTAQLTREVTDAI 300
 QY 301 GTVHPHPSFTSTTWNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
 Db 301 GTVHPHPSFTSTTWNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
 QY 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFTOPVN-VPR 419
 Db 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFTOPVNGVPR 420
 QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQODSENELPPEATQPNYESYSHRLSHIGLIS 479
 Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQODSENELPPEATQPNYESYSHRLSHIGLIS 480
 QY 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
 QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
 Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
 QY 600 TFXTVGFTTTPFSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 659
 Db 601 TFXTVGFTTTPFSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 660
 QY 660 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718
 Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
 O85796 PRELIMINARY; PRT; 719 AA.
 ID O85796;
 AC O85796;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Insecticidal protein.
 GN Name=cryVI01;
 OS Bacillus thuringiensis (subsp. kurstaki).
 OG Plasmid large plasmid.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=29339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S101;
 RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF076953; AAC26910.1; -.
 DR HSSP; P02965; 1CIY.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal_bind_like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.

KW Plasmid.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 99.1%; Score 3716.5; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 6.4e-251;
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINOKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSOYIALELMFVKLPSPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSOYIALELMFVKLPSPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
DB 241 TGLNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360

QY 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNV 419
DB 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNV 419

QY 420 VDFHKKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 479
DB 420 VDFHKKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 479

QY 480 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
DB 480 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539

QY 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

QY 540 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 599
DB 540 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 599

QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600

QY 600 TFXTVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 659
DB 600 TFXTVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 659

QY 601 TFRVVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 660
DB 601 TFRVVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 660

QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
Q8KY61 PRELIMINARY; PRT; 719 AA.
AC Q8KY61;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278797; AAM73516.1; -
DR PIR; B42459; B42459.

DR HSSP; P02965; ICIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 95.7%; Score 3587.5; DB 2; Length 719;
Best Local Similarity 95.7%; Pred. No. 6.6e-242;
Matches 688; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINOKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSOYIALELMFVKLPSPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSOYIALELMFVKLPSPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
DB 241 TGLNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360

QY 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNV 419
DB 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNV 419

QY 420 VDFHKKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 479
DB 420 VDFHKKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 479

QY 480 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
DB 480 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539

QY 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

QY 540 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 599
DB 540 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 599

QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600

QY 600 TFXTVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 659
DB 600 TFXTVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 659

QY 601 TFRVVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 660
DB 601 TFRVVGFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQEKV 660

QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6
Q9FOP8 PRELIMINARY; PRT; 719 AA.
AC Q9FOP8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)


```
DE Name=cryII;
GN Bacillus thuringiensis.
OS Plasmid pBRC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007;
RX MEDLINE=22837682; PubMed=12957903;
RY DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
RA Hu Y., Li G., Huang D.;
RT "Identification of cryII-type genes from Bacillus thuringiensis
RT strains and characterization of a novel cryII-type gene.";
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL: AF211190; AAG43526.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid.
KW SEQUENCE 719 AA; 81024 MW; 7E17481922C435B6 CRC64;

Query Match 93.7%; Score 3513.5; DB 2; Length 719;
Best Local Similarity 93.0%; Pred. No. 9.9e-237;
Matches 669; Conservative 26; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSYENVEPVSASTI 60

Qy 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIQKISTYA 120
Db 61 QTGIGIAGKILGTLGVFPAGQIASLYSFLGELMPKGNQWEIFMEHVEELIDQKISTYA 120

Qy 121 RNKALTDLKLGLDALAVYHDSLESVGNRNTRSVKSNQYIALELMPVQKLPSEAVSG 180
Db 121 RNIALADLKLGLDALAVYHDSLESVGNRNTRSVKSNQYIALELMPVQKLPSEAVSG 180

Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240
Db 181 BEVPLPIYAQAANLHLLLRDASVFGKGLSNSQISTFYNRQVERTSDYSDHCVKWS 240

Qy 241 TGLNNLRGTNAESWRYNQFRDRTMLVLDLVALPSPYDQMPYIKTTAQLTREYVTDAL 300
Db 241 TGLNNLRGTNAESWRYNQFRDRTMLVLDLVALPSPYDQMPYIKTTAQLTREYVTDAL 300

Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
Db 301 GTVHPNAPSFSTTWYNNAPSFSAIESAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360

Qy 361 GGHKLEPRTIGTTLNSTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVN-VPR 419
Db 361 GGHRLFPRTIGGLVNSTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

Qy 420 VDFHWKFTPIASDNFYYPGAGIGTQLQDSENELPPATGPQNYESYSHRLSHIGLIS 479
Db 421 VDFHWKFTPIASDNFYYPGAGIGTQLQDSENELPPATGPQNYESYSHRLSHIGLIS 480

Qy 480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

Qy 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGCDLDYK 599
Db 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGCDLDYK 599
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Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGCDLDYK 600
Qy 600 TFXTVGFTTTPESLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659
Db 601 TFXTVGFTTTPESFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLYDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLYDKRELFEIVKYAKQLHIERNM 719

RESULT 7
CLIB_BACTE STANDARD; PRT; 719 AA.
AC Q45709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIb (Insecticidal delta-endotoxin
DE CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Names=cryIIb; Synonyms=cryII(b), cryV, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=953114293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U07642; AAA82114.1; -.
CC PIR: I40590; I40590.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C_1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
KW SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

Query Match 92.9%; Score 3482.5; DB 1; Length 719;
Best Local Similarity 92.4%; Pred. No. 1.4e-234;
Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHCLKMSYENVEPVSASTI 60
```


QY	61	QTGIGIAGKILGTLGVFPAGQVAVSLYSFILGELWPKGNQWEIFMEHVVEIINOKISTYA	120	CC	terminus.
Db	61	QTGIGIAGKILGTLGVFPAGQVAVSLYSFILGELWPKGNQWEIFMEHVVEIINOKISTYA	120	CC	-!- SIMILARITY: Belongs to the delta endotoxin family.
QY	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRRSVKSQYIALELMFVKQLPSFAVSG	180	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
Db	121	RNKALSDRLGLGDALAVYHDSLESWGNRNTRRSVKSQYIALELMFVKQLPSFAVSG	180	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSISTFYNNQVERAGDYSYHCVKWS	240	CC	the European Bioinformatics Institute. There are no restrictions on its
Db	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSISTFYNNQVERAGDYSYHCVKWS	240	CC	use by non-profit institutions as long as its content is in no way
QY	241	TGLNLRGNTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTRVYTDAL	300	CC	modified and this statement is not removed. Usage by and for commercial
Db	241	TGLNLRGNTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTRVYTDAL	300	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
QY	301	GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWNSNTQYMNW	360	CC	or send an email to license@isb-sib.ch).
Db	301	GTVHPNQAFASITWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWNSNTQYMNW	360	CC	EMBL; AF047579; AAD44366.1; -.
QY	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQVNV-VPR	419	DR	HSSP; P02965; ICIV.
Db	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQVNV-VPR	419	DR	InterPro; IPR001178; Endotoxin.
QY	420	VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	479	DR	InterPro; IPR005638; endotoxin C.
Db	420	VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	479	DR	InterPro; IPR005639; endotoxin N.
QY	480	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDLRRTN	539	DR	InterPro; IPR008979; Gal_bind_like.
Db	480	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDLRRTN	539	DR	Pfam; PF03944; Endotoxin C; 1.
QY	540	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK	599	DR	Pfam; PF00555; Endotoxin M; 1.
Db	540	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK	599	DR	Pfam; PF03945; Endotoxin N; 1.
QY	600	TEXTVGFTTFFSLLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	659	KW	Sporulation; Toxin.
Db	600	TEXTVGFTTFFSLLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	659	SQ	SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
QY	660	TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	718		
Db	661	TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	719		
RESULT 8					
CLIP_BACTU					
ID	CLIP_BACTU	STANDARD;	PRT;	719 AA.	
AC	Q9XDL1;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Pesticidal crystal protein cryII (Insecticidal delta-endotoxin				
DE	CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).				
GN	Name=cryIId; Synonyms=cryII(d), NRCryV;				
OS	Bacillus thuringiensis				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1428;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BR30;				
RX	MEDLINE=20374042; PubMed=10919402;				
RA	Choi S.-K.; Shin B.-S.; Kong E.-M.; Rho H.M.; Park S.-H.;				
RT	"Cloning of a new Bacillus thuringiensis cryII-type crystal protein				
RT	gene."				
RL	Curr. Microbiol. 41:65-69(2000).				
CC	-!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut				
CC	epithelial cells of many lepidopteran larvae. Active on Plutella				
CC	xylostella and on Bombyx mori.				
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during				
CC	sporulation and is accumulated both as an inclusion and as part of				
CC	the spore coat.				
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-				

CC	Query Match	89.6%;	Score 3359.5;	DB 1;	Length 719;
CC	Best Local Similarity	89.3%;	Pred. NO. 5.7e-226;		
CC	Matches	642;	Conservative	35;	Mismatches 41;
CC				Indels	1;
CC				Gaps	1;
QY	1	MKLKNDKHQFSSNAKVDKISLKNETDIELQNIHEDCLKMSEYENVEPFVSASTI	60		
Db	1	MKSKNQMYRFSFNATVDKSTDPLEHNTMELQNSHEDCLKMSEYEVPEFVSSTI	60		
QY	61	QTGIGIAGKILGTLGVFPAGQVAVSLYSFILGELWPKGNQWEIFMEHVVEIINOKISTYA	120		
Db	61	QTGIGIAGKILGTLGVFPAGQVAVSLYSFILGELWPKGNQWEIFMEHVVEIINOKISTYA	120		
QY	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRRSVKSQYIALELMFVKQLPSFAVSG	180		
Db	121	RNKALADLGLGDALAVYHDSLESWGNRNTRRSVKSQYIALELMFVKQLPSFAVSG	180		
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSISTFYNNQVERAGDYSYHCVKWS	240		
Db	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSISTFYNNQVERAGDYSYHCVKWS	240		
QY	241	TGLNLRGNTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTRVYTDAL	300		
Db	241	TGLNLRGNTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTRVYTDAL	300		
QY	301	GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWNSNTQYMNW	360		
Db	301	GTVHPNASFASTWYNNNAPSFTIEAAVVRNPHLLDFLEQVITYSLLSRWNSNTQYMNW	360		
QY	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQVNV-VPR	419		
Db	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQVNV-VPR	420		
QY	420	VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	479		
Db	421	VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480		
QY	480	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDLRRTN	539		
Db	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDLRRTN	540		
QY	540	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK	599		
Db	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK	600		
QY	600	TEXTVGFTTFFSLLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	659		
Db	601	TEXTVGFTTFFSLLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660		
QY	660	TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	718		
Db	661	TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	718		


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Db 661 TAMFTSTNLRRLKTNVTDCHIDQVSNLVSLSDFYLDKRELFEIVKAKQLNIERNM 719
RESULT 9
CLIC_BACTU
ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin)
DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; AF056933; AAC62933.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
DR Plasmid; Sporulation; Toxin.
KW SEQUENCE 719 AA; 81210 MW; 8370B3P06B905DFF CRC64;
Query Match 89.6%; Score 3358.5; DB 1; Length 719;
Best Local Similarity 89.6%; Pred. No. 6.7e-226;
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MKLKNQDKHQSFSNAKVDKISTDSIKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNPDKHQTLSSNAKVDKIATDSLKNETDIELKNMNEYLRMSEHESIDPVSASTI 60
Qy 61 QTGIGTAGKILGTLPVFPAGQVASYLFIQELWPKGNQWEIFMEHVEEIIQKISTYA 120
Db 61 QTGIGTAGKILGTLPVFPAGQVASYLFIQELWPKGNQWEIFMEHVEEIIQKISTYA 120
Qy 121 RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVKVSQYIALELMFVQKLPSPFVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVKVSQYIALELMFVQKLPSPFVSG 180
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNROVERAGDYSYHCVKWSY 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNROVERAGDYSYHCVKWSY 240
Qy 241 TGLNLRGNTNAESWRYNQFRDWTMLVLDLVALPPSYDTQMPYIKTTAQLTREYTDAL 300
Db 241 TGLNLRGNTNAESWRYNQFRDWTMLVLDLVALPPSYDTQMPYIKTTAQLTREYTDAL 300
Db 241 TGLNLRATNGQSWRYNQFRKDIELMWLDLVRVPSPYDTLVYPIKTTSQLTREYTDAL 300
Qy 301 GTVHPHPSPTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 360
Db 301 GTVDPNQLRSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGGTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVN-VPR 419
Db 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVN-VPR 420
Qy 420 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTIENPSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRTN 539
Db 481 GSHVKALVYSWTHRSADRTNTIENPSITQIPLVKAFNLSGGAAVVRGPGFTGGHILRTK 540
Qy 540 TGTGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 541 SGTFGHIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 600 TFXTVGFTTTPSLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQSKV 659
Db 601 TFRTVGFTTTPSFDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTVYEAEDFEKAQSKV 660
Qy 660 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKRELFEIVKAKQLNIERNM 718
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKRELFEIVKAKQLNIERNM 719
RESULT 10
CLIB_BACTU
ID C1BB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbB (Insecticidal delta-endotoxin)
DE CryIb(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbB; Synonyms=cryET5, cryIb(b);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NREL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L32020; AAA22344.1; --
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
DR Plasmid; Sporulation; Toxin.
KW SEQUENCE 719 AA; 81210 MW; 8370B3P06B905DFF CRC64;
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Qy 542 TFGDIRVNIWPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGSDLDVKTFF 601
Db 541 TFGDIRVNIWPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGSDLDVKTFF 600
Qy 602 XTGVFTTFFSLDDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 661
Db 601 RTAGFTTFFSLDDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 659
Qy 662 LFTSTNPRGLKTDVTDYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 660 LFTSTNPRGLKTDVTDYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 12
ID Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAKS1084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF05555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match
Best Local Similarity 60.0%; Score 2249; DB 2; Length 1228;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

Qy 23 TDSLKNETDIELQINIH;-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNEEIIAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVFPAGQVASYFLGELWPKGNQWEIEMHVEIINQIKISTVARNKALTDLKG 130
Db 62 LGVLGVFPAGQLASFVFLGELWPKGRDQWEIEMHVEIINQIKISTVARNKALTDLKG 121
Qy 131 LGDALAVYHDSLESVGNRNNTARSVVKQYIALELMFVQKLPFAVSAGEEVPLLPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRDARTSVLHTQYIALELDFLNAFPLFAIRNQVEPPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKEWGLSSSISTFNQVERAGDYSYHCVKYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQIQRYERQVERTRDYSYCVVWNTGLNLRGTN 241
Qy 251 ASWVRNQFRDMLVLDLVALFESYDTQMPYIKTTAQLTRVYTDAGTVHPHSFT 310
Db 242 ASWVRNQFRDMLVLDLVALFESYDTQMPYIKTTAQLTRVYTDAGTVHPHSFT 299
Qy 311 STTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLERTI 370
Db 300 SMWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLERTI 359

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Qy 371 GGTINISTQSTNTSINPVTLPTSDRVYRTESLAGLNF--LTQPVN-VPRVDEHMKFV 427
Db 360 GGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLMGYILEPIHGVPTRFNF-- 416
Qy 428 THP-----IASDNFYYPGAGIGTQLQSENELPPEATGQPNYESYSHRLSHIGLISASH 482
Db 417 TNPQINISDRGTANYSQP-YESPGQLKQSETLPPETTERPNYESYSHRLSHIGLILQSR 475
Qy 483 VKALVYSWTHRSADRTNTIENPSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGT 542
Db 476 VNPVYSWTHRSADRTNTIENPSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGT 535
Qy 543 FGDIRVNIWPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGSDLDVKTFF 602
Db 536 FGDIRVNIWPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGSDLDVKTFF 595
Qy 603 TVGFTTFFSLDDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662
Db 596 RRAFTTFFSLDDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 655
Qy 663 FTSTNPRGLKTDVTDYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 656 FTSTNPRGLKTDVTDYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 13
C1BA_BACTK
ID C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIaB (insecticidal delta-endotoxin
DE CryIaB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIaB; Synonyms=cryA4, cryIaB(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339; 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; X06711; CAA29898.1; -.
CC EMBL; X95704; CAA65003.1; -.
CC PIR; S00873; S00873.
CC HSSP; P07130; 1DLC.

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DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match      60.0%; Score 2248; DB 1; Length 1228;
Best Local Similarity 62.3%; Pred. No. 5.8e-148;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLDPARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVFPAGQVASLYSFIIGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALDILKG 130
DB 62 LGVLGVFPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRLQG 121

QY 131 LGDALAVYHDSLESWGNRNNTARSVKQYIALELMFVQKLPFSFVSGEEVPLPIYA 190
DB 122 LGDSFRAYQQSLEDWLENRDDARTSVLYTQYIALELDLFLNAMPFLAIRNQEVPLLMVYA 181

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTGTLNLRGTN 250
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYRYERQVTRDYSDYCVIEWYNTGLNLRGTN 241

QY 251 AESWVRNQFRDMLTLMVLVDFPSYDTQMYPIKTTAQLTRVYTDAGTVVHPHSFT 310
DB 242 AASWVRNQFRDMLTLMVLVDFPSYDTQMYPIKTTAQLTRVYTDAGTVVHPHSFT 299

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFTI 370
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFTI 359

QY 371 GGTNLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVN-VPRVDFHMKFV 427
DB 360 GGLNTSTHGATNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVN-VPRVDFHMKFV 416

QY 428 THP-----IASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHSHIGLISASH 482
DB 417 TNPQNSDRGTANYSQP-YESPGLQKDSLETLPETTERPNYESYSHRSLHSHIGLISASH 475

QY 483 VKALVYSWTHRSADRTNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTGT 542
DB 476 VNPVYVSWTHRSADRTNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTGT 535

QY 603 TVGFTTFFSLDVGSTFTTGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTAL 662
DB 596 RRAFTTFFFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLEAQAQAVNAL 655

QY 663 FTSTNPRGLKTDVKDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 711
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RESULT 14

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AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry1Ba.
GN Name=cry1Ba;
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OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
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SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;
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Query Match      59.7%; Score 2240; DB 2; Length 1228;
Best Local Similarity 62.2%; Pred. No. 2.1e-147;
Matches 445; Conservative 80; Mismatches 165; Indels 26; Gaps 7;
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DB 2 TSNRKNENEIINAVSNHSAQMDLLDPARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVFPAGQVASLYSFIIGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALDILKG 130
DB 62 LGVLGVFPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRLQG 121

QY 131 LGDALAVYHDSLESWGNRNNTARSVKQYIALELMFVQKLPFSFVSGEEVPLPIYA 190
DB 122 LGDSFRAYQQSLEDWLENRDDARTSVLYTQYIALELDLFLNAMPFLAIRNQEVPLLMVYA 181

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTGTLNLRGTN 250
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYRYERQVTRDYSDYCVIEWYNTGLNLRGTN 241

QY 251 AESWVRNQFRDMLTLMVLVDFPSYDTQMYPIKTTAQLTRVYTDAGTVVHPHSFT 310
DB 242 AASWVRNQFRDMLTLMVLVDFPSYDTQMYPIKTTAQLTRVYTDAGTVVHPHSFT 299

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFTI 370
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFTI 359

QY 371 GGTNLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVN-VPRVDFHMKFV 427
DB 360 GGLNTSTHGATNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVN-VPRVDFHMKFV 416

QY 428 THP-----IASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHSHIGLISASH 482
DB 417 TNPQNSDRGTANYSQP-YESPGLQKDSLETLPETTERPNYESYSHRSLHSHIGLISASH 475

QY 483 VKALVYSWTHRSADRTNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTGT 542
DB 476 VNPVYVSWTHRSADRTNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTGT 535

QY 603 TVGFTTFFSLDVGSTFTTGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTAL 662
DB 596 RRAFTTFFFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLEAQAQAVNAL 655

QY 663 FTSTNPRGLKTDVKDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 711
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5604 Seconds
(without alignments)
4171.616 Million cell updates/sec

Title: US-10-019-823B-54
Perfect score: 3749
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3732.5	99.6	719	2 S25383	parasporal crystal
2	3724.5	99.3	719	2 I39814	insecticidal prote
3	3722.5	99.3	719	2 I39815	insecticidal prote
4	3482.5	92.9	719	2 I40590	crvY465 protein -
5	2248	60.0	1228	2 S00873	parasporal crystal
6	1891	50.4	380	2 B42459	hypothetical prote
7	1480.5	39.5	1157	1 S49247	parasporal crystal
8	1462	39.0	1166	2 S32645	parasporal crystal
9	1455.5	38.8	1174	2 S32649	parasporal crystal
10	1448.5	38.6	1155	2 A26513	parasporal crystal
11	1441.5	38.5	1155	2 J00002	parasporal crystal
12	1441.5	38.5	1156	2 A29125	parasporal crystal
13	1433	38.2	934	2 A22798	parasporal crystal
14	1432	38.2	1176	2 J02041	parasporal crystal
15	1426	38.0	1176	2 J02219	parasporal crystal
16	1424.5	38.0	1155	2 S02134	parasporal crystal
17	1424	38.0	1181	2 A41052	parasporal crystal
18	1422	37.9	1176	2 A22617	parasporal crystal
19	1422	37.9	1176	2 S02215	parasporal crystal
20	1420.5	37.9	1155	2 I39838	parasporal crystal
21	1354.5	36.1	1174	2 A42459	parasporal crystal
22	1340.5	35.8	1138	2 A48944	parasporal crystal
23	1319	35.2	1156	2 A29838	parasporal crystal
24	1310	34.9	823	2 S04181	parasporal crystal
25	1298	34.6	1189	2 S00944	parasporal crystal
26	1288.5	34.4	1154	2 S39536	parasporal crystal
27	1257.5	33.5	1171	2 I40572	parasporal crystal
28	1257.5	33.5	1171	2 A37829	parasporal crystal
29	1248.5	33.3	1176	2 A48970	parasporal crystal

30	1205.5	32.2	1160	2 S32647	parasporal crystal
31	1197	31.9	1165	2 S11446	parasporal crystal
32	1185	31.6	655	2 JC7140	protoxin - Bacillu
33	1184.5	31.6	1172	2 S32689	parasporal crystal
34	1179.5	31.5	1160	2 I40589	parasporal crystal
35	1149.5	30.7	1177	2 A49785	parasporal crystal
36	1146	30.6	1178	1 USBSXH	parasporal crystal
37	1136.5	30.3	652	2 A27323	parasporal crystal
38	1114.5	29.7	659	2 S10228	parasporal crystal
39	1082	28.9	652	2 I39811	parasporal crystal
40	977.5	26.1	649	1 JH0261	parasporal crystal
41	921.5	24.6	618	2 S11445	parasporal crystal
42	875.5	23.4	1156	2 S19306	parasporal crystal
43	818.5	21.8	1136	1 USBS81	parasporal crystal
44	686	18.3	934	2 B29838	parasporal crystal
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ALIGNMENTS

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S25383
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N;Alternate names: delta-endotoxin; parasporal crystal protein cryv
C;Species: Bacillus thuringiensis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25383
R;Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin
A;Reference number: S25383; MUID:92269582; PMID:1588820
A;Accession: S25383
A;Molecule type: DNA
A;Residues: 1-719 <TAI>
A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290
C;Genetics:
A;Gene: cryV
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 99.6%; Score 3732.5; DB 2; Length 719;
Best Local Similarity 99.6%; Pred. No. 2.2e-250;
Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db	61	QTGIGIAGKILGTGVPFAGQVASLYSFTILGELWPKGNQWEIEMHVEEIIINQISTYA	120
Qy	121	RNKALTDLKGIGDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKLPFAVSG	180
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Qy	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNNRQVERAGDYSYHCVKWS	240
Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNNRQVERAGDYSYHCVKWS	240
Qy	241	TGLNNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMYPIKTTAQLTREVYTDAI	300
Db	241	TGLNNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMYPIKTTAQLTREVYTDAI	300
Qy	301	GTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
Db	301	GTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
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Tue Feb 15 10:07:49 2005

QY	420	VDHFKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	479
DB	421	VDHFKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
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QY	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHSTINGKAINQGNFSATMNRGEDLDYK	599
DB	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHSTINGKAINQGNFSATMNRGEDLDYK	600
QY	600	TFXTVGTFTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV	659
DB	601	TFRTVGTFTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV	660
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DB	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
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C:Species: Bacillus thuringiensis			
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999			
C:Accession: I39814			
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			
Appl. Environ. Microbiol. 61, 2402-2407, 1995			
A:Title: Distribution of cryI-type insecticidal protein genes in Bacillus thuringiensis			
tomocidus.			
A:Reference number: I39814; MUID:95314293; PMID:7793960			
A:Accession: I39814			
A:Status: preliminary; translated from GB/EMBL/DBJ			
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A:Gene: cryv1			
C:Superfamily: parasporal crystal protein			
Query Match 99.3%; Score 3724.5; DB 2; Length 719;			
Best Local Similarity 99.3%; Pred. No. 7.8e-250;			
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DB	61	QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA	120
QY	121	RNKALTDLKLGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG	180
DB	121	RNKALTDLKLGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG	180
QY	181	EEVPLLPYIAQAANLHLLLRDASI FGKEWGLSSSEISTFPYNNRQVERAGDYSYHCVKWS	240
DB	181	EEVPLLPYIAQAANLHLLLRDASI FGKEWGLSSSEISTFPYNNRQVERAGDYSYHCVKWS	240
QY	241	TGLNNLRGTNAESWVRVYNNQFRDMLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI	300
DB	241	TGLNNLRGTNAESWVRVYNNQFRDMLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI	300
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DB	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
QY	361	GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVRESLACLNFLTPQVN-VPR	419
DB	361	GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVRESLACLNFLTPQVNGVPR	420

QY	420	VDHFKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	479
DB	421	VDHFKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
QY	480	ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN	539
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QY	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHSTINGKAINQGNFSATMNRGEDLDYK	599
DB	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHSTINGKAINQGNFSATMNRGEDLDYK	600
QY	600	TFXTVGTFTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV	659
DB	601	TFRTVGTFTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV	660
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C:Species: Bacillus thuringiensis			
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004			
C:Accession: I39815			
R:Gleave, A.P.; Williams, R.; Hedges, R.J.			
Appl. Environ. Microbiol. 59, 1683-1687, 1993			
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis			
iensis subsp. kurstaki.			
A:Reference number: I39815; MUID:93298009; PMID:8517758			
A:Accession: I39815			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
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A:Gene: cryV			
C:Superfamily: parasporal crystal protein			
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Best Local Similarity 99.4%; Pred. No. 1.1e-249;			
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DB	61	QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA	120
QY	121	RNKALTDLKLGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG	180
DB	121	RNKALTDLKLGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG	180
QY	181	EEVPLLPYIAQAANLHLLLRDASI FGKEWGLSSSEISTFPYNNRQVERAGDYSYHCVKWS	240
DB	181	EEVPLLPYIAQAANLHLLLRDASI FGKEWGLSSSEISTFPYNNRQVERAGDYSYHCVKWS	240
QY	241	TGLNNLRGTNAESWVRVYNNQFRDMLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI	300
DB	241	TGLNNLRGTNAESWVRVYNNQFRDMLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI	300
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Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELPEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELPEIVKYAKQLHIERNM 719
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C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40590
R;Shin, B.S.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I40590
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Gene: cryV465
C;Superfamily: parasporal crystal protein
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Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;
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Qy 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVN-VPR 419
Db 361 GGHRLBSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPR 420

Qy 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSSENLPPPEATGPNYESYSHRLSHIGLIS 479
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSSENLPPPEATGPNYESYSHRLSHIGLIS 480
Qy 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 540 TGTFGDIRVINNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 541 TGTFGDIRVINNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 600 TFXTVGTTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 659
Db 601 TFRTVGTTTPFSLDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELPEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELPEIVKYAKQLHIERNM 719
RESULT 5
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
Query Match 60.0%; Score 2248; DB 2; Length 1228;
Best Local Similarity 62.3%; Pred. No. 3.2e-147;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;
Qy 23 TDSLKNETDIELQINIH-----EDCLKMSEYENVEPVFSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIPMEHVVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPFAGQLASFSYFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNATALARLQ 121
Qy 131 LGDALAVYHDSLESVWGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSGEVPLLPIYA 190
Db 122 LGDSPRAYQOSLEDWLENRDDARTRSVLTYQYIALELDFLNAFLFAIRNQEVPLLMUYA 181
Qy 191 QAANLHLLLRDASIFGKEMGLSSSEISFTYNROVERAGDYSYHCWKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYRQVTRTRDYSYCVWEYNTGLNSLRGTN 241
Qy 251 AESWRYNQPRDWTLMVLDLVALPSPDYTMQYPIKTTAQLTREVTYDAIGTVHPHPSFT 310
Db 242 AASWRYNQPRDWTLMVLDLVALPSPDYTRTYPINTSQAQLTREVTYDAIGAT--GVNMA 299
Qy 311 STTWYNNAPFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNWGGHKLFEPTI 370
Db 300 SMWYNNAPFSAIEAAVRS PHLLDFLEQVITYSLLSRWSNTRHMTYWRGHTIQSRPI 359
Qy 371 GGTLANSTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVN-VPRVDFHMKFV 427
Db 360 GGGLANSTHGATNTSINPVTLPFTSRDVRATESYAGVLLWGIYLEPIHGVPTVRFNF--- 416

Db	722	AAKRLSRERL 732	
RESULT 8			
S32645			
parasporeal crystal protein crylGal - Bacillus thuringiensis			
C;Species: Bacillus thuringiensis			
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004			
C;Accession: S32645			
R;Lambert, B.			
submitted to the EMBL Data Library, April 1993			
A;Reference number: S32645			
A;Accession: S32645			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-1166 <LAM>			
A;Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958			
C;Superfamily: parasporeal crystal protein			
C;Keywords: delta-endotoxin			
Query Match 39.0%; Score 1462; DB 2; Length 1166;			
Best Local Similarity 45.7%; Pred. No. 7.9e-93;			
Matches 322; Conservative 101; Mismatches 207; Indels 74; Gaps 17;			
Qy	41	DCLKMSYE-----NVEPFVSASTIQTGIGIAGKILGTLGVFPAGQVASLYSFILGELWPK 96	
Db	13	NCLNPESEIFNARNNSFGLVQVSSGL-----TRFLEAAVPEAGFALGLDIIWGAL--- 66	
Qy	97	GKNQWEIFMEHVEEIIINQKISTYARNKALTDKLGIDALAVYHDSLSWSVGNRNTRARS 156	
Db	67	GVDQSWLFRQIEQLRQIELELRNRAVAILTGLSSSYNLYVEALREWENDPNPASQE 126	
Qy	157	VKSKQVIALELMFVQKLPSPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSE 216	
Db	127	RVRTRELTDDAIVTGLPTLAIRNLEVNLVSVYQAANLHLSLLRDVYFGERWGLTQAN 186	
Qy	217	ISTFYNRQVERAGDYSYHCVKMYSTGLNNLRGTNAESWVRYNQFRDRMTLVLVDLALFP 276	
Db	187	IEDLYRLTNSIQEYSDHCAWYNOGLNEIGGISR----RYLDFQRDUTISVLVDIVLALFP 242	
Qy	277	SYDTQMYPIKTTAQLTRVYTDAL--GTVHPHPSPSTSTWYNNNAPSFAIEAAVVRNPH 334	
Db	243	NYDIRTYPIPTQSQLTREIYTPVVAGNI-----NFGLSIANVLRLAPH 285	
Qy	335	LLDFLEQVTIYLLSRWSNTQYMMWGGHKLFRITIG-GTLN-----ISTQGSTNTS 385	
Db	286	LMDFIDRIVITNSVR--STPY---WAGHEVISRRTGQSQGNEIRFPFLYGVAAAEPPVT 340	
Qy	386	INPVTLPFTSRDVRYES-----LAGNLFLTPQVNVPRVDFHMKFVTHPIASDNFYYP 439	
Db	341	IRPTGFTDEQWYRARSRVVFSRSSGQDFSLVDVAVG-----FLT-IFSASVIYRN 390	
Qy	440	GVAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVKALVYSWTHRS 494	
Db	391	GF-GFNT---DTIDEPIEGTDP--FTGYSHRLCHVGLFCLASSPFIQSARAPIFSWTHRS 444	
Qy	495	ADRTNTEPNSITQIPLVKAFNLSSGAADVVRGPGTGGDILRRNTGTGFDIRVNINPPF 554	
Db	445	ATLTNTIAPDVITQIPLVKAFNLHSGATIVKPGPGTGGDILRRNTVSGFDGMRVNIAPL 504	
Qy	555	AQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNRGEDLDYKTFXTVGTTPPFSLLD 614	
Db	505	SQRYRVRIRYASTTDLQFYTNINGTTINIGNFSSIMDSGDDQLQGRFRVAGFTTPFTFSD 564	
Qy	615	VQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYEAEDPEKAEKVATLTFTSTNPRGLKTD 674	
Db	565	ANSTFTIGAFGFSNNEVYIDRIEFVPAEVTFEAEYDLEKAQKAVNALFTSSNQIGLTKD 624	
Qy	675	VQDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718	
Db	625	VTDYHIDKVSNLVECLSDFCFLDKRELSEKVKHAKRLSDERNL 668	

RESULT 9			
S32649			
parasporeal crystal protein crylPa3 - Bacillus thuringiensis			
C;Species: Bacillus thuringiensis			
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004			
C;Accession: S32649			
R;Lambert, B.			
submitted to the EMBL Data Library, April 1993			
A;Reference number: S32645			
A;Accession: S32649			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-1174 <LAM>			
A;Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g2958			
C;Superfamily: parasporeal crystal protein			
C;Keywords: delta-endotoxin			
Query Match 38.8%; Score 1455.5; DB 2; Length 1174;			
Best Local Similarity 44.7%; Pred. No. 2.3e-92;			
Matches 324; Conservative 101; Mismatches 205; Indels 95; Gaps 17;			
Qy	36	NINHE----DCLKMSYENVEPFVSASTIQTGIGIA-GKILGTLGVFPAGQVASLYSFIL 90	
Db	4	NIQNCVPYNCLSNPEVEILSEERSTGRPLDLSLSTRFLSEFPVGVGVAFGLFDLIW 63	
Qy	91	GELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDKLGIDALAVYHDSLSWSVGNRN 150	
Db	64	GFITP---SEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALREWEENPN 120	
Qy	151	NTRARSVKSQVIALELMFVQKLPSPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW 210	
Db	121	NAQLREDVRIRFANTDDALITAINNFTLSFEIPLSVVYQAANLHLSLLRDVAVSFGQGW 180	
Qy	211	GLSSSEISTFYNRQVERAGDYSYHCVKMYSTGLNNLRGTNAESWVRYNQFRDRMTLVLVD 270	
Db	181	GLDIATVNNHYNRLINLIHRYTEHCLDITYNOGLENLRTNROWSRFNQFRRELTTLTVLD 240	
Qy	271	LVALPESYDTQMYPIKTTAQLTRVYTDALGTVHPHPSPSTSTWYNNNAPS-PSAIEAAV 329	
Db	241	IVALFPNYDARAYPIQTSSQLTREIYTSV--IEDSP-----VSANIPNGFNRAEFG- 290	
Qy	330	VRNPHLLDFLEQVTIYLLSRWSNTQYMMWGGHKLFRITIGTGLNISTQGSTNTSINPV 389	
Db	291	VRPPHLMDFWN-----SLFVTAETVRSQTVWGGHLV-----SSRNTAGNPI 331	
Qy	390	TLFP-----TSRDVYRTESLAGNLFLTPQVNVPRVDFHMKFVTHPIASD 434	
Db	332	NFPYIGVIFNPGGAIWAIEDPPFPYRT-----LSDPVFV-RGGF-----GN 371	
Qy	435	NFYYPGVAGIGTQLQ-----DSENELPPEATGQPNYESYSHRLSHI----- 475	
Db	372	PHYVLGLRGVAFQQTGTHNTRTFERNSTGTTDSLDEIPQONSGAPWNDYSHVLNHTVTVRW 431	
Qy	476	-GLISASHV-KALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAADVVRGPGTGGD 533	
Db	432	PGEIAGSDSNRAPMFSWTHRSADRTNINPNITQIPAVKAHNLHSGSTVVRGPGTGGD 491	
Qy	534	ILRRNTGTGFDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNRG 593	
Db	492	LLRRNTGTADIRVNITGPLSQRYRVRIRYASTTDLQFTRINGTSVNOGNFQRTWMNRG 551	
Qy	594	EDLDYKTEXTVGTTPFSLLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYEAEDPE 653	
Db	552	GNLESNGNFRTAGFSTPFSNAQSTFTLTGTQAFSN-QEYVIDRIEFVPAEVTFEAESDLE 610	
Qy	654	KAQEKVTALTSTNPRGLTKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLH 713	
Db	611	RAQKAVNALFTSTSQLGLKTNVTGVYHIDQVSNLVACLSDFCFLDKRELSEKVKHAKRLS 670	
Qy	714	IERNM 718	
Db	671	DKRNL 675	

Db 120 DPTNPALEEMRIQFNDMNSALTITPLFAVQNVPLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRTGTAESWVRYNQFRDRTLM 267
Db 180 QRMGDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDWIRYNQFRRELTLT 239
Qy 268 VLDLVALPSPDYDTOMPIKTAQLTREVYTDAGTVHPPHPSFTSTTWNNNAPSF----S 323
Db 240 VLDIVSLFPNVDSTYPIRTVSLTREIYNPV-----LENFDSFRGSAQ 285
Qy 324 ATEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGGHKLFRFTIGTGLNI 376
Db 286 GIEGS-IRSPHLMIDLNSITIYTDHRGEYYSWGHIQIMASPVGSGPFTFPLYGTWNA 344
Qy 377 STQGSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNV-PRVDFHWKFTVTHPIASDN 435
Db 345 APQORIVAQLGGGVYRTLSSTLYRRPFNIGN---NQLSVLDTGTEPAYG-----TSSN 395
Qy 436 FYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHIGLI-----SASHVKALVY 488
Db 396 LPSAVYRKSGT--VDSLDEIPQNNNVPPRQGFHSHLSHVSMFRSGFSNSSVSIIRAPMF 453
Qy 489 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFDIRV 548
Db 454 SWTHRSAEFNLIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSPQISTLRV 513
Qy 549 NINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFXTVGFTT 608
Db 514 NITAPLSQRVVRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLNQSFSRTVGFTT 573
Qy 609 PFSLLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQKVTALFTSTNP 668
Db 574 PNFNSGSSVFTLSAHVFNSENEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633
Qy 669 RGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 634 IGLKTDVTDYHIDQVSNLVESLSDEFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 12

A29125
Parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9P296; UNIPROT:Q93T21
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.5%; Score 1441.5; DB 2; Length 1156;
Best Local Similarity 44.2%; Pred. No. 2.1e-91;
Matches 314; Conservative 111; Mismatches 228; Indels 57; Gaps 14;

Qy 36 NINHEDCLKMEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVFPAGQVASYLS 87
Db 4 NPNINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESVWG 147
Db 63 IIWGIPI--GPSQWDAFLVQIEQLINQRIEFAFNQAIARLEGSLNLYQIYAESFREWEA 119
Qy 148 NRNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALEEMRIQFNDMNSALTITPLFAVQNVQVPLSVYVQAANLHLSVLDRDVSFG 179

Qy 208 KEWGLSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRTGTAESWVRYNQFRDRTLM 267
Db 180 QRMGDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDWIRYNQFRRELTLT 239
Qy 268 VLDLVALPSPDYDTOMPIKTAQLTREVYTDAGTVHPPHPSFTSTTWNNNAPSF----S 323
Db 240 VLDIVSLFPNVDSTYPIRTVSLTREIYNPV-----LENFDSFRGSAQ 285
Qy 324 ATEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGGHKLFRFTIGTGLNI 376
Db 286 GIEGS-IRSPHLMIDLNSITIYTDHRGEYYSWGHIQIMASPVGSGPFTFPLYGTWNA 344
Qy 377 STQGSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNV-PRVDFHWKFTVTHPIASDN 435
Db 345 APQORIVAQLGGGVYRTLSSTLYRRPFNIGN---NQLSVLDTGTEPAYG-----TSSN 395
Qy 436 FYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHIGLI-----SASHVKALVY 488
Db 396 LPSAVYRKSGT--VDSLDEIPQNNNVPPRQGFHSHLSHVSMFRSGFSNSSVSIIRAPMF 453
Qy 489 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFDIRV 548
Db 454 SWTHRSAEFNLIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSPQISTLRV 513
Qy 549 NINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFXTVGFTT 608
Db 514 NITAPLSQRVVRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLNQSFSRTVGFTT 573
Qy 609 PFSLLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQKVTALFTSTNP 668
Db 574 PNFNSGSSVFTLSAHVFNSENEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633
Qy 669 RGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 634 IGLKTDVTDYHIDQVSNLVESLSDEFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 13

A22798
Parasporal crystal protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: A22798
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A:Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thurin
A:Reference number: A22798; MUID:85232070; PMID:2989108
A:Accession: A22798
A:Molecule type: DNA
A:Residues: 1-934 <SHI>
A:Cross-references: UNIPROT:Q9SSV8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:G551713
C:Comment: The authors translated the codon ACA for residue 264 as Ser.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.2%; Score 1433; DB 2; Length 934;
Best Local Similarity 43.1%; Pred. No. 5.7e-91;
Matches 308; Conservative 119; Mismatches 221; Indels 66; Gaps 13;

Qy 36 NINHEDCLKMEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVFPAGQVASYLS 87
Db 4 NPNINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESVWG 147
Db 63 IIWGIPI--GPSQWDAFLVQIEQLINQRIEFAFNQAIARLEGSLNLYQIYAESFREWEA 119
Qy 148 NRNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALEEMRIQFNDMNSALTITPLFAVQNVQVPLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRTGTAESWVRYNQFRDRTLM 267

Db 180 QRWGFDAAATNSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRWVRYNQFRRELTUT 239
Qy 268 VLDLVALPSPYDQMPYIKTTAQLTREVYTDAGTVHPHPSTSTTWYNNAPPSAIEA 327
Db 240 VLDLVALFNSYDSRRYPRTVSQLTREIYNPV-----LENFDSFRGMAQ 285
Qy 328 AV----VRNPHLLDFLEQVTIYSLLSRWSNTQYMMNMGHKLFRITGTT---LNISTQGS 381
Db 286 RIEQNIRQPHLMDILNRIITYTDVHRG-----FNYWSGHQITASPVGSGPEFAFPLFGN 340
Qy 382 TMTSINPVTLPFTSRDVRVRESL-----AGLN---LFLTPQVNVPRVDFHMKFVTH 429
Db 341 AGNAAPPVLVSLTGLGIFRTLSPPLRYRRIILSGGPNQELFV-----LDGTEFSFASLT 395
Qy 430 PIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVK 484
Db 396 NLPSTIYRQGTV-----DSLVDVIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLR 448
Qy 485 ALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVVGPGFTGGDILRRNTGTGTF 544
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRNTSPGQIS 508
Qy 545 DIRVNIAPPQARYRIRYASTDLOFHTSINGKAINQGNFSAVMNRGBDLDTYKTFXTV 604
Db 509 TLRVNITAPLSQRYRIRYASTNLQFHTSIDGRPINQGNFSAVMNRGBDLDTYKTFXTV 568
Qy 605 GFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTALFT 664
Db 569 GFTTFFNFSSGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFT 628
Qy 665 STNPGKLTVDKDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
Db 629 SSNQIGLKTVDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 682

RESULT 14

JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N;Alternate names: 135K insecticidal protein
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JT0241
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
Agric. Biol. Chem. 52, 1565-1573, 1988
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A;Reference number: JT0241
A;Accession: JT0241
A;Molecule type: DNA
A;Residues: 1-1176 <SHI>
A;Cross-references: UNIPROT:P02965
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.2%; Score 1432; DB 2; Length 1176;
Best Local Similarity 43.1%; Pred. No. 9.6e-91;
Matches 308; Conservative 118; Mismatches 222; Indels 66; Gaps 13;
Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGQVASLYS 87
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGDLALAVYHDSLESVWG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESPREWEA 119
Qy 148 NRNNTARSVVKSQYIALELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTTPAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179
Qy 208 KEWGLSSSEISTFTYNNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLM 267

Db 180 QRWGFDAAATNSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRWVRYNQFRRELTUT 239
Qy 268 VLDLVALPSPYDQMPYIKTTAQLTREVYTDAGTVHPHPSTSTTWYNNAPPSAIEA 327
Db 240 VLDLVALFNSYDSRRYPRTVSQLTREIYNPV-----LENFDSFRGMAQ 285
Qy 328 AV----VRNPHLLDFLEQVTIYSLLSRWSNTQYMMNMGHKLFRITGTT---LNISTQGS 381
Db 286 RIEQNIRQPHLMDILNRIITYTDVHRG-----FNYWSGHQITASPVGSGPEFAFPLFGN 340
Qy 382 TMTSINPVTLPFTSRDVRVRESL-----AGLN---LFLTPQVNVPRVDFHMKFVTH 429
Db 341 AGNAAPPVLVSLTGLGIFRTLSPPLRYRRIILSGGPNQELFV-----LDGTEFSFASLT 395
Qy 430 PIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVK 484
Db 396 NLPSTIYRQGTV-----DSLVDVIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLR 448
Qy 485 ALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVVGPGFTGGDILRRNTGTGTF 544
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRNTSPGQIS 508
Qy 545 DIRVNIAPPQARYRIRYASTDLOFHTSINGKAINQGNFSAVMNRGBDLDTYKTFXTV 604
Db 509 TLRVNITAPLSQRYRIRYASTNLQFHTSIDGRPINQGNFSAVMNRGBDLDTYKTFXTV 568
Qy 605 GFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTALFT 664
Db 569 GFTTFFNFSSGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFT 628
Qy 665 STNPGKLTVDKDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
Db 629 SSNQIGLKTVDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 682

RESULT 15

JC2219
parasporal crystal protein cryIAa - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2219
R;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biochem. Biotechnol. 58, 830-835, 1994
A;Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and analysis of its function
A;Reference number: JC2219; MUID:94289859; PMID:7764972
A;Accession: JC2219
A;Molecule type: DNA
A;Residues: 1-1176 <UDA>
A;Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:9506190; PIDN:BAA04468.1; PID:953578
C;Genetics:
A;Gene: cryIA(a)
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1426; DB 2; Length 1176;
Best Local Similarity 43.0%; Pred. No. 2.5e-90;
Matches 307; Conservative 118; Mismatches 223; Indels 66; Gaps 13;
Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGQVASLYS 87
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGDLALAVYHDSLESVWG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESPREWEA 119
Qy 148 NRNNTARSVVKSQYIALELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTTPAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179
Qy 208 KEWGLSSSEISTFTYNNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLM 267

Db 180 QRMGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRYNQFRRELTLT 239
QY 268 VLDLVALPPSYDTOMYPIKTTAQLTREYVTDAGTVHPHPSFTSTTWYNNNAPSFAIEA 327
Db 240 VLDLVALFSNYDSRRYFIRTVSQTREIYNPV-----LENFDGSRFGMAQ 285
QY 328 AV---VRNPHLDLEQVYIYSLLSRWSNTQYMMNMGHKLFRITIGT--LNISTQGS 381
Db 286 RIEQNIQPHLMDILNSITIYTDVHRG-----FNWSGHOITAPVGFSGPPEFAPPLFGN 340
QY 382 TWTISNPVTLPTSRDVRVTESL-----AGLN--LFLTQPVNVPRVDFHWKFVTH 429
Db 341 AGNAAPPVLSVTLGLGIFRTLSSPLYRRIILGSGPNNQELFV-----LDGTEFSFASLTT 395
QY 430 PIASDNFYYPGYAGIGTQLOQSENELPPEATGQPNYESYSHRSLHIGLISAS-----HVK 484
Db 396 NLPSTIYRQGTV-----DSLDPVPPQDMSVPPRAGFSHRLSHVMTLSQAAGAVYTLR 448
QY 485 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFG 544
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTSPGOIS 508
QY 545 DIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTXTV 604
Db 509 TLRVNIITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSGNLSQSGSFRTV 568
QY 605 GFTTPFSLLDVOSTFTIGAWPSSGNEVYIDRIEFVVPVEVYEAHYDFEKAQKVTAFT 664
Db 569 GFTTPFNFSNGSSVFTLSAHVFNBSGNEVYIDRIEFVPAEVTFEAYDLEAQAQVNELFT 628
QY 665 STNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 629 SSNQIGLKTVDYDHYDQVSNLVESLSDEFCLDEKQELSEKVKHAKRLSDERNL 682

Search completed: February 14, 2005, 21:00:45
Job time : 19.5604 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.011 Seconds
(without alignments)
3909.384 Million cell updates/sec

Title: US-10-019-823B-54

Perfect score: 3749

Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFVIVKYLHIERNM 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3722.5	99.3	719	16	US-10-782-020-10
2	3722.5	99.3	719	16	US-10-782-141-8
3	3439	91.7	710	15	US-10-428-961-42
4	2249	60.0	1228	16	US-10-809-953-10
5	2236	59.6	1207	10	US-09-988-462-7
6	2156	57.5	1227	15	US-10-428-961-63
7	2141	57.1	1186	9	US-09-826-660-23
8	2085.5	55.6	1228	15	US-10-428-961-38
9	2085.5	55.6	1228	15	US-10-614-524-2
10	1902	50.7	643	9	US-09-826-660-25
11	1708	45.6	1167	14	US-10-089-678-1
12	1658	44.2	653	15	US-10-428-961-6
13	1652	44.1	1157	16	US-10-782-141-16

14	1500.5	40.0	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1500.5	40.0	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1500.5	40.0	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1477.5	39.4	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1477.5	39.4	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1477.5	39.4	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1474	39.3	1156	14	US-10-099-285-72	Sequence 72, Appl
21	1474	39.3	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1441.5	38.5	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1441.5	38.5	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1441.5	38.5	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1441.5	38.5	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1441.5	38.5	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1441.5	38.5	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1441.5	38.5	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1441.5	38.5	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1441.5	38.5	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1441.5	38.5	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1441.5	38.5	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1441.5	38.5	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1441.5	38.5	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1436.5	38.3	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1434.5	38.3	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1433.5	38.2	1177	14	US-10-102-469-24	Sequence 24, Appl
38	1422	37.9	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1400	37.3	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1400	37.3	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1380.5	36.8	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1360.5	36.3	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1360.5	36.3	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1360.5	36.3	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1360.5	36.3	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782, 020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 99.3%; Score 3722.5; DB 16; Length 719;
Best Local Similarity 99.4%; Pred. No. 4.5e-303;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy	1	MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQININHEDCLKMSEVENVEPVSASTI	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQININHEDCLKMSEVENVEPVSASTI	60
Qy	61	QTGIGIAGKILGTGLGVFFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120
Db	61	QTGIGIAGKILGTGLGVFFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120

QY	121	RNKALTDLKGGLDALAVYHDSLESWGNRNTRARVVKSQYIALELMFVQKLPSPFAVSG	180
DB	121	RNKALTDLKGGLDALAVYHDSLESWGNRNTRARVVKSQYIALELMFVQKLPSPFAVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISSTFYNRQVERAGDYSYHCVKWS	240
DB	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISSTFYNRQVERAGDYSYHCVKWS	240
QY	241	TGLNLRGNAESWVRNQFRDMLMVLVDFPSYDTQMPYIKTTAQLTREVTDAI	300
DB	241	TGLNLRGNAESWVRNQFRDMLMVLVDFPSYDTQMPYIKTTAQLTREVTDAI	300
QY	301	GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW	360
DB	301	GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW	360
QY	361	GGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVRESLGLNLFQTQPVN-VPR	419
DB	361	GGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVRESLGLNLFQTQPVN-VPR	419
QY	420	VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS	479
DB	420	VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS	479
QY	480	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	539
DB	480	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	539
QY	540	TGTFGDIRVNIINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK	599
DB	540	TGTFGDIRVNIINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK	599
QY	600	TEXTVGTTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	659
DB	600	TEXTVGTTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	659
QY	660	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	718
DB	660	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	718
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.3%; Score 3722.5; DB 16; Length 719;			
Best Local Similarity 99.4%; Pred. No. 4.5e-303;			
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
QY	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI	60

NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match
Best Local Similarity 91.7%; Score 3439; DB 15; Length 710;
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;

Qy 1 MGLKQKQKQSSNAKVDKISTDLKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60
Db 1 MKSKQNMHQSLSNATVDRKFTGLENNTNTELQNFN-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKIILGTGVPFAGQVASYLSPFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIAGKILGNLGVFPAGQVASYLSPFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 111

Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGGLDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPSPFAVSG 171

Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKWKYS 240
Db 172 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQSGSKESYSDHCVKWKYN 231

Qy 241 TGLNVLGRTNAGSWRYNQFRDMLVLDLVALPSPSYDTOMYPIKTTAQLTREYVYDAI 300
Db 232 TGLNRLMGNAESWRYNQFRDMLVLDLVALPSPSYDTOMYPIKTTAQLTREYVYDAI 291

Qy 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYNNMW 351

Qy 361 GGHKLEPRTIGTTLNTSTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVN-VPR 419
Db 352 GGHKLEPRTIGTTLNTSTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 411

Qy 420 VDFHWKFTVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 412 VDFHWKFTVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 480 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
Db 472 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 531

Qy 540 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK 599
Db 532 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK 591

Qy 600 TFXTVGTTTPESLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 659
Db 592 TFXTVGTTTPESLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 651

Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 718
Db 652 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Van Mellaert, Herman
APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10:
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match
Best Local Similarity 60.0%; Score 2249; DB 16; Length 1228;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

Qy 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

Qy 71 LGTLGVFPAGQVASYLSPFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGTLGVFPAGQVASYLSPFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121

Qy 131 LGDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPSPFAVSGEVEPVLPIYA 190
Db 122 LGDSFRAYQOSLEDWLENRDDARTSRVLHTQYIALELDPLNAMPFLFAIRNQEVPLLMVYA 181

Qy 191 QAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKWKYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASIFGSEGLTSQEIQYRYERQVTRDYSDYCVWEYNTGLNSLRGTN 241

Qy 251 AESWRYNQFRDMLVLDLVALPSPSYDTOMYPIKTTAQLTREYVYDAIGTVHPHPSFT 310
Db 242 AASWRYNQFRDMLVLDLVALPSPSYDTOMYPIKTTAQLTREYVYDAIGAT--GVNMA 299

Qy 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYNNMWGKHLEPRTI 370
Db 300 SMWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYNNMWGKHLEPRTI 359

Qy 371 GGTNLISQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVN-VPRVDFHWKFTV 427
Db 360 GGTNLISQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVN-VPRVDFHWKFTV 416

Qy 428 THP-----IASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 482
Db 417 TNPQNISDRGTANYSQP-YESPGQLKQDSETELPETTERPNYESYSHRLSHIGLISASH 475

Qy 483 VKALVYSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 542
Db 476 VNVVYVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 535

Qy 543 FGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYKTFX 602
Db 536 FGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYKTFX 595

Qy 603 TVGTTTPESLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 662
Db 596 RRAFTTTPESLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 655

Qy 663 FTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 718
Db 656 FTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

Db 122 ARLOGLGNSFRAYQOQSLDNLNRRDARTSRVLYTQYIALELDFLNAMEPLFAIRNQEVPL 181

Qy 186 LPIYAQAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNN 245

Db 182 LMVYAQAANLHLLLRDASIFGSEFGLTSQEIORYERYERQVEKTRYSYCARWYNTGLNN 241

Qy 246 LRGTNASWVRNQFRDRLTGLVLDLVALPSPYDQMPYIKTTAQLTREYVYDAIGTVHP 305

Db 242 LRGTNASWVRNQFRDRLTGLVLDLVALPSPYDQMPYIKTTAQLTREYVYDAIGTVHP 301

Qy 306 HPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMWGGHKL 365

Db 302 PSFGASTNWFNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMWGGHKL 361

Qy 366 EFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLOTQPVN-VPRVDFHW 424

Db 362 ESRTIRGSLSTWHTGNTSINPVTLPFTSRDVRVYTESLAGNLFLOTQPVN-VPRVDFHW 421

Qy 425 KFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 484

Db 422 RNPLNSLRGSLTYTIGTGVGTQDFSETELPETTERPNYESYSHRLSNIRLISGNTLR 481

Qy 485 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTFFG 544

Db 482 APVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTFFG 541

Qy 545 DIRVNIHPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGEDLDYKTFXTV 604

Db 542 SMGLNFNTSLQRYVRVRYAASQTMVLRVTVGSGTTFDQGFPTMSANESLTSQSPRFA 601

Qy 605 GFTTPFSLDVQSTFTIGAMFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKAVTALFT 664

Db 602 EFPVGISASGSQ-TAGISISNAGRTTFHDFKIEFIPITATFEAEYDLERAQKAVNALFT 660

Qy 665 STNPRGLKTDVVDYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 718

Db 661 NTNPRRLKTVTDYHIDEVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 714

RESULT 7

US-09-826-660-23

; Sequence 23, Application US/09826660

; Patent No. US20010026940A1

; GENERAL INFORMATION:

; APPLICANT: Cardineau, Guy A.

; APPLICANT: Stelman, Steven J.

; APPLICANT: Narva, Kenneth E.

; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

; FILE REFERENCE: MA-714XC2D1

; CURRENT APPLICATION NUMBER: US/09/826,660

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/178,252

; PRIOR FILING DATE: 1998-10-23

; PRIOR APPLICATION NUMBER: 60/065,215

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/076,445

; PRIOR FILING DATE: 1998-03-02

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 23

; LENGTH: 1186

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene

US-09-826-660-23

Query Match 57.1%; Score 2141; DB 9; Length 1186;

Best Local Similarity 58.5%; Pred. No. 5e-170;

Matches 418; Conservative 108; Mismatches 174; Indels 14; Gaps 4;

Qy 13 SSNAKVDKISTSLKN-----ETDIELQNHEDCLMKSEYENVEPFPVSASTIQTGIG 65

Db 7 NENEIINALSIPAVSNHSAQMNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

Qy 66 IAGKILGTGVFPAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125

Db 62 IAGRILGVLGVFPAGQIASFYSLVGELWPRGRDPWEIHEVQELIRQOVTEINTRDTAL 121

Qy 126 TDLKGLGDALAVYHDSLESVWGNRNNTARSVVKSQYIALELMFVQKLPSPFAVSAGEEYPL 185

Db 122 ARLOGLGNSFRAYQOQSLDNLNRRDARTSRVLYTQYIALELDFLNAMEPLFAIRNQEVPL 181

Qy 186 LPIYAQAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNN 245

Db 182 LMVYAQAANLHLLLRDASIFGSEFGLTSQEIORYERYERQVEKTRYSYCARWYNTGLNN 241

Qy 246 LRGTNASWVRNQFRDRLTGLVLDLVALPSPYDQMPYIKTTAQLTREYVYDAIGTVHP 305

Db 242 LRGTNASWVRNQFRDRLTGLVLDLVALPSPYDQMPYIKTTAQLTREYVYDAIGTVHP 301

Qy 306 HPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMWGGHKL 365

Db 302 PSFGASTNWFNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMWGGHKL 361

Qy 366 EFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLOTQPVN-VPRVDFHW 424

Db 362 ESRTIRGSLSTWHTGNTSINPVTLPFTSRDVRVYTESLAGNLFLOTQPVN-VPRVDFHW 421

Qy 425 KFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 484

Db 422 RNPLNSLRGSLTYTIGTGVGTQDFSETELPETTERPNYESYSHRLSNIRLISGNTLR 481

Qy 485 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTFFG 544

Db 482 APVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTFFG 541

Qy 545 DIRVNIHPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGEDLDYKTFXTV 604

Db 542 SMGLNFNTSLQRYVRVRYAASQTMVLRVTVGSGTTFDQGFPTMSANESLTSQSPRFA 601

Qy 605 GFTTPFSLDVQSTFTIGAMFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKAVTALFT 664

Db 602 EFPVGISASGSQ-TAGISISNAGRTTFHDFKIEFIPITATFEAEYDLERAQKAVNALFT 660

Qy 665 STNPRGLKTDVVDYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 718

Db 661 SSNQIGLKTVDYHIDVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 714

RESULT 8

US-10-428-961-38

; Sequence 38, Application US/10428961

; Publication No. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; FILE REFERENCE: MECO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 38

; LENGTH: 1228

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-428-961-38


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US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111a1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 44.2%; Score 1658; DB 15; Length 653;
Best Local Similarity 51.3%; Pred. No. 6.6e-130;
Matches 345; Conservative 104; Mismatches 175; Indels 48; Gaps 15;

QY 13 SSNAKVDKISTDSLKN---ETDIELQNIHEDCLKMSEYENVEPVFSASTIQTGIGTAGK 69
Db 2 NENEIINALSIPAVSNHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINAGR 60

QY 70 ILGTLGVPPAGQVASLYSPILGELMPKGNOWEIFMEHVEBEIINQKISTYARNKALTDLK 129
Db 61 ILGVLGVPPAGQASLYSFLVGLMPSGRDPWEIFLEYVEQLIRQQVTEENTRTAIRLE 120

QY 130 GLGDALAVYHDSLESWVGVRNNTRARSVVKSQVIALELMFQKLPSPFVSGEVPLLPIY 189
Db 121 GLGGRVRSYQQALETWLDNRNDARSRSIILERYVALEDDITTAIPLFIRNEEVPLLMVY 180

QY 190 AQAAHLHLLLRDASIFGKEWGLSSSEISTFNRQVERAGDYSYHCVKMYSTGNNLRGT 249
Db 181 AQAAHLHLLLRDASIFGSEWGMASSDVNQYQEQIRYTBESYHCVQWYNTGLNNLRGT 240

QY 250 NAESWVRYNQFRDRLTMLVDLVALFPSTQYPIKTTAQLTREYVTDAGTVHPHPSF 309
Db 241 NAESWLRYNQFRDLTLGLVDLVALFPSTQYPIKTTAQLTREYVTDAGTVHPHPSF 300

QY 310 TSTTWYNNAPSFSATEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLERT 369
Db 301 ASTNWFNNAAPSFSATEAAIFRPPHLLDFPEQVTIYSSASSRWSSTQHMNVWGHRLNRP 360

QY 370 IGTGLNTSTQGST-NTSINPVTLPF-TSRDVARTESLAGNLFLTPQVN-VPRVDFHWKF 426
Db 361 IGTGLNTSTQGLTNTSINPVTLVHVSRRDVRTESNAGTNILFTTPVNGVPWAFEN--F 418

QY 427 VTHPIADSNFYYP-----GYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIG-- 476
Db 419 ITLRIFMKEAPLPTVNRIRRELGNLYIQKLNHYQK-----QQNDQIMNHIVIDISYR 470

QY 477 LISASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRPGFGTGGDILR 536
Db 471 LIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIPAVKGRFLFNG-SVISGPGFTGGDVVR 529

QY 537 -RTNTGT--GDIRVNN-PPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNN 591
Db 530 LNRNNGNIQNRGIVIEPIQFTSTSTRYRVRVRYASVTSIELNVNLGNSSIFTNIPATAA 589

QY 592 RGEDLDYKTFXTVGTFTPFSLLDVQSTFT-----IGAWNFSSGNEVYIDRIEFVPEVT 645
Db 590 SLQDLQ-----SGDFGVGEVYINNAFTSATGNIVGARNFSANAEEVIIDRFEPIDVAT 640

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Qy	646	YEAAYDFEKAQE 657	: :
Db	641	FEVEYDLERAQK 652	: :
RESULT 13			
US-10-782-141-16			
; Sequence 16, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Kozziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 16			
; LENGTH: 1157			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-16			
Query Match 44.1%; Score 1652; DB 16; Length 1157;			
Best Local Similarity 48.8%; Pred. No. 5.1e-129;			
Matches 369; Conservative 100; Mismatches 229; Indels 58; Gaps 19			
Qy	1	M L K N Q D K H Q S F S S N A K V D K I S T D S - - - - L K N E T D I E L Q N I N H E D C L K M S E Y E - - - - - N 50	
Db	1	M S P N N Q N E Y E I I D A T P S T - S V S S D S N R Y P F A N E P T D A L Q N M Y K D Y L K M S G G E N P E L F G N 59	
Qy	51	V E P F V S A S I Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S I F I G E L M P - K G K N Q W E I F M E H V E 109	
Db	60	P E T F I S S T I Q T G I G I V G R I L G A L G V P P A S Q I A S F Y S F I V Q L W P S K S V D I W G E I M E R V E 119	
Qy	110	E I I N Q K I S T Y A R N K A L T D L K G L G D A L A V H D S L E S V G N R N N T R A R S V V K S Q Y I A L E L M F 169	
Db	120	E L V D Q K I E Y V K D A L A E L K G L G N A L D V Y Q O S L E D W L E N R D A R T R S V S N Q F I A L D L N F 179	
Qy	170	V Q K L P S F A V S G E E V P L L P I Y A Q A A N H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G 229	
Db	180	V S S I P S F A V S G H E V L L A V A Q A V N L H L L L R D A S I F G E E W G F T P G E I S R F Y N R Q V L T A 239	
Qy	230	D Y S Y H C V K W Y S T G L N L R G N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A 289	
Db	240	E Y S D Y C V K W Y K I G L D K L K G T T S K W L N Y H Q F R R E M T L L V L D L V A L F P N Y D T H M Y P I E T T A 299	
Qy	290	Q L T R E V Y T D A I G T V H P H P S F T S T - - - - T W Y N N N A P S F S A E A A V V R N P H L L D F L E Q T I Y 345	
Db	300	Q L T R D V Y T D I A - - - - F N I V T S T G C N P W S T H S G I L F Y E V E N N V I R P P H L F D I L S S V E I N 355	
Qy	346	S L L S R - - - - W S N T Q Y M N W G H K L B F R - - - - T I G T L N I S T Q G S T N T S I N P V T L P F T S R 396	
Db	356	T - - - S R G G I T L N D A V I N W S G H T L K Y R T A D S T V Y T A N Y G R I T S E K N S - - - - - F A L E D R 408	
Qy	397	D V Y R T E S - L A G L N L F I T Q P V N V P R V D F H K F V T H P I A S D N E Y - - - - - Y P G A G I G T Q L O D 450	
Db	409	D I F E I N S T V A N L A N Y Q K A Y G V P G S W F H - - M V K R G T S S T T A Y L Y S K T H T A L O G C - T Q V Y E 465	
Qy	451	S E N E L P P E A T Q P N Y E S Y S H R L S H I - - - - - G L I S A S H V K A L V Y S W T H S A D R T N T I E 502	
Db	466	S S D E I P L D R T - V P V A E S Y S H R L S H I T S H S F S K N G - - S A Y Y G S F P V F V W T H T S A D L N N T I Y 522	
Qy	503	P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N T G T G D I R V N I N P P A Q R Y V R I 562	


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Db 523 SDKITQIPAVKGMVLYLGGVVQGPFTGGDILKRTNPSILGTFPAVTNGSLSQRYRVI 582
Qy 563 RYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFXTVGTFTPPFSLLDVQSTFTIG 622
Db 583 RYASTTDEEF-TLYLGTITIEKRNFKMTDNGASLYETFEASFITDFQFRETQDKILLS 641
Qy 623 AMNPFSSGNEVYIDRIEIPVVEYEAEDFEKAQKVLTALFTSTNPRGLKTDVVKDYHIDQ 682
Db 642 MGFPSGGQEVYIDRIEIPVDEYEAQDLEAAKKAVALFTNTKD-GLRPGVTDYEVNQ 700
Qy 683 VSNLVESLSDFEYLDKRELFVIVKAKQLHIERNM 718
Db 701 AANLVECLSDDLYPNEKRLFLDAVREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 40.0%; Score 1500.5; DB 13; Length 1206;
Best Local Similarity 44.2%; Pred. No. 2.8e-116;
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQININHEDECLM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVNSDNRYPFANEPTNALQNDYKDYLKMSAGNASEYPGS 59

Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNOMEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVFPVIVSLYTLQIDILWPSEKSKQWEIFMEQV 119

Qy 109 EEIINQKISTYARNKALTDLKGLGDALAVYHDSLSVWGNRNTRARSVVKSQVIALEIM 168
Db 120 EEIINQKIAEYARNKALSELEGLGNNYQLYLTALEEWEENPNGSRALRDVNRNFEILDSL 179

Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 228
Db 180 FTQYMPSFRVTNFEVPFLTVYAMAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 239

Qy 229 GDYSYHCVKWYSGLNNLRGTNAESVRYNQFRDMLVLDLVALFPSVDYQMPYIKTT 288
Db 240 AEYSDHCVKWYETGLAKLGTSAKQWVDYDYNQFRRENTLAVLDVVALFPNYDTRYPMETK 299

Qy 289 AQLTREYVTDALGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSL 348
Db 300 AQLTREYVTDPLGAVNVS--SIGSWY-DKAPSFVIESSVIRPHVFDYITGLTVYITQS 355

Qy 349 SRWSNTQYNNMGGHKLFRITGGTILNISTQGSTNTSINPV-TLPFTSRDVTYRTESLAGL 407
Db 356 RSISSARYIRHWAGHQISYHRVSRGSLQMQMYGTNQNLHSTSTFDFTNYDIYKTLSDAV 415
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Qy 408 NLFLTOP-----VNVPRVDFHMKFVTHPIASDN---FYYPGYAGIGITQLODSENELPPE 458
Db 416 LLDIVVPGYTYIFFGMPEVEF---FMVNLNTRKTLKYNPVSXDIIASTRDSELELPE 472
Qy 459 ATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRNTWIEPNSITQIPLVKAP 515
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKCM 532
Qy 516 NLSSGAAVVRGPGFTGGDILR-RTNVTGTFGDI---RVNINPPFAQRYRVRIRVASTTDLQ 571
Db 533 DNLFPVVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRVLRLVATDADIV 592
Qy 572 FHTSINGKAINQGNFSATMNRGEDLDYKTF-----XTVGFTTTPFSL-----DVOST 618
Db 593 LH--VNDQAI---QMPKTMNPGEDLTSKTPKVAADAITTLNLTATDSSSLAKHNIGEDPNST 647
Qy 619 FTIGAWNFSGNEVYIDRIEIPVVEYEAEDFEKAQKVLTALFTSTNPRGLKTDVVKDY 678
Db 648 LS-----GIVYVDRIEIPVDEYEAQDLEAAKKAVALFTNTKD-GLRPGVTDY 697

Qy 679 HIDQVSNLVESLSDFEYLDKRELFVIVKAKQLHIERNM 718
Db 698 EVNQAANLVECLSDDLYPNEKRLFLDAVREAKRLSGARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 40.0%; Score 1500.5; DB 14; Length 1206;
Best Local Similarity 44.2%; Pred. No. 2.8e-116;
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQININHEDECLM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVNSDNRYPFANEPTNALQNDYKDYLKMSAGNASEYPGS 59

Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNOMEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVFPVIVSLYTLQIDILWPSEKSKQWEIFMEQV 119

Qy 109 EEIINQKISTYARNKALTDLKGLGDALAVYHDSLSVWGNRNTRARSVVKSQVIALEIM 168
Db 120 EEIINQKIAEYARNKALSELEGLGNNYQLYLTALEEWEENPNGSRALRDVNRNFEILDSL 179

Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 228
Db 180 FTQYMPSFRVTNFEVPFLTVYAMAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 239
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.2992 Seconds
(without alignments)
2403.590 Million cell updates/sec

Title: US-10-019-823B-54
Perfect score: 3749
Sequence: 1 MKLKNDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/1/1aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B COMB.pep.*
5: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3718.5	99.2	719	3	US-08-286-870A-8
2	3439	91.7	710	4	US-09-661-322A-42
3	3360.5	89.6	648	3	US-08-286-870A-4
4	3358.5	89.6	719	2	US-09-003-217-2
5	3356.5	89.5	719	3	US-09-218-942-2
6	2778.5	74.1	535	3	US-08-286-870A-6
7	2415	64.4	1229	1	US-08-100-709-4
8	2415	64.4	1229	1	US-08-176-865-4
9	2415	64.4	1229	1	US-08-474-038-4
10	2415	64.4	1229	2	US-08-779-046-4
11	2415	64.4	1229	2	US-08-881-340-4
12	2319	61.9	488	1	US-08-448-170-10
13	2319	61.9	488	3	US-08-961-803-10
14	2236	59.6	1207	1	US-07-951-715A-7
15	2236	59.6	1207	2	US-08-459-448A-7
16	2236	59.6	1207	3	US-08-459-595A-7
17	2236	59.6	1207	3	US-08-459-504B-7
18	2236	59.6	1207	3	US-08-459-444-7
19	2236	59.6	1207	3	US-09-053-549-8
20	2236	59.6	1207	3	US-09-547-422-7
21	2236	59.6	1207	4	US-09-988-462-7
22	2235	59.6	1227	3	US-09-053-549-2
23	2165	57.7	1227	1	US-08-448-170-8
24	2165	57.7	1227	3	US-08-961-803-9
25	2156	57.5	1227	4	US-09-661-322A-63
26	2141	57.1	1186	3	US-09-178-252-23
27	2141	57.1	1186	4	US-09-826-660-23

28	2085.5	55.6	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1902	50.7	643	3	US-09-178-252-25	Sequence 25, Appl
30	1902	50.7	643	4	US-09-826-660-25	Sequence 25, Appl
31	1891	50.4	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1658	44.2	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1652	44.1	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1652	44.1	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1652	44.1	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1652	44.1	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1482	39.5	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1480.5	39.5	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1480.5	39.5	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1480.5	39.5	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1480.5	39.5	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1480.5	39.5	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1480.5	39.5	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1474	39.3	1156	3	US-09-002-285-72	Sequence 72, Appl
45	1474	39.3	1156	4	US-09-589-477-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/286.870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Query Match 99.2%; Score 3718.5; DB 3; Length 719;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEHDCIKMSEYENVEPVSASTI 60
1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEHDCIKMSEYENVEPVSASTI 60
61 QTGIGIAGKILGTLGVPPAGQVVASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
61 QTGIGIAGKILGTLGVPPAGQVVASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
121 RNKALTDLKGLDALAVYHDSLESWGNNRNRTRSVKSOYIALELMFVQKLPSPFAVSG 180
121 RNKALTDLKGLDALAVYHDSLESWGNNRNRTRSVKSOYIALELMFVQKLPSPFAVSG 180
181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVYDAI 300
241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVYDAI 300
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301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTQPVN-VPR 419
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661 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719
661 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719
-RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (2007..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 91.7%; Score 3439; DB 4; Length 710;
Best Local Similarity 91.9%; Pred. No. 1.2e-299;
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;
1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEHDCIKMSEYENVEPVSASTI 60
1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEHDCIKMSEYENVEPVSASTI 60
61 QTGIGIAGKILGTLGVPPAGQVVASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
61 QTGIGIAGKILGTLGVPPAGQVVASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
121 RNKALTDLKGLDALAVYHDSLESWGNNRNRTRSVKSOYIALELMFVQKLPSPFAVSG 180
121 RNKALTDLKGLDALAVYHDSLESWGNNRNRTRSVKSOYIALELMFVQKLPSPFAVSG 180
181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
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241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVYDAI 300
301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTQPVN-VPR 419
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600 TEXTVGTTPFSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659
660 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
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661 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719
-RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 89.6%; Score 3360.5; DB 3; Length 648;
Best Local Similarity 99.4%; Pred. No. 1.1e-292;
Matches 644; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
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Db 121 RNKALTDLKGIDALAVYHDSLESWGVRNNTNRRSVVKSQYIALELMFVQKLPSPAVSG 180
Qy 181 EYVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNNQVERAGDYSYHCVKWS 240
Db 181 EYVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNNQVERAGDYSYHCVKWS 240
Qy 241 TGLNLRGTNAESWVRNQNPRDMLTDLVALPSPYDTQMYPIKTTAQLTREYVYTDI 300
Db 241 TGLNLRGTNAESWVRNQNPRDMLTDLVALPSPYDTQMYPIKTTAQLTREYVYTDI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Qy 361 GGKLEFRITGTLNISTQGTNTSINPVLPTFTRDVRVYTESLAGLNLFLTQPVNGVPR 419
Db 361 GGKLEFRITGTLNISTQGTNTSINPVLPTFTRDVRVYTESLAGLNLFLTQPVNGVPR 420
Qy 420 VDFHWKFTVTHPIASDNFYPGAGIGTQLODSENLPEATGQPNYESYSHRISHIGLIS 479
Db 421 VDFHWKFTVTHPIASDNFYPGAGIGTQLODSENLPEATGQPNYESYSHRISHIGLIS 480

Qy 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGFGTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGFGTGGDILRRTN 540
Qy 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMRGDELDYK 599
Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMRGDELDYK 600
Qy 600 TFXTVGFTTFFSLDDVQSTFTIGAWNFSGNEVYIDRIEFVPEVYTYE 647
Db 601 TFXTVGFTTFFSLDDVQSTFTIGAWNFSGNEVYIDRIEFVPEVYTYE 648
RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.6%; Score 3358.5; DB 2; Length 719;
Best Local Similarity 89.6%; Pred. No. 2e-292;
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGIDALAVYHDSLESWGVRNNTNRRSVVKSQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGIDALAVYHDSLESWGVRNNTNRRSVVKSQYIALELMFVQKLPSPAVSG 180
Qy 181 EYVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNNQVERAGDYSYHCVKWS 240
Db 181 EYVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNNQVERAGDYSYHCVKWS 240

Db 181 EEVPLLPYIAQAANLHLLLRDASIFKNGGLSASEISFYNRQVTRDYSHCVKWN 240
Qy 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVYTDI 300
Db 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVYTDI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Db 301 GTVDPNQALRSITWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRITIGTINI STQGSTNTSINPVTLPTSRDVRVYTESLAGLNLFLTOPVN-VPR 419
Db 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPTSRDVRVYTESLAGLNLFLTOPVNGVPR 420
Qy 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 479
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 GSHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
Qy 540 TGTGDIRVNNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
Db 541 SGTFGHIRVNNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 600 TFXTVGFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659
Db 601 TFRVGTFTTFFSDFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVQHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVQHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Oman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; TITLE OF INVENTION: Activity
; FILE REFERENCE: Cry1I
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

Query Match 89.5%; Score 3356.5; DB 3; Length 719;
Best Local Similarity 89.6%; Pred. No. 3e-292;
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDLKNETDIELQINHEDECKMSEVENVEPVSASTI 60
Db 1 MKLKNPDKHQTSSNAKVDKIATDSLKNETDIELKNNNDYLRNHEHSIDPVSASTI 60

Qy 61 QTGIGIAGKILGTIGVPPAGVVALSYFILGELWPKGKNQWEIFMEHVEEILNOKISTYA 120
Db 61 QTGIGIAGKILGTIGVPPGQIASLYFILGELWPKGKSQWEIFMEHVEAIINRKISTYA 120

Qy 121 RNKALTDLKGDLALAVHDSLSWVGNNRNTARSVVKSQYIALELMFVKLPSPFAVSG 180
Db 121 RNKALTDLKGDLALAVHDSLSWVGNNRNTARSVVKQYIALELMFVKLPSPFAVSG 180

Qy 181 EEVPLLPYIAQAANLHLLLRDASIFKNGGLSASEISFYNRQVTRDYSHCVKWN 240
Db 181 EEVPLLPYIAQAANLHLLLRDASIFKNGGLSASEISFYNRQVTRDYSHCVKWN 240
Qy 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVYTDI 300
Db 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVYTDI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Db 301 GTVDPNQALRSITWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRITIGTINI STQGSTNTSINPVTLPTSRDVRVYTESLAGLNLFLTOPVN-VPR 419
Db 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPTSRDVRVYTESLAGLNLFLTOPVNGVPR 420
Qy 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 479
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
Qy 540 TGTGDIRVNNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
Db 541 SGTFGHIRVNNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 600 TFXTVGFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659
Db 601 TFRVGTFTTFFSDFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVQHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVQHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.1%; Score 2778.5; DB 3; Length 535;
Best Local Similarity 99.6%; Pred. No. 1.5e-240;
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDECKMSEVENVEPVFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDECKMSEVENVEPVFSASTI 60

QY 61 QTGIGIAGKILGTLPVFPAGQVASYLFIKELWPKGKQWEIEMHEVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLFIKELWPKGKQWEIEMHEVEEIIINQKISTYA 120

QY 121 RNKALTDKGLGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPSPFAVSG 180
DB 121 RNKALTDKGLGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPSPFAVSG 180

QY 181 EEPVLLPIYAQAANTLHLLLRDASIFGKWLSSSEISFYNNQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANTLHLLLRDASIFGKWLSSSEISFYNNQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREYTDAT 300
DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREYTDAT 300

QY 301 GTVHPHPSFTSTTWYNNAPSFSAEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMW 360

QY 361 GGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVN-VPR 419
DB 361 GGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420

QY 420 VDFHWKFTVHTPIASDNFYPGYAGICTQLQDSNELPPEATQPNYESYSHRISHIGLIS 479
DB 421 VDFHWKFTVHTPIASDNFYPGYAGICTQLQDSNELPPEATQPNYESYSHRISHIGLIS 480

QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 534
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECKMSEVENVEPVFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQNLSPDIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLFIKELWPKGKQWEIEMHEVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQVASYLFIKELWPKGKQWEIEMHEVEEIIINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPSPFAVSGEVEPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRNEEVEPLLMVYA 186

QY 191 QAANLHLLLRDASIFGKWLSSSEISFYNNQVERAGDYSYHCVKWSYTGNNLRGTN 250
DB 187 QAANLHLLLRDASIFGSEWGMASDDVQYEQIRYTESYHCVQWYNTGLNLRGTN 246

QY 251 AESWRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREYTDATGTVHPHPSFT 310
DB 247 AESWRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREYTDATGTVHPHPSFT 306

QY 311 STTWYNNAPSFSAEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMWGGHKLERTI 370
DB 307 STTWYNNAPSFSAEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMMWGGHKLERTI 366

QY 371 GGTGLNISTQST-NTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVN-VPRVDFHWKEVT 428
DB 367 GGTGLNISTQST-NTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVN-VPRVDFHWKEVT 422

QY 429 HPIASDNFYPG------YAGICTQLQDSNELPPEATQPNYESYSHRISHIGLISAS 481
DB 423 --INPQNIYERGATTYSQPYQGVIGLDFSETELPETTERPNYESYSHRISHIGLIIGN 480

QY 482 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDLRRNTWG 541
DB 481 TLRAPVYSWTHRSADRTNTIEPNSITQIPLVKALNLSGVTVVGGPGFTGGDLRRNTWG 540

QY 542 TFGDIRVNIPLPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYKTF 601
DB 541 TFGDIRVNIPLPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYKTF 600

QY 602 XTVGFTTTPFSLLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKTYA 661
DB 601 RTAGFTSTPFNLNAQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKTYA 659

Tue Feb 15 10:07:49 2005

Db 247 AESWLYNQFRDLTLGLVLDLVALFSDYTRTYPIINTSQALETREIYTDPIGRNAPSGFA 306
 QY 311 STTWNNAPSAIEAAVVRPHLLDLEOVITYSLLSRWSTNTQYMNWGHKLEPRTI 370
 Db 307 STWNNAPSAIEAAIFRPPHLLDPEQLTIYSASSRWSTQHMVWVGHRLNFRPI 366
 QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVTESLAGLNLFLTOPVN-VPRVDFHWKFTV 428
 Db 367 GGTLNISTQGST-NTSINPVTLPFTSRDVTESLAGLNLFLTOPVN-VPRVDFHWKFTV 422
 QY 429 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNVESYSHRLSHIGLISAS 481
 Db 423 --INPQNIYERGATYISQYQGVGIQLFDSETELPPEATERPNEYSYSHRLSHIGLIGN 480
 QY 482 HVKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDIILRTNTG 541
 Db 481 TLRAPVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDIILRTNTG 540
 QY 542 TFGDIRVNINPFAQRYVRIRYASTTDLQFHTSINGKAINOGNFSATMNGEDLDYKTF 601
 Db 541 TFGDIRVNINPFAQRYVRIRYASTTDLQFHTSINGKAINOGNFSATMNGEDLDYKTF 600
 QY 602 XTGVFTTFFSLDQVSTETIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDEKAEKVT 661
 Db 601 RTAGFSTPFNFLNAQSTFTLGAQSFNS-QVYIDRVEFVPAEVTFEAEYDLERAQKAVNA 659
 QY 662 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFKIVKAKQLHIERNM 718
 Db 660 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFKIVKAKQLHIERNM 716

RESULT 9

US-08-474-038-4
 ; Sequence 4, Application US/08474038
 ; Patent No. 5679343
 ; GENERAL INFORMATION:
 ; APPLICANT: Donovan, William P.
 ; APPLICANT: Tan, Yuping
 ; APPLICANT: Jany, Christine S.
 ; APPLICANT: Gonzalez Jr., Jose M.
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
 ; ADDRESSEE: Nadel
 ; STREET: 1601 Market Street, 36th Floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,038
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/176,865
 ; FILING DATE: 30-DEC-1993
 ; APPLICATION NUMBER: US 08/100,709
 ; FILING DATE: 29-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Egolf, Christopher
 ; REGISTRATION NUMBER: 27633
 ; REFERENCE/DOCKET NUMBER: 7205-49
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-757-1590
 ; INFORMATION FOR SEQ ID NO: 4:

QY 662 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFKIVKAKQLHIERNM 718
 Db 660 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFKIVKAKQLHIERNM 716
 ;
 ; RESULT 8
 ; US-08-176-865-4
 ; Sequence 4, Application US/08176865
 ; Patent No. 5616319
 ; GENERAL INFORMATION:
 ; APPLICANT: Donovan, William P.
 ; APPLICANT: Tan, Yuping
 ; APPLICANT: Jany, Christine S.
 ; APPLICANT: Gonzalez Jr., Jose M.
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
 ; ADDRESSEE: Nadel
 ; STREET: 1601 Market Street, 36th Floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/176,865
 ; FILING DATE: 30-DEC-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/100,709
 ; FILING DATE: 29-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Egolf, Christopher
 ; REGISTRATION NUMBER: 27633
 ; REFERENCE/DOCKET NUMBER: 7205-49
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-757-1590
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1229 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-176-865-4
 ; Query Match 64.4%; Score 2415; DB 1; Length 1229;
 ; Best Local Similarity 65.1%; Pred. No. 2.5e-207;
 ; Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;
 ;
 ; QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEVENPEPVSASTIOTGIGIAGKI 70
 ; 7 NENEIINALSIFTVSNPSTQNLSPDARIEDSLCVAEYNIIDPFVSASTVOTGINAGRI 66
 ; 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVHEEILNKISTYARNKALTDLKG 130
 ; 67 LGVLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVHEEILNKISTYARNKALTDLKG 126
 ; 131 LGDALAVHDSLSSEWGNRNTRARSVVKSQYIALELMFVKQLPSPAVSGEEVPLPIYA 190
 ; 127 LGRGYRSYQOALETWLDRNDARSILERYVALELDTTATPLFRIRNEEVPPLMVYA 186
 ; 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGYSYHCVKWYSTGLNNLRGTN 250
 ; 187 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGYSYHCVKWYSTGLNNLRGTN 246
 ; 251 AESWRYNQFRDLTLGLVLDLVALFSDYTRTYPIINTSQALETREIYTDPIGRNAPSGFA 310


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SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-038-4

Query Match      64.4%; Score 2415; DB 1; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDCLKMSYENVEPVFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQOVTRNTAIAARLEG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVKQYIALELMFVQKLPFAVSGEVEPLLPPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPFLMVA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSYHCVKYSTGLNLRGTN 250
DB 187 QAAHLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSYHCVKYSTGLNLRGTN 246

QY 251 AESWRYNQFRDMLTMDLVALFPPSYDTQMPYIKTTAQLTREYVTDATGTVHPHPSFT 310
DB 247 AESWLRYNQFRDLTLGVLDLVALFPPSYDTRTPINTSAQLTREIYDPIGRNAPSFA 306

QY 311 STTWYNNAPFSAIEAAVVRNPVHLLDFLEQVITYSLSRWSNTQYMMNMGHKLFRPTI 370
DB 307 STNWFNNAPFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMYVWGHRLNRP 366

QY 371 GGTLLNSTQGST-NTSINPVTLPFTSRDVRVTSAGLNLFLTPQVN-VPRVDFHWKFW 428
DB 367 GGTLLNSTQGLTNTNTSINPVTLPFTSRDVRVTSAGLNLFLTPQVNVPWAFRNF 422

QY 429 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLISAS 481
DB 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPETTERPNYESYSHRLSHIGLI 480

QY 482 HVKALVYSWTHRSADRTNTRIPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRNTG 541
DB 481 TLRAPVYSWTHRSADRTNTRIPNRTIQIPLVKALNLHSGTVVGGPGFTGGDILRRNTG 540

QY 542 TFGDIRVNINPFAQYRVRIRYASTDLOPHTSINGKAINQGNFSAWNRGDDLYKTF 601
DB 541 TFGDIRLNINPLSQRYRVRIRYASTDLOPHTRINGTWNIGNFSRTMNRGDNLEYSF 600

QY 602 XTGVFTTFFLLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 661
DB 601 RTAGFSTFPFNFLNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFEAEYDLERAQKAVNA 659

QY 662 LFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKRELFEIVKAKOLHIERNM 718
DB 660 LFTSTNPRRLKTDVTDHYDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLSDERNL 716
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RESULT 10
US-08-779-046-4
Sequence 4, Application US/08779046
Patent No. 5854053
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jan, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-046-4
```

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Query Match      64.4%; Score 2415; DB 2; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDCLKMSYENVEPVFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQOVTRNTAIAARLEG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVKQYIALELMFVQKLPFAVSGEVEPLLPPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPFLMVA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSYHCVKYSTGLNLRGTN 250
DB 187 QAAHLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSYHCVKYSTGLNLRGTN 246

QY 251 AESWRYNQFRDMLTMDLVALFPPSYDTQMPYIKTTAQLTREYVTDATGTVHPHPSFT 310
DB 247 AESWLRYNQFRDLTLGVLDLVALFPPSYDTRTPINTSAQLTREIYDPIGRNAPSFA 306

QY 311 STTWYNNAPFSAIEAAVVRNPVHLLDFLEQVITYSLSRWSNTQYMMNMGHKLFRPTI 370
DB 307 STNWFNNAPFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMYVWGHRLNRP 366

QY 371 GGTLLNSTQGST-NTSINPVTLPFTSRDVRVTSAGLNLFLTPQVN-VPRVDFHWKFW 428
DB 367 GGTLLNSTQGLTNTNTSINPVTLPFTSRDVRVTSAGLNLFLTPQVNVPWAFRNF 422

QY 429 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLISAS 481
DB 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPETTERPNYESYSHRLSHIGLI 480

QY 482 HVKALVYSWTHRSADRTNTRIPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRNTG 541
DB 481 TLRAPVYSWTHRSADRTNTRIPNRTIQIPLVKALNLHSGTVVGGPGFTGGDILRRNTG 540

QY 542 TFGDIRVNINPFAQYRVRIRYASTDLOPHTSINGKAINQGNFSAWNRGDDLYKTF 601
DB 541 TFGDIRLNINPLSQRYRVRIRYASTDLOPHTRINGTWNIGNFSRTMNRGDNLEYSF 600

QY 602 XTGVFTTFFLLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 661
DB 601 RTAGFSTFPFNFLNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFEAEYDLERAQKAVNA 659

QY 662 LFTSTNPRGLKTDVKDHYDQVNLVESLSDEFYLDKRELFEIVKAKOLHIERNM 718
DB 660 LFTSTNPRRLKTDVTDHYDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLSDERNL 716
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Tue Feb 15 10:07:49 2005

127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPFRIRNEBVLIMVYA 186
191 QANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWSYGLNNLRGTN 250
187 QANLHLLLDASLFGSEWGMASDVNQYQEQIRYEEYSHCVQWYNTGLNNLRGTN 246
251 AESWVRNQFRDMTLMVLDVALPSPYDTQWYPIKTTAQLTREYVYDAIGTVHPHSFT 310
247 AESWLRNQFRDRLTLGVLDLVALPSPYDTQWYPIKTTAQLTREYVYDAIGTVHPHSFT 306
311 STTWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYMMWGGHKLFRFTI 370
307 STWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYMMWGGHKLFRFTI 366
371 GGTNLNISTQGST-NTSINPVTLPFTSRDVTRESLGLNLFLTOPVN-VPRVDFHMKFVT 428
367 GGTNLNISTQGST-NTSINPVTLPFTSRDVTRESLGLNLFLTOPVN-VPRVDFHMKFVT 422
429 HPIASDNFYYPG-----YAGITQLODSNELPPEATQPNVYESYSHLSHIGLISAS 481
423 --INPQNIYERGATTYSQPYQGVIGLFDSELTPEPTTERPNVYESYSHLSHIGLISAS 480
482 HVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRWTG 541
481 TLRAVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRWTG 540
542 TFGDIRVNINPPLPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTYTF 601
541 TFGDIRVNINPPLPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTYTF 600
602 XTVGFTTTPSLLDVQSTFTIGANVSSNEVYDRIEFVPEVTVYEAEDFEKAEKVTA 661
601 RTAGFSTPFNFNAQSTFTLGAQSFN-QEVIYDRVFPVPAEVTFAEYDLERAKAVNA 659
662 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
660 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-881-340-4

Query Match 64.4%; Score 2415; DB 2; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;
13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDCIKMSVENVPEVFPVSASTQTGTGIGIAGKI 70
7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNIDPFPVSASTVQTGINIAGRI 66
71 LGTLGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
67 LGVLGVFPAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQQVTRNTARLEG 126
131 LGDALAVYHDSLSLVGNGNRNTRARSVKSYQYIALELMFVKLPSPAVSGEVPVLLPIYA 190

RESULT 12

US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758

GENERAL INFORMATION:

APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve

TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,170

FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 424


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 61.9%; Score 2319; DB 1; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.3e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSIKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKSKQNQHQSLSNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIQKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGQWEIFMEHVVEELINQISTYA 111

Qy 121 RNKALTDLKGDLALAVYHDSLEWVGNNRNNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWIENRNNTRRSVVKSQYITLELMFVQSLPSPFAVSG 171

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISITFYNNRQVERAGDYSYHCVKWS 240
Db 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISITFYNNRQSGKSEYSDHCVKWYN 231

Qy 241 TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREYVTDI 300
Db 232 TGLNRLMGNNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 292 GTVHPHPSFTSTTWYNNNAPSFSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 351

Query Match 61.9%; Score 2319; DB 3; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.3e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSIKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKSKQNQHQSLSNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIQKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGQWEIFMEHVVEELINQISTYA 111

Qy 121 RNKALTDLKGDLALAVYHDSLEWVGNNRNNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWIENRNNTRRSVVKSQYITLELMFVQSLPSPFAVSG 171

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISITFYNNRQVERAGDYSYHCVKWS 240
Db 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISITFYNNRQSGKSEYSDHCVKWYN 231

Qy 241 TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREYVTDI 300
Db 232 TGLNRLMGNNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 292 GTVHPHPSFTSTTWYNNNAPSFSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 351

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 61.9%; Score 2319; DB 3; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.3e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSIKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKSKQNQHQSLSNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIQKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGQWEIFMEHVVEELINQISTYA 111

Qy 121 RNKALTDLKGDLALAVYHDSLEWVGNNRNNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWIENRNNTRRSVVKSQYITLELMFVQSLPSPFAVSG 171

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISITFYNNRQVERAGDYSYHCVKWS 240
Db 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISITFYNNRQSGKSEYSDHCVKWYN 231

Qy 241 TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREYVTDI 300
Db 232 TGLNRLMGNNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 292 GTVHPHPSFTSTTWYNNNAPSFSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 351

; TITLE OF INVENTION: Bacillus thuringiensis Isolate Denoted
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
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QY 361 GGKLEFRITGGTINISQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNVPR 419
Db 352 GGKLEFRITGGTINISQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNVPR 411
QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPPEATGQPNYESYSHRLSHIGLIS 479
Db 412 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPPEATGQPNYESYSHRLSHIGLIS 471
QY 480 ASHKALVYSWTHRSAD 496
Db 472 ASHKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-951-715A-7

Query Match 59.6%; Score 2236; DB 1; Length 1207;

Best Local Similarity 63.9%; Pred. No. 2.8e-191;
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;
QY 40 EDCIKMSYENVEPVSASTIQTGTIGIAGIKLTGLVPPAGQVASYLSFILGELWPKGN 99
Db 10 EDSLCIAEGNNIDPFVSASTVQTGINIAGRILGLVGPVAGQVASYLSFILGELWPKGN 69
QY 100 QWEIFMEHVEEIIINOKISTYARNKALTDLKGGLDALAVVHDSLESVGNRNTRARSVVK 159
Db 70 QWEIFMEHVEEIIINOKISTYARNKALTDLKGGLDALAVVHDSLESVGNRNTRARSVVK 129
QY 160 SQYIALELMFVQKLPSPAVSGEEVPLPIYAAQANLHLLLRDASIFGKELSSSEIST 219
Db 130 TOYIALELDFLNAMPLFAIRNQEVPLLMVYAAQANLHLLLRDASIFGKELSSSEIST 189
QY 220 FYNROVERAGDYSYHCVKMYSTGLNNLRGTNAESWRYNOFRDRMTLMLDLVALFPSYD 279
Db 190 YFERQVTRDYSYHCVKMYSTGLNNLRGTNAESWRYNOFRDRMTLMLDLVALFPSYD 249
QY 280 TOMYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFL 339
Db 250 TRTYPINTSAQLTREVTDAIGTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFL 307
QY 340 EQVTIYSLRSWNTQYMMWGGHKLERTIGTTLNTSTQGSTNTSINPVTLPFTSRDVS 399
Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDVS 367
QY 400 RTESLAGLNLF--LTQPVN--VPRVDFHWKFVTHP-----IASDNFYYPGYAGIGTQLODS 451
Db 368 RTESYAGVLLWGIYLEPIHGVTVRNF--TNPQNISDRGTANYSQP--YESPGQLKDS 423
QY 452 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 511
Db 424 ETELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 483
QY 512 VKAFNLSSGAADVVRGPGFTGGDILRRTNTGTGDIRVNIINPFAQRYRVRIRYASTDLQ 571
Db 484 VKASELPQGTTVVRGPGFTGGDILRRTNTGTGDIRVNIINPFAQRYRVRIRYASTDLQ 543
QY 572 FHTSINKAINQGNFSATMNRGDELDTFTXVTGFTTTPFSLDLVQSTFTIGAWNFSGNE 631
Db 544 FVSRGGTTVNNFRFLRTMNSGDELKYGVRRAFTTFTTQIOTDIIRTSIQGLSNGE 603
QY 632 VYIDRIEFVPEVTEAEYDEKAEQKVLTFTSTNPRGLKTDVYHIDQVSNLVESLS 691
Db 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRKLTVDYHIDQVSNLVESLS 663
QY 692 DEFYLDKRELFEIVKYAKQIHIERNM 718
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.2147 Seconds
(without alignments)
2827.419 Million cell updates/sec

Title: US-10-019-823B-54
Perfect score: 3749
Sequence: 1 MKLKNQDKHQSPSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3747	99.9	718	4 AAB66907	Aab66907 Insectici
2	3747	99.9	718	6 AAE36271	Aae36271 B. thurin
3	3736.5	99.7	719	2 AAR08041	Aar08041 81 kD end
4	3732.5	99.6	719	4 AAU02095	Aau02095 Bacillus
5	3724.5	99.3	719	4 AAB66909	Aab66909 Insectici
6	3724.5	99.3	719	6 AAE36273	Aae36273 B. thurin
7	3722.5	99.3	719	4 AAB66908	Aab66908 Insectici
8	3722.5	99.3	719	6 AAE36272	Aae36272 B. thurin
9	3722.5	99.3	719	8 ADR89421	Adr89421 crylla. 1
10	3718.5	99.2	719	4 AAB66910	Aab66910 Insectici
11	3718.5	99.2	719	6 AAE36274	Aae36274 B. thurin
12	3711.5	99.0	719	4 AAB66911	Aab66911 Insectici
13	3711.5	99.0	719	6 AAE36275	Aae36275 B. thurin
14	3513.5	93.7	719	7 ADM74717	Adm74717 B. thurin
15	3482.5	92.9	719	4 AAB66912	Aab66912 Insectici
16	3482.5	92.9	719	6 AAE36276	Aae36276 B. thurin
17	3439	91.7	710	4 AAU02041	Aau02041 B. thurin
18	3359.5	89.6	719	3 ABB07073	Abb07073 Bacillus
19	3358.5	89.6	719	2 AAW49089	Aaw49089 Bacillus
20	3280.5	87.5	719	2 AAU02092	Aau02092 Bacillus
21	2704.5	72.1	1208	4 AAU02093	Aau02093 Bacillus
22	2416.5	64.5	1230	8 ADK98484	Adk98484 B thuring
23	2416.5	64.5	1230	8 ADK98489	Adk98489 B thuring
24	2416.5	64.5	1230	8 ADK98481	Adk98481 B thuring
25	2416.5	64.5	1230	8 ADK98491	Adk98491 B thuring

26	2416.5	64.5	1230	8 ADK98487	Adk98487 B thuring
27	2415	64.4	1229	2 AAR54074	Aar54074 CryET5. 2
28	2415	64.4	1229	2 AAW35259	Aaw35259 Bacillus
29	2415	64.4	1229	2 AAW17699	Aaw17699 CryET5. 3
30	2415	64.4	1229	2 AAW87633	Aaw87633 CryET5 pr
31	2415	64.4	1229	2 AAY30923	Aay30923 B. thurin
32	2415	64.4	1229	8 ADK98479	Adk98479 B thuring
33	2319	61.9	488	2 AAW44322	Aaw44322 Bacillus
34	2319	61.9	488	4 AAB19947	Aab19947 Bacillus
35	2249	60.0	1228	2 AAR50955	Aar50955 Bacillus
36	2244	59.9	1209	4 AAU02094	Aau02094 Bacillus
37	2235	59.6	1227	2 AAY31990	Aay31990 Chimeric
38	2165	57.7	1227	2 AAW44321	Aaw44321 Bacillus
39	2165	57.7	1227	4 AAB19950	Aab19950 Bacillus
40	2156	57.5	1227	4 AAU02046	Aau02046 B. thurin
41	2141	57.1	1186	2 AAY16796	Aay16796 Amino aci
42	2121	56.6	1221	4 AAU00421	Aau00421 B. thurin
43	2107	56.2	1221	4 AAU00420	Aau00420 B. thurin
44	2085.5	55.6	1228	4 AAB84628	Aab84628 Amino aci
45	2085.5	55.6	1228	4 AAU02039	Aau02039 B. thurin

ALIGNMENTS

RESULT 1
AAB66907
ID AAB66907 standard; protein; 718 AA.
XX
AC AAB66907;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIaI.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
production.
XX
PS Claim 14; Page 53-55; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66909 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 718 AA;

Query Match 99.9%; Score 3747; DB 4; Length 718;
Best Local Similarity 100.0%; Pred. No. 9.4e-296;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
Db
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
Db
QY 61 QTGIGIAGKILGTGLGVPFAGQVASYLFGELMWPKNQWEIFMEHVEEIIINQKISTYA 120
Db
QY 61 QTGIGIAGKILGTGLGVPFAGQVASYLFGELMWPKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180
Db
QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLVDLVALFSPSYDTQMPYIKTTAQLTREYVTDAL 300
Db
QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLVDLVALFSPSYDTQMPYIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNPRV 420
Db
QY 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNPRV 420
QY 421 DFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISA 480
Db
QY 421 DFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISA 480
QY 481 SHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRNT 540
Db
QY 481 SHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRNT 540
QY 541 GTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKT 600
Db
QY 541 GTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKT 600
QY 601 FXTVGFTTFFSLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVT 660
Db
QY 601 FXTVGFTTFFSLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVT 660
QY 661 ALFTSTNPRGLKTDVKDHYHIDQVSNLVSDEFLDEKRELFEIVKYAKQLHIERNM 718
Db
QY 661 ALFTSTNPRGLKTDVKDHYHIDQVSNLVSDEFLDEKRELFEIVKYAKQLHIERNM 718

RESULT 2
AAE36271
ID AAE36271 standard; protein; 718 AA.
XX AC AAE36271;
XX DT 26-JUN-2003 (first entry)
XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.
XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX OS Bacillus thuringiensis.
XX PN WO2000298911-A2.
PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-GB002666.
XX PR 07-JUN-2001; 2001GB-00013900.
XX PA (SYGN) SYNGENTA LTD.
XX XX

PI Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
XX Claim 12; Page 42-44; 67pp; English.
XX
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX
XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
XX
XX Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
XX Sequence 718 AA;
XX

Query Match 99.9%; Score 3747; DB 6; Length 718;
Best Local Similarity 99.9%; Pred. No. 9.4e-296;
Matches 717; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
Db
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
Db
QY 61 QTGIGIAGKILGTGLGVPFAGQVASYLFGELMWPKNQWEIFMEHVEEIIINQKISTYA 120
Db
QY 61 QTGIGIAGKILGTGLGVPFAGQVASYLFGELMWPKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180
Db
QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLVDLVALFSPSYDTQMPYIKTTAQLTREYVTDAL 300
Db
QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLVDLVALFSPSYDTQMPYIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNPRV 420
Db
QY 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNPRV 420
QY 421 DFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISA 480
Db
QY 421 DFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISA 480
QY 481 SHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRNT 540
Db
QY 481 SHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRNT 540
QY 541 GTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKT 600
Db
QY 541 GTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKT 600
QY 601 FXTVGFTTFFSLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVT 660
Db
QY 601 FXTVGFTTFFSLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVT 660
QY 661 ALFTSTNPRGLKTDVKDHYHIDQVSNLVSDEFLDEKRELFEIVKYAKQLHIERNM 718
Db
QY 661 ALFTSTNPRGLKTDVKDHYHIDQVSNLVSDEFLDEKRELFEIVKYAKQLHIERNM 718

CC and II, to make the hybrid protoxins of the invention. The hybrid toxins
CC of the invention, having structural domains I, II and III in this order
CC starting from the N-terminal derived from at least 2 different crystal
CC proteins, are useful for protecting plants against pest insects, e.g.
CC moths, butterflies and Colorado potato beetle or for combating insects
XX
SQ Sequence 719 AA;

Query Match 99.6%; Score 3732.5; DB 4; Length 719;
Best Local Similarity 99.6%; Pred. No. 1.4e-294;
Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240

QY 241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S F T S T T W Y N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 360
Db 301 G T V H P H P S F T S T T W Y N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 360

QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419
Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419

QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479
Db 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479

QY 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539
Db 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539

QY 540 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599
Db 540 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599

RESULT 5
ID AAB66909 standard; protein; 719 AA.
XX
AC AAB66909;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa3.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX

Paecilomyces sp.
WO200100841-A1.
04-JAN-2001.
23-JUN-2000; 2000WO-GB002457.
29-JUN-1999; 99GB-00015215.
23-DEC-1999; 99GB-00030536.
(ZENE) ZENECA LTD.
Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
Vincent JL, Lee MD;
WPI; 2001-123015/13.
Novel insecticidal protein obtained from species of Paecilomyces for
controlling insects, and for insect-resistant transgenic plant
production.
Claim 14; Page 57-59; 72pp; English.
The present invention relates to novel insecticidal proteins obtained
from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
insecticidal proteins can be used to produce transgenic plants, which are
insect-resistant. Also, the insecticidal proteins are useful for
controlling insects by providing them at a locus where insects feed
Sequence 719 AA;

Query Match 99.3%; Score 3724.5; DB 4; Length 719;
Best Local Similarity 99.3%; Pred. No. 6.4e-294;
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240

QY 241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S F T S T T W Y N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 360
Db 301 G T V H P H P S F T S T T W Y N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 360

QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419
Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419

QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479
Db 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479

QY 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539
Db 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539

QY 540 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599
Db 540 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599

Db 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFNSATMNGEDLDYK 600
Qy 600 TFXTVGTTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQSKV 659
Db 601 TFRVTGTTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQSKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEEYLDKRELFEIVKAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEEYLDKRELFEIVKAKQLHIERNM 719

RESULT 6
AAE36273
ID AAE36273 standard; protein; 719 AA.
XX
AC AAE36273;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT
XX
PS Claim 12; Page 47-50; 67pp; English.
XX
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 719 AA;
Query Match 99.3%; Score 3724.5; DB 6; Length 719;
Best Local Similarity 99.3%; Pred. No. 6.4e-294;
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120
Qy 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVKWSQYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVKWSQYIALELMFVQKLPFAVSG 180

Qy 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSYHCVKWYS 240
Db 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSYHCVKWYS 240
Qy 241 TGLNNLRGTNAESWRYNQPRRDMTLMVLDLVALFPSPDYDTOMYPIKTTAQLTREVYTDAI 300
Db 241 TGLNNLRGTNAESWRYNQPRRDMTLMVLDLVALFPSPDYDTOMYPIKTTAQLTREVYTDAI 300
Qy 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDLFLEQVTIYLSLSRWSNTQYMMNM 360
Db 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDLFLEQVTIYLSLSRWSNTQYMMNM 360
Qy 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESIAGLNLFLTQPVN-VPR 419
Db 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESIAGLNLFLTQPVN-VPR 420
Qy 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 540 TGTFGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFNSATMNGEDLDYK 599
Db 541 TGTFGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFNSATMNGEDLDYK 600
Qy 600 TFXTVGTTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQSKV 659
Db 601 TFRVTGTTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQSKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEEYLDKRELFEIVKAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEEYLDKRELFEIVKAKQLHIERNM 719

RESULT 7
AAB66908
ID AAB66908 standard; protein; 719 AA.
XX
AC AAB66908;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa2.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
XX
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.
XX
PS Claim 14; Page 55-57; 72pp; English.
XX

CC The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

Query Match 99.3%; Score 3722.5; DB 4; Length 719;
Best Local Similarity 99.4%; Pred. No. 9.3e-294;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180

QY 181 EVVPLPIYAQAANLHLLLRDASIFGKESWGLSSSEISTFYNNQVRAGDYSYHCVKWS 240
DB 181 EVVPLPIYAQAANLHLLLRDASIFGKESWGLSSSEISTFYNNQVRAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMNW 360
DB 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMNW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNV-VR 419
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNV-VR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELEPPPEATGQPNYESYSHRLSHIGLIS 479
DB 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELEPPPEATGQPNYESYSHRLSHIGLIS 479

QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
DB 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539

QY 540 TGTGDIRVNNPFAQRYRIRYASTTDIQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
DB 540 TGTGDIRVNNPFAQRYRIRYASTTDIQFHTSINGKAINQGNFSAATMNRGEDLDYK 599

QY 600 TFXTVGFTTFFSLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659
DB 600 TFXTVGFTTFFSLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659

QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLDEYFVDEKRELFEIVKAKQLHIERNM 718
DB 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLDEYFVDEKRELFEIVKAKQLHIERNM 718

RESULT 8
ID AAE36272 standard; protein; 719 AA.
XX AAE36272;
AC AAE36272;
XX AAE36272;
DT 26-JUN-2003 (first entry)
XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX

OS Bacillus thuringiensis.
XX WO200298911-A2.
PN 12-DEC-2002.
PD 30-MAY-2002; 2002WO-GB002666.
PF 07-JUN-2001; 2001GB-00013900.
XX (SYGN) SYNGENTA LTD.
PR Vincent J.L, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PS Claim 12; Page 44-47; 67pp; English.
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX Sequence 719 AA;

Query Match 99.3%; Score 3722.5; DB 6; Length 719;
Best Local Similarity 99.4%; Pred. No. 9.3e-294;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180

QY 181 EVVPLPIYAQAANLHLLLRDASIFGKESWGLSSSEISTFYNNQVRAGDYSYHCVKWS 240
DB 181 EVVPLPIYAQAANLHLLLRDASIFGKESWGLSSSEISTFYNNQVRAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMNW 360
DB 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMNW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNV-VR 419
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNV-VR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELEPPPEATGQPNYESYSHRLSHIGLIS 479
DB 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELEPPPEATGQPNYESYSHRLSHIGLIS 479

QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
DB 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539

QY 540 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 599
|||||
Db 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
|||||
QY 600 TFXTVGFTTFFSLDLVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659
|||||
Db 601 TFRTVGFTTFFSLDLVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
|||||
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
|||||
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
|||||

RESULT 9
ADR89421
ID ADR89421 standard; protein; 719 AA.
XX
AC ADR89421;
XX
DT 18-NOV-2004 (first entry)
XX
DE cryIIa.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX
DR WPI; 2004-635574/61.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Example 6; SEQ ID NO 33; 178pp; English.

XX
CC This sequence represents a delta-endotoxin crystal protein. This protein
CC was included in the scope of the invention as a comparison to the delta-
CC endotoxins of the invention. Some of the delta-endotoxin coding sequences
CC of the invention have alternative start codons, producing more than one
CC protein from a single open reading frame. The nucleic acid sequences of
CC the invention are useful in DNA constructs or expression cassettes for
CC transformation and expression in plants and bacteria. The nucleic acids
CC and corresponding polypeptides are useful for killing lepidopteran or
CC coleopteran pests. Compositions containing the delta-endotoxins of the
CC invention, and methods for their production, are useful for the
CC production of organisms with pesticide resistance, specifically bacteria
CC and plants. These organisms are useful for generating altered or improved

CC delta-endotoxin or delta-endotoxin-associated proteins that have
CC pesticidal activity, or for detecting the presence of delta-endotoxin or
CC delta-endotoxin-associated proteins or nucleic acids in products or
CC organisms.
XX
SQ Sequence 719 AA;
Query Match 99.3%; Score 3722.5; DB 8; Length 719;
Best Local Similarity 99.4%; Pred. No. 9.3e-294;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60
|||||
Db 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60
|||||
QY 61 QTGIGIAGKILGTGLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
|||||
Db 61 QTGIGIAGKILGTGLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
|||||
QY 121 RNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMEVQKLPSPFAVSG 180
|||||
Db 121 RNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMEVQKLPSPFAVSG 180
|||||
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSYHCVKWS 240
|||||
Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSYHCVKWS 240
|||||
QY 241 TGLNLRGTNAESWVRYNQFRDRMTLMVLVLPSPSYDTQMPYIKTTAQLTRVYTDAL 300
|||||
Db 241 TGLNLRGTNAESWVRYNQFRDRMTLMVLVLPSPSYDTQMPYIKTTAQLTRVYTDAL 300
|||||
QY 301 GTVHPHPSFTSTTWYNNAPSFSIAEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 360
|||||
Db 301 GTVHPHPSFTSTTWYNNAPSFSIAEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 360
|||||
QY 361 GGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419
|||||
Db 361 GGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 420
|||||
QY 420 VDFHWKPVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479
|||||
Db 421 VDFHWKPVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
|||||
QY 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
|||||
Db 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
|||||
QY 540 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 599
|||||
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
|||||
QY 600 TFXTVGFTTFFSLDLVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659
|||||
Db 601 TFRTVGFTTFFSLDLVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
|||||
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
|||||
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
|||||

RESULT 10
AAB66910
ID AAB66910 standard; protein; 719 AA.
XX
AC AAB66910;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa4.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.

Tue Feb 15 10:07:49 2005

XX WO200100841-A1.
XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
XX 29-JUN-1999; 99GB-00015215.
XX 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
XX Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
XX Novel insecticidal protein obtained from species of Paecilomyces for
XX controlling insects, and for insect-resistant transgenic plant
XX production.
XX Claim 14; Page 60-62; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained
XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
XX insecticidal proteins can be used to produce transgenic plants, which are
XX insect-resistant. Also, the insecticidal proteins are useful for
XX controlling insects by providing them at a locus where insects feed
XX
XX Sequence 719 AA;
SQ Query Match 99.2%; Score 3718.5; DB 4; Length 719;
Best Local Similarity 99.3%; Pred. No. 2e-293; Indels 1; Gaps 1;
Matches 714; Conservative 0; Mismatches 4;
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSEAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSEAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFTFNQVERAGDYSYHCVKWS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFTFNQVERAGDYSYHCVKWS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMDTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMDTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300
QY 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRTIGTTLNISTQSTNTSINPVTLPFTRSDRYRTESLAGNLFITQPVN-VPR 419
DB 361 GGHKLEFRTIGTTLNISTQSTNTSINPVTLPFTRSDRYRTESLAGNLFITQPVN-VPR 420
QY 420 VDFHWKFTVTHPIASDNFYYPGYAGTQLODSENELPPEATQPNVYESYHRLSHIGLIS 479
DB 421 VDFHWKFTVTHPIASDNFYYPGYAGTQLODSENELPPEATQPNVYESYHRLSHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRTN 539
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 599
DB 540 TGTGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 599

DB 541 TGTGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600
QY 600 TFXTVGFTTPESLDDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 659
DB 601 TFXTVGFTTPESLDDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFVLDKRELFEIVKYAKQLHIERNM 718
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFVLDKRELFEIVKYAKQLHIERNM 719
RESULT 11
AAE36274
ID AAE36274 standard; protein; 719 AA.
XX AAE36274;
AC AAE36274;
XX 26-JUN-2003 (first entry)
DT B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
DE Bacillus thuringiensis.
XX WO200298911-A2.
XX 12-DEC-2002.
XX 30-MAY-2002; 2002WO-GB002666.
XX 07-JUN-2001; 2001GB-00013900.
XX (SYGN) SYNGENTA LTD.
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Claim 12; Page 50-53; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX Sequence 719 AA;
SQ Query Match 99.2%; Score 3718.5; DB 6; Length 719;
Best Local Similarity 99.3%; Pred. No. 2e-293; Indels 1; Gaps 1;
Matches 714; Conservative 0; Mismatches 4;
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSEAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKLPSEAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFTFNQVERAGDYSYHCVKWS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFTFNQVERAGDYSYHCVKWS 240

Db 181 EEVPLPIYAQAANLHLLLDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVKWYS 240
Qy 241 TGLNLRGTNAESWRYNQPRDMLMVLVALFPSPYDTQMPYPIKTTAQLTREYVYDAI 300
Db 241 TGLNLRGTNAESWRYNQPRDMLMVLVALFPSPYDTQMPYPIKTTAQLTREYVYDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 479
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 540 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 599
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Qy 600 TFXTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 659
Db 601 TFRTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12
AAB66911
ID AAB66911 standard; protein; 719 AA.
XX AC AAB66911;
XX DT 12-APR-2001 (first entry)
XX DE Insecticidal protein cryIIa5.
XX KW Insecticide; transgenic plant; insect-resistance.
XX OS Paecilomyces sp.
XX PN WO200100841-A1.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-GB002457.
XX PR 29-JUN-1999; 99GB-00015215.
XX PR 23-DEC-1999; 99GB-00030536.
XX PA (ZENE) ZENECA LTD.
XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
XX PI Vincent JL, Lee MD;
XX DR WPI; 2001-123015/13.
XX PT Novel insecticidal protein obtained from species of Paecilomyces for
XX PT controlling insects, and for insect-resistant transgenic plant
XX PT production.
XX PS Claim 14; Page 62-64; 72pp; English.
XX CC The present invention relates to novel insecticidal proteins obtained

CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX SQ Sequence 719 AA;
Query Match 99.0%; Score 3711.5; DB 4; Length 719;
Best Local Similarity 99.0%; Pred. No. 7.4e-293;
Matches 712; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNEDTIELQINIHEDCLKMSEVENVEFVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNEDTIELQINIHEDCLKMSEVENVEFVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFTLGELMPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFTLGELMPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTARSVVKSOYIALELMFVQKLPSFAVSG 180
Db 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTARSVVKSOYIALELMFVQKLPSFAVSG 180
Qy 181 BEVPLPIYAQAANLHLLLDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVKWYS 240
Db 181 BEVPLPIYAQAANLHLLLDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVKWYS 240
Qy 241 TGLNLRGTNAESWRYNQPRDMLMVLVALFPSPYDTQMPYPIKTTAQLTREYVYDAI 300
Db 241 TGLNLRGTNAESWRYNQPRDMLMVLVALFPSPYDTQMPYPIKTTAQLTREYVYDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 479
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 540 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 599
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Qy 600 TFXTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 659
Db 601 TFRTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
RESULT 13
AAE36275
ID AAE36275 standard; protein; 719 AA.
XX AC AAE36275;
XX DT 26-JUN-2003 (first entry)
XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.
XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX OS Bacillus thuringiensis.

XX	PN	WO200298911-A2.	Db	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLPHTSINGKAINQGNFSATMNRGEDLDYK	600
XX	PD	12-DEC-2002.	QY	600	TFXTVGTTPPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV	659
XX	PF	30-MAY-2002; 2002WO-GB002666.	Db	601	TFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV	660
XX	PR	07-JUN-2001; 2001GB-00013900.	QY	660	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKRELFELVYKAKOLHIERNM	718
XX	PA	(SYGN) SYNGENTA LTD.	Db	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKRELFELVYKAKOLHIERNM	719
XX	PI	Vincent JL, Viner R;				
XX	XX	WPI; 2003-175137/17.				
XX	DR	New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.				
XX	PT	Claim 12; Page 53-56; 67pp; English.				
XX	PS	The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.				
XX	CC	Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention				
XX	CC	Sequence 719 AA;				
XX	SQ	Query Match 99.0%; Score 3711.5; DB 6; Length 719; Best Local Similarity 99.0%; Pred. No. 7.4e-293; Matches 712; Conservative 2; Mismatches 4; Indels 1; Gaps 1;				
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFVSASTI	QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFVSASTI	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFVSASTI	Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFVSASTI	60
QY	61	QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA	QY	61	QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA	120
Db	61	QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA	Db	61	QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA	120
QY	121	RNKALTDLKLGLDALAYVHDSLESWVGNNRNNTRARSVKSQYIALELMFVQKLPFAVSG	QY	121	RNKALTDLKLGLDALAYVHDSLESWVGNNRNNTRARSVKSQYIALELMFVQKLPFAVSG	180
Db	121	RNKALTDLKLGLDALAYVHDSLESWVGNNRNNTRARSVKSQYIALELMFVQKLPFAVSG	Db	121	RNKALTDLKLGLDALAYVHDSLESWVGNNRNNTRARSVKSQYIALELMFVQKLPFAVSG	180
QY	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS	QY	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS	240
Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS	Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS	240
QY	241	TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYPIKTTAQLTREVYTDAL	QY	241	TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYPIKTTAQLTREVYTDAL	300
Db	241	TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYPIKTTAQLTREVYTDAL	Db	241	TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYPIKTTAQLTREVYTDAL	300
QY	301	GTVHPHPSFTSTTWNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSTNQYMMNW	QY	301	GTVHPHPSFTSTTWNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSTNQYMMNW	360
Db	301	GTVHPHPSFTSTTWNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSTNQYMMNW	Db	301	GTVHPHPSFTSTTWNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSTNQYMMNW	360
QY	361	GCHKLEFRITGGTLNISTOGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR	QY	361	GCHKLEFRITGGTLNISTOGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR	419
Db	361	GCHKLEFRITGGTLNISTOGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR	Db	361	GCHKLEFRITGGTLNISTOGSTNTSINPVLPTSRDVRTESLAGLNFLTQPVN-VPR	420
QY	420	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS	QY	420	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS	479
Db	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS	Db	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS	480
QY	480	ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGGAHVVRGPGTGGDILRRTN	QY	480	ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGGAHVVRGPGTGGDILRRTN	539
Db	481	ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGGAHVVRGPGTGGDILRRTN	Db	481	ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGGAHVVRGPGTGGDILRRTN	540
QY	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLPHTSINGKAINQGNFSATMNRGEDLDYK	QY	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLPHTSINGKAINQGNFSATMNRGEDLDYK	599

Db 121 RNIALADUKGLDALAVHESLESWKNNRATSVKQYIALELLFVKQLPSFAVSG 180
Qy 181 EEVPLLPYQAANLHLLLRDASIFGKESWGLSSSEISTFYNNROVERAGDYSVHCWKYS 240
Db 181 EEVPLLPYQAANLHLLLRDASVFGKESWGLSNSQISTFYNNROVERTSDYSDHCWKYS 240
Qy 241 TGLNLRGCTNAESWVRNQFRDMLVLDLVALPSPYDQMYPIKTTAQLTREVTYDAI 300
Db 241 TGLNLRGCTNAESWVRNQFRDMLVLDLVALPSPYDQMYPIKTTAQLTREVTYDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIAAARNVPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
Db 301 GTVHPNASFASTWYNNAPSFSAIAESAVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 420 VDFHWKFTVHTPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHWKFTATLPASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 540 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 600 TFXTVGFTTPEFSLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 659
Db 601 TFRFTIGFTTPEFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQIHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQIHIERNM 719

RESULT 15
AAB66912
ID AAB66912 standard; protein; 719 AA.

XX AAB66912;
AC AAB66912;
XX 12-APR-2001 (first entry)
XX Insecticidal protein cryIb1.
DE Insecticide; transgenic plant; insect-resistance.
XX Paecilomyces sp.
XX WO200100841-A1.
XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
XX 29-JUN-1999; 99GB-00015215.
XX 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.

XX Claim 14; Page 64-66; 72pp; English.
PS The present invention relates to novel insecticidal proteins obtained
XX from Paecilomyces sp. (see AAB66899 to AAB6901 and AAB6913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;
SQ
Query Match 92.9%; Score 3482.5; DB 4; Length 719;
Best Local Similarity 92.4%; Pred. No. 3.2e-274;
Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;
Qy 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVFVASTI 60
Db 1 MKLKNPDKHOSLSSNAKVDKIATDSLKNETDIELQNMNEDYLRMSEHESIDPFVASTI 60
Qy 61 QTGIGTAGKILGTGVPFAGQIASLYSFTILGELWPKGKQWEIFMEHVVEIINQKILTYA 120
Db 61 QTGIGTAGKILGTGVPFAGQIASLYSFTILGELWPKGKQWEIFMEHVVEIINQKILTYA 120
Qy 121 RNKALTDKGLGDALAVYHDSLESWVGNRNNTARSVVKSQYIALELMPVKQLPSFAVSG 180
Db 121 RNKALSDRLGDLALAVYHDSLESWVENNTRARSVVKQYIALELMPVKQLPSFAVSG 180
Qy 181 BEVPLLPYQAANLHLLLRDASIFGKESWGLSSSEISTFYNNROVERAGDYSVHCWKYS 240
Db 181 BEVPLLPYQAANLHLLLRDASIFGKESWGLSSSEISTFYNNROVERTSDYSDHCWKYN 240
Qy 241 TGLNLRGCTNAESWVRNQFRDMLVLDLVALPSPYDQMYPIKTTAQLTREVTYDAI 300
Db 241 TGLNLRGCTNAESWVRNQFRDMLVLDLVALPSPYDQMYPIKTTAQLTREVTYDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIAAARNVPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
Db 301 GTVHPNQAFASFTWYNNAPSFSAIAAARVSRPHLLDFLEKVTIYSLSRWSNTQYMNW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419
Db 361 GGHKLESRPISGALNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 420 VDFHWKFTVHTPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHWKFTPLPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 480 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 540 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 600 TFXTVGFTTPEFSLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 659
Db 601 TFRFTIGFTTPEFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 660
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQIHIERNM 718
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQIHIERNM 719

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OM protein - protein search, using sw model

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(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-54
Perfect score: 3749
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3718.5	99.2	719	3 US-08-286-870A-8	Sequence 8, Appli
2	3439	91.7	710	4 US-09-661-322A-42	Sequence 42, Appl
3	3360.5	89.6	648	3 US-08-286-870A-4	Sequence 4, Appli
4	3358.5	89.6	719	2 US-09-003-217-2	Sequence 2, Appli
5	3356.5	89.5	719	3 US-09-218-942-2	Sequence 2, Appli
6	2778.5	74.1	535	3 US-08-286-870A-6	Sequence 6, Appli
7	2415	64.4	1229	1 US-08-100-709-4	Sequence 4, Appli
8	2415	64.4	1229	1 US-08-176-865-4	Sequence 4, Appli
9	2415	64.4	1229	1 US-08-474-038-4	Sequence 4, Appli
10	2415	64.4	1229	2 US-08-779-046-4	Sequence 4, Appli
11	2415	64.4	1229	2 US-08-881-340-4	Sequence 4, Appli
12	2319	61.9	488	1 US-08-448-170-10	Sequence 10, Appl
13	2319	61.9	488	3 US-08-961-803-10	Sequence 10, Appl
14	2236	59.6	1207	1 US-07-951-715A-7	Sequence 7, Appli
15	2236	59.6	1207	2 US-08-459-448A-7	Sequence 7, Appli
16	2236	59.6	1207	3 US-08-459-595A-7	Sequence 7, Appli
17	2236	59.6	1207	3 US-08-459-504B-7	Sequence 7, Appli
18	2236	59.6	1207	3 US-08-459-444-7	Sequence 7, Appli
19	2236	59.6	1207	3 US-09-053-549-8	Sequence 8, Appli
20	2236	59.6	1207	3 US-09-547-422-7	Sequence 7, Appli
21	2236	59.6	1227	4 US-09-988-462-7	Sequence 7, Appli
22	2235	59.6	1227	3 US-09-053-549-2	Sequence 2, Appli
23	2165	57.7	1227	1 US-08-448-170-8	Sequence 8, Appli
24	2165	57.7	1227	3 US-08-961-803-9	Sequence 9, Appli
25	2156	57.5	1227	4 US-09-661-322A-63	Sequence 63, Appl
26	2141	57.1	1186	3 US-09-178-252-23	Sequence 23, Appl
27	2141	57.1	1186	4 US-09-826-660-23	Sequence 23, Appl

28	2085.5	55.6	1228	4 US-09-661-322A-38	Sequence 38, Appl
29	1902	50.7	643	3 US-09-178-252-25	Sequence 25, Appl
30	1902	50.7	643	4 US-09-826-660-25	Sequence 25, Appl
31	1891	50.4	380	5 PCT-US91-02560-4	Sequence 4, Appli
32	1658	44.2	653	4 US-09-661-322A-6	Sequence 6, Appli
33	1652	44.1	1157	1 US-07-876-280-30	Sequence 30, Appl
34	1652	44.1	1157	1 US-07-812-180A-2	Sequence 2, Appli
35	1652	44.1	1157	1 US-08-315-468-2	Sequence 2, Appli
36	1652	44.1	1157	3 US-07-941-650A-2	Sequence 2, Appli
37	1482	39.5	1176	1 US-08-257-999-2	Sequence 2, Appli
38	1480.5	39.5	1157	2 US-08-532-547-5	Sequence 5, Appli
39	1480.5	39.5	1157	2 US-08-379-658B-5	Sequence 5, Appli
40	1480.5	39.5	1157	3 US-08-455-838-5	Sequence 5, Appli
41	1480.5	39.5	1157	3 US-09-019-809-5	Sequence 5, Appli
42	1480.5	39.5	1157	4 US-09-471-177-5	Sequence 5, Appli
43	1480.5	39.5	1157	4 US-09-220-806-5	Sequence 5, Appli
44	1474	39.3	1156	3 US-09-002-285-72	Sequence 72, Appl
45	1474	39.3	1156	4 US-09-589-477-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/230720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Thu Mar 10 14:26:03 2005

Query Match 99.2%; Score 3718.5; DB 3; Length 719;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
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1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q I A L E L M F V Q K L P S F A V S G 180
121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q I A L E L M F V Q K L P S F A V S G 180
181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
361 G G H K L E F R T I G G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419
361 G G H K L E F R T I G G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N V P R 420
420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 479
421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
480 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 539
481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 540
540 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599
541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
600 T F T V G F T T P F S L D V O S T F T I G A M N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 659
601 T F T V G F T T P F S L D V O S T F T I G A M N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 718
661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661.322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (2007..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 91.7%; Score 3439; DB 4; Length 710;
Best Local Similarity 91.9%; Pred. No. 1.2e-299;
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;
1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
1 M K S K N Q N M H Q S L S N N A T V D K N F T G S L E N N T N T E L Q N F N H -----EGIEPFSVSTI 51
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
52 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K S Q W E I F M E H V E E I I N Q K I S T Y A 111
121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q I A L E L M F V Q K L P S F A V S G 180
112 R N K A L A D L K G L D A L A V H S E S L E S W I E N R N N T R T R S V V K S Q I T L E L M F V Q S L P S F A V S G 171
181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
172 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S K S K E Y S D H C V K W Y N 231
241 T G L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
232 T G L N R L M G N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 291
301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
292 G T V H P H P S F T S T T W Y N N N A P S F S I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 351
361 G G H K L E F R T I G G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419
352 G G H K L E F R T I G G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N V P R 411
420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 479
412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 471
480 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 539
472 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R K N 531
540 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599
532 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591
600 T F T V G F T T P F S L D V O S T F T I G A M N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 659
592 T F T V G F T T P F S D V O S T F T I G A M N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E E V 651
660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 718
652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D K F Y L D E K R E L F E I V K A Q L H I E R N M 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 89.6%; Score 3360.5; DB 3; Length 648;
Best Local Similarity 99.4%; Pred. No. 1.1e-292;
Matches 644; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSG 180
DB 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQROVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQROVERAGDYSYHCVKWS 240
QY 241 TGLNLRGNTAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300
DB 241 TGLNLRGNTAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300
QY 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPTSRDVRRTESLAGNLFLTQPVN-VPR 419
DB 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPTSRDVRRTESLAGNLFLTQPVN-VPR 420
QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 479
DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLQFHTSINGKAINQGNFSATWNRGDELIDYK 599
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLQFHTSINGKAINQGNFSATWNRGDELIDYK 600
QY 600 TFXTVGFTTFFSLDDVQSTFTTICAWNFSNGNEVYIDRIEFVPEVTYIE 647
DB 601 TFXTVGFTTFFSLDDVQSTFTTICAWNFSNGNEVYIDRIEFVPEVTYIE 648
RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.6%; Score 3358.5; DB 2; Length 719;
Best Local Similarity 89.6%; Pred. No. 2e-292;
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSG 180
DB 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQROVERAGDYSYHCVKWS 240

181 EEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSYHCVKWN 240
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 300
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 300
301 GTVPHPSFTSTWYNNAPSAIEAARVNPPLHLDLFLQVTVIYLLSRWSNTQYNNMW 360
301 GTVDNQALRSTWYNNAPSAIEAARVNPPLHLDLFLQVTVIYLLSRWSNTQYNNMW 360
361 GGHKLEFRITGGTINISQGSTNTSINPVTLPFTSRDVRVRESLGLNLFQVGVPR 419
361 GGHKLEFRITGGTINISQGSTNTSINPVTLPFTSRDVRVRESLGLNLFQVGVPR 420
420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 479
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 480
480 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDLRRTN 539
481 GSHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDLRRTN 540
540 TGTGDIRVNIINPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 599
541 SGTGDIRVNIINPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
600 TFXVTGTTTSPSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 659
601 TFXVTGTTTSPSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660
660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 718
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: Civ11
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

Query Match 89.5%; Score 3356.5; DB 3; Length 719;
Best Local Similarity 89.6%; Pred. No. 3e-292;
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNTNHEDLKMSYEYENVEPVSASTI 60
1 MKLKNPDKHQTLSNAKVDKIATDSLKNETDIELKNNEDYLMSEHESIDPFFVSASTI 60
61 QTGIGIAGKILGTLGVFPAGQVSLYSFTLGEKLPKQKQWEIFMEHVEEIIQNKISTYA 120
61 QTGIGIAGKILGTLGVFPAGQVSLYSFTLGEKLPKQKQWEIFMEHVEEIIQNKISTYA 120
121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNTNRARSVVKSVQIALELMFVKLPSPAVSG 180
121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNTNRARSVVKSVQIALELMFVKLPSPAVSG 180

181 EEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSYHCVKWN 240
181 EEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSYHCVKWN 240
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 300
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 300
301 GTVPHPSFTSTWYNNAPSAIEAARVNPPLHLDLFLQVTVIYLLSRWSNTQYNNMW 360
301 GTVDNQALRSTWYNNAPSAIEAARVNPPLHLDLFLQVTVIYLLSRWSNTQYNNMW 360
361 GGHKLEFRITGGTINISQGSTNTSINPVTLPFTSRDVRVRESLGLNLFQVGVPR 419
361 GGHKLEFRITGGTINISQGSTNTSINPVTLPFTSRDVRVRESLGLNLFQVGVPR 420
420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 479
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSHIGLIS 480
480 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDLRRTN 539
481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDLRRTN 540
540 TGTGDIRVNIINPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 599
541 SGTGDIRVNIINPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
600 TFXVTGTTTSPSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 659
601 TFXVTGTTTSPSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660
660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 718
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989


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;
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match      74.1%; Score 2778.5; DB 3; Length 535;
Best Local Similarity 99.6%; Pred. No. 1.5e-240;
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60
DB 1 MCLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLAVYHDSLESWGNNRNTARSVVKSVQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGDLAVYHDSLESWGNNRNTARSVVKSVQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240
QY 241 TGLNLRGNTNAESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300
DB 241 TGLNLRGNTNAESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300
QY 301 GTVHPHPSTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMMNW 360
DB 301 GTVHPHPSTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMMNW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPNV-VPR 419
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPNVGVPR 420
QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 479
DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480
QY 480 ASHKVAVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 534
DB 481 ASHKVAVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

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;
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match      64.4%; Score 2415; DB 1; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLKMSYENVEPFFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCVAEWNNDPFFVASTVQTGINIAGRI 66
QY 71 LGTLGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARKALTDLKG 130
DB 67 LGVLGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARKALTDLKG 126
QY 131 LGDALAVYHDSLESWGNNRNTARSVVKSVQYIALELMFVQKLPFAVSGEVPVLLPIYA 190
DB 127 LGRGYSYQAALETWLDNRDARSRIILRYVALELDITTAIPLFRIRNEEVPVLLMVA 186
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWSYTGNNLRGTN 250
DB 187 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWSYTGNNLRGTN 246
QY 251 AESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDIAGTVHPHPST 310
DB 247 AESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDIAGTVHPHPST 306
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMMNWGGHKLFRFTI 370
DB 307 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMMNWGGHKLFRFTI 366
QY 371 GGTGLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNFLTQPNV-VPRVDFHWKFTV 428
DB 367 GGTGLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNFLTQPNV-VPRVDFHWKFTV 422
QY 429 HPIASDNFYYPG-----YAGIGTQDSENELPPEATQPNYESYSHRLSHIGLISAS 481
DB 423 --INPQNIYERGATTYSQYQVGIQIFDSETELPPTTERPNERYESYSHRLSHIGLIIGN 480
QY 482 HVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 541
DB 481 TLAPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540
QY 542 TFGDIRVNNPPFAQRVVRIRYASTTDLQFTHSINGKAINQGNFATMNRGDLDYKTF 601
DB 541 TFGDIRVNNPPFAQRVVRIRYASTTDLQFTHSINGKAINQGNFATMNRGDLDYKTF 600
QY 602 XTGVFTTTPFSLDVQSTFTTIGAMNFSNGEVYIDIRIFVPVEVTEYAEYDFEKAQSKVTA 661
DB 601 RTAGFSTPFNFLNAQSTFTTIGAMNFSNGEVYIDIRIFVPVEVTEYAEYDFEKAQSKVTA 659

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match          64.4%; Score 2415; DB 1; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDTKSTDSLKN-ETDIELQ-NINHEDCLKMSVENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINAGRI 66

QY 71 LGTLGVPPAGQVASFYLFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQLASFYFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLSWVGNRNTRARSVVKSQXTALELMFVQKLPSFAVSGEEVPLPIYA 190
Db 127 LGRGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVPMLMVA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCVKWYSTGLNNLRGTN 250
Db 187 QAANLHLLLRDASIFGSEWGMASDVNQYQOIRYTEEYSHNHCQWYNTGLNNLRGTN 246

QY 251 AESWRYNQFRDRTMLVLDLVALFPSYDTOMYPIKTAQTALREVYTDAGTVPHPSPFT 310
Db 247 AESWLRYNQFRDRTMLVLDLVALFPSYDTOMYPIKTAQTALREVYTDAGTVPHPSPFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMVGSHKLEFRTI 370
Db 307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMVGSHKLEFRTI 366

QY 371 GGTNLNISTOGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPRVDFHVKFVT 428
Db 367 GGTNLNISTOGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPRVDFHVKFVT 422

QY 429 HPIASDNFYYPG-----YAGIGTQLQDSENEPPEATGQPNYESYSHRLSHIGLISAS 481
Db 423 --INPQNIYERGATTYSQYQYQVGIQLFDSLETLPETTERPNYESYSHRLSHIGLIGN 480

QY 482 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 541
Db 481 TLRAPIVSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGPGFTGGDILRRNTG 540

QY 542 TFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINOGNFATMNGEDLDYKTF 601
Db 541 TFGDIRLNINPLSQRYRIRYASTTDLQFFTRINGTTVNIQNFSTMRNGDNLEYSF 600

QY 602 XTGVTTPPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVTEYAEYDPEKAQKVTA 661
Db 601 RTAGFSTPFLNAQSTFTLGAQFSN-QEVYIDRVEFPVPAEVTFAEYDLERAQKAVNA 659

QY 662 LFTSTNPRGLKTDVKDYHIDOVNLSVESISDEFYLDKRELPEIKVYAKQLHIERNM 718
Db 660 LFTSTNPRGLKTDVYHIDQVSNMVAACLSDEFCLDEKRELPEIKVYAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/100,709
; APPLICATION DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-779-046-4

Query Match          64.4%; Score 2415; DB 2; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDTKSTDSLKN-ETDIELQ-NINHEDCLKMSVENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINAGRI 66

QY 71 LGTLGVPPAGQVASFYLFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQLASFYFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLSWVGNRNTRARSVVKSQXTALELMFVQKLPSFAVSGEEVPLPIYA 190
Db 127 LGRGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVPMLMVA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCVKWYSTGLNNLRGTN 250
Db 187 QAANLHLLLRDASIFGSEWGMASDVNQYQOIRYTEEYSHNHCQWYNTGLNNLRGTN 246

QY 251 AESWRYNQFRDRTMLVLDLVALFPSYDTOMYPIKTAQTALREVYTDAGTVPHPSPFT 310
Db 247 AESWLRYNQFRDRTMLVLDLVALFPSYDTOMYPIKTAQTALREVYTDAGTVPHPSPFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMVGSHKLEFRTI 370
Db 307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMVGSHKLEFRTI 366

QY 371 GGTNLNISTOGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPRVDFHVKFVT 428
Db 367 GGTNLNISTOGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPRVDFHVKFVT 422

QY 429 HPIASDNFYYPG-----YAGIGTQLQDSENEPPEATGQPNYESYSHRLSHIGLISAS 481
Db 423 --INPQNIYERGATTYSQYQYQVGIQLFDSLETLPETTERPNYESYSHRLSHIGLIGN 480

QY 482 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 541
Db 481 TLRAPIVSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGPGFTGGDILRRNTG 540
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127	LGRGYSYQQALETWLDNRDARSRIILERYVALELDTTALPLFRIRNEEVPLLMVYA	180
191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKVYSTGLNNLRGTN	250
187	QAANLHLLLRDASLFGSEGWMASSDVNQYQEQIRYITEYSNHCQWYNTGLNNLRGTN	246
251	AESWVRNORRDMTLMWLDLVALPSPSYDTQMYPKTTAQLTREYVYTDAGTVHPPHSFT	310
247	AESWLRYNQFRDLTLGVLDLVALPSPSYDTRYPINTSAQLTREIYTDPIGRTNAPSGFA	306
311	SITWYNNNAPSASIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRFTI	370
307	SITWFNNNAPSASIAEAAIFRPHLLDFPEQLTIYASRWSSTQHMVYVWGHRLNFRPI	366
371	GGTLNISTQGST-NTSINPVTLPFTSRDVTYESLAGLNFLTPQVYV-VRVDFHWKFTV	428
367	GGTLNSTQGLTNNTSINPVTLPFTSRDVTYESNAGTNILFTTPVNGVPWARFNF---	422
429	HPIASDNFYPG-----YAGITQLQDSNELPPEATGQPNYESYSHRLSHIGLISAS	481
423	--INPQNIYERGATTYSQPYQGVGILQFDSQTELPPETTERPNYESYSHRLSHIGLI	480
482	HVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAUVVRGPGFTGGDILRRTNG	541
481	TLRAPVYSWTHRSADRNTIGNRITQIPLVKALNLHSGVTVVGPGFTGGDILRRTNG	540
542	TFGDIRVNINPPFAQRVRIYASTTDLQFHTSINKAINQGNFSATMNRGEDLDYKTF	601
541	TFGDIRLNVNVPUSQRYRVRIYASTTDLQFFTRINGTTVAINGFSRTMNRGDNLEYSR	600
602	XTVGFTTPESLDQSTFTTIGAMNFSGNEVYIDIRBFVPVEVITYEAYDFEKAQKVTA	661
601	RTAGFSTPFLNAQSTFTTLAGQSFN--QEVYIDRVEFVPAEVTFEAYDILERAQAVNA	659
662	LFTSTNPRGLKTDVYHIDQVSNLVESLDSFEYLDKRELPKEIVKYAKQLHIERNM	718
660	LFTSTNPRGLKTDVYHIDQVSNLVESLDSFEYLDKRELPKEIVKYAKQLHIERNM	716

RESULT 12
 US-08-448-170-10
 ; Sequence 10, Application US/08448170
 ; Patent No. 5723758
 ; GENERAL INFORMATION:
 ; APPLICANT: Payne, Jewel
 ; APPLICANT: Cummings, David A.
 ; APPLICANT: Cannon, Raymond J.C.
 ; APPLICANT: Narva, Kenneth E.
 ; APPLICANT: Stelman, Steve
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
 ; TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/448,170
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/069,902
 ; FILING DATE: 01-JUNE-1993
 ; CLASSIFICATION: 424

Best Local Similarity 63.9%; Pred. No. 2.8e-191;
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;
40 EDCLKMSYENVEPFVSASTIQTGIGIAGKILGTGVPFAGQVASYLFIILGELWPKGN 99
10 EDSLCIAEGNNIDPFVSASTVQTGINIAGIRLGLVGPVAGQLASFYFLVGLWPRGRD 69
100 QWEIFMEHVEEINOKISTYARKKALTDLKGLGDALAVVHDSLESWVGNRNNTRARSVVK 159
70 QWEIFLEHVEQLINQITENARNTALARLQGLGDSFRAYQOSLEDWLENRDDARTSRVLY 129
160 SQYIALELMFVQKLPFAVSGEEVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEIST 219
130 TOYIALELDFLNAMPLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEFGLTSQEQIR 189
220 FYNROVERAGDYSYHCVKWYSTGLNNLRGTNAESWRYNQFRDRLTMLVLDLVALFPSYD 279
190 YVERQVERTRDYSYCVENYNTGLNSLRGTNAASWRYNQFRDRLTMLVLDLVALFPSYD 249
280 TOMYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFL 339
250 TRTYPINTSAQLTREVTDAIGAT--GVNMAWYNNNAPSFAIEAAVVRNPHLLDFL 307
340 EQVTIYSLRSWNTQYNNMGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVTY 399
308 EQLTIFSASSRWSNTRHMTYWRGTIQSRPIGGGLNTSTHGATNTSINPVTLPFASRDVTY 367
400 RTESLAGLNF--LTOPVN--VPRVDFHMKFVTHP-----IASDNFYYPGYAGIGTQLODS 451
368 RTESYAGVLLWGIYLEPIHGVPTVRFNF---TNPNQISDRGTANYSQP--YESPGLQKDS 423
452 ENELPPEATGQPNYESYSHRLSHLIGLISASHVKALVYSWTHESADRTNTIEPNSTIQIPL 511
424 ETELPPETTERPNYESYSHRLSHLIGLISASHVKALVYSWTHESADRTNTIEPNSTIQIPL 483
512 VKAFNLSSGAADVVRGFGTGDILRRNTGTGDIRVNIINPPPAQRYRIRYASTTDLQ 571
484 VKASELPQGTTVVRGFGTGDILRRNTGTGDIRVNIINPPPAQRYRIRYASTTDLQ 543
572 FHTSINGKAINQCNFSATMNRGDLDTKFTXTVGTFTTFFSLLDVQSTFTIGAWNFFSSGNE 631
544 FVSRGGTTVNNFRFLTMNSGDELKYGNEVRRAPTFTTQIQDIIRTSIQGLSGNGE 603
632 VIIDRIEFVPEVTEYAEYDEKAEKVATLFTSTNPRGLKTDVKYHIDQVSNLVESLS 691
604 VIIDKIEIIPVTATFEAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663
692 DEFYLDKRELFELVYKAKQHLIERNM 718
664 DEFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNLFLTPQVN--VPR 419
352 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNLFLTPQVNGVPR 411
420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSSENELPPEATGQPNYESYSHRLSHLIGLIS 479
412 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSSENELPPEATGQPNYESYSHRLSHLIGLIS 471
480 ASHVKALVYSWTHRSAD 496
472 ASHVKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951.715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-951-715A-7

Query Match 59.6%; Score 2236; DB 1; Length 1207;

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-7

Query Match 59.6%; Score 2236; DB 2; Length 1207;
Best Local Similarity 63.9%; Pred. No. 2.8e-191;
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;
QY 40 EDCLKMEYENVEPVFASTIQTGIGIAGKILGTLPVFPAGQVAVSLYSPILGELMPKGN 99
Db 10 EDSLCIAEGNNIDPFVSASTVQGINIAGRILGVLPFPAGQVAVSLYSPILGELMPKGRD 69
QY 100 QWEIFMEHVEEIIKOKISTYARNKALTDLKLGDALAVYHDSLESWYGNRNNTARSVVK 159
Db 70 QWEIFLEHVEQLINQOITENARNALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLY 129
QY 160 SOYIALELMFVQKLPSFAVSGEEVPLPIYAAQAAHLHLLLRDASIFGKEWGLSSSEIST 219
Db 130 TOYIALELDFLNPFLFAIRNQEVPLLMVYAAANLHLLLRDASLFGSEFGLTSQEIQR 189
QY 220 FYNQVERAGDYSYCHVKWYSTGLNNLRTGNAESWRYNQFRDMLMVLVLPSPSYD 279
Db 190 YVERQVETRDYSDYCVWEYNTGLNSLRTGNAESWRYNQFRDMLMVLVLPSPSYD 249
QY 280 TOMYPIKTTAQLTRREYTDAGTVHPHPSFTSTWYNNAPSFAEAAVVRNPHLLDFL 339
Db 250 TRTPYINTSAQLTRREYTDAGTAT--GVNMAWMWYNNAPSFAEAAAIRSPHLLDFL 307
QY 340 EQVTIYSLSRWSNTQYNNMWGCHKLEFRTIGTGLNSTQSGTNTSINPVTLPFTSRDXY 399
Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGLNTSTHGATNTSINPVTLPFTSRDXY 367
QY 400 RTESLAGLNLFF--LTQPNV-VPRVDFHWKFVTHP-----IASDNFYYPGYAGIGTQLQDS 451
Db 368 RTESYAGVLLWGIYLEPIHGVPVTRFNF---TNPQNSDRGTANYSQP-YESPGQLQKDS 423

QY 452 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIBPNSITQIPL 511
Db 424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVVPVYSWTHRSADRTNTIGNRITQIPM 483
QY 512 VKAFNLSSGAAVVRGPGTGGDILRRNTGTGDIRVNNINPFPAPQRYRVRIRYASTDLQ 571
Db 484 VKASELPQGTTVVRGPGTGGDILRRNTGTGDIRVNNINPFPAPQRYRVRIRYASTVDFD 543
QY 572 FHTSINGKAINQGNFSAWNRGDDLDYKFTXVGTTPPFLSLDDVQSTFTTIGAWNPFSSGNE 631
Db 544 FFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRAFTTTPFTTQIQDIIRTSIQGLSGNGE 603
QY 632 VYIDRIEFVPEVVEYAEYDFEKAQEKVLTFTSTNPRGLKTDVKDYHIDQVSNLVESLS 691
Db 604 VYIDKIEIIPVTATFEAYDLEKRAQEAVALFTNTNPRRLKTDVTDHIDQVSNLVACLS 663
QY 692 DEFYLDKRELFELVKYAKQLHIERNM 718
Db 664 DEFCLDEKRELEKVKYAKRLSDERNL 690

Search completed: March 9, 2005, 17:27:38
Job time : 26.119 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.5047 Seconds
(without alignments)
3350.901 Million cell updates/sec

Title: US-10-019-823B-54
Perfect score: 3749
Sequence: 1 MLKNQDKHQSFSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3722.5	99.3	719	16	US-10-782-020-10
2	3722.5	99.3	719	16	US-10-782-141-8
3	3439	91.7	710	15	US-10-428-961-42
4	2249	60.0	1228	16	US-10-809-953-10
5	2236	59.6	1207	10	US-09-988-462-7
6	2156	57.5	1227	15	US-10-428-961-63
7	2141	57.1	1186	9	US-09-826-660-23
8	2085.5	55.6	1228	15	US-10-428-961-38
9	2085.5	55.6	1228	15	US-10-614-524-2
10	1902	50.7	643	9	US-09-826-660-25
11	1708	45.6	1167	14	US-10-089-678-1
12	1658	44.2	653	15	US-10-428-961-6
13	1652	44.1	1157	16	US-10-782-141-16

14	1500.5	40.0	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1500.5	40.0	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1500.5	40.0	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1477.5	39.4	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1477.5	39.4	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1477.5	39.4	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1474	39.3	1156	14	US-10-099-285-72	Sequence 72, Appli
21	1474	39.3	1156	15	US-10-428-961-28	Sequence 28, Appli
22	1441.5	38.5	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1441.5	38.5	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1441.5	38.5	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1441.5	38.5	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1441.5	38.5	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1441.5	38.5	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1441.5	38.5	1181	10	US-09-988-462-15	Sequence 15, Appli
29	1441.5	38.5	1181	10	US-09-988-462-17	Sequence 17, Appli
30	1441.5	38.5	1181	10	US-09-988-462-28	Sequence 28, Appli
31	1441.5	38.5	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1441.5	38.5	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1441.5	38.5	1181	15	US-10-136-998A-10	Sequence 10, Appli
34	1441.5	38.5	1181	15	US-10-136-998A-12	Sequence 12, Appli
35	1436.5	38.3	1177	14	US-10-035-060-8	Sequence 2, Appli
36	1434.5	38.3	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1433.5	38.2	1177	14	US-10-102-469-24	Sequence 24, Appli
38	1422	37.9	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1400	37.3	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1400	37.3	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1380.5	36.8	1167	15	US-10-428-961-40	Sequence 40, Appli
42	1360.5	36.3	1177	9	US-09-873-873-26	Sequence 26, Appli
43	1360.5	36.3	1177	10	US-09-916-956A-26	Sequence 26, Appli
44	1360.5	36.3	1177	10	US-09-997-914-26	Sequence 26, Appli
45	1360.5	36.3	1177	14	US-10-365-645-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1

US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 99.3%; Score 3722.5; DB 16; Length 719;
Best Local Similarity 99.4%; Pred. No. 3.4e-303;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY	1	MLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFVSASTI	60
Db	1	MLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFVSASTI	60
QY	61	QTGIGIAGKILGTLPFAGQVNASLYSPILGELWPKGNQWEIFMEHVEEINQIKISTYA	120
Db	61	QTGIGIAGKILGTLPFAGQVNASLYSPILGELWPKGNQWEIFMEHVEEINQIKISTYA	120

QY	121	RNKALTDKGLDALAVYHDSLESWVGNRNTRRSVVKSOYIALELMFVKLPSPFAVSG	180
DB	121		
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS	240
DB	181		
QY	241	TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSTYDQMPYIKTTAQLTREYTTDAI	300
DB	241		
QY	301	GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
DB	301		
QY	361	GGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTQPVN-VPR	419
DB	361		
QY	420	VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS	479
DB	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS	480
QY	480	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	539
DB	481	ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAWMNRGEDLDYK	599
DB	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAWMNRGEDLDYK	600
QY	600	TFXTVGFTTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	659
DB	601	TFRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
QY	660	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM	718
DB	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Kozziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: Fast-SEQ for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PR			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.3%; Score 3722.5; DB 16; Length 719;			
Best Local Similarity 99.4%; Pred. No. 3.4e-303;			
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
QY	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPVSASTI	60

; NAME/KEY: misc feature
; LOCATION: (200)....(200)
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 91.7%; Score 3439; DB 15; Length 710;
Best Local Similarity 91.9%; Pred. No. 2.1e-279;
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFFVSASTI 60
DB 1 MKSKNQNMHQSLSNATVDKNFTGSLNNTNTELOQNFH-----EGIEPFFVSSTI 51
QY 61 QTGIGIAGKITGLTGVPPAGQVASYSLFILGELWPKGNQWEIFMEHVEEIIQNKISTYA 120
DB 52 QTGIGIAGKITGLNLPAGQVASYSLFILGELWPKGKSQWEIFMEHVEEIIQNKISTYA 111
QY 121 RNKALTDLKGDLALAVHDSLESVGNRNTRARSVVKSQVIALELMFVQKLPSPAVSG 180
DB 112 RNKALADLKGDLALAVHDSLESVGNRNTRARSVVKSQVIALELMFVQKLPSPAVSG 171
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWS 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWN 231
QY 241 TGLNLRGNTNAESVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTD 300
DB 232 TGLNLRGNTNAESVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTD 291
QY 301 GTVPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYMMNW 360
DB 292 GTVPHPSFTSTWYNNAPSPSTIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYMMNW 351
QY 361 GGHKLEFRITIGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFTQPVN-VPR 419
DB 352 GGHKLEFRITIGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFTQPVN-VPR 411
QY 420 VDFHFWKFTVTHPIASDNFYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 479
DB 412 VDFHFWKFTVTHPIASDNFYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 471
QY 480 ASHKALVYTSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
DB 472 ASHKALVYTSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531
QY 540 TGTGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 599
DB 532 TGTGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 591
QY 600 TFXTVGFTTTPFSLDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 659
DB 592 TFXTVGFTTTPFSDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 651
QY 660 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 652 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 710

RESULT 4

US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016

; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 60.0%; Score 2249; DB 16; Length 1228;
Best Local Similarity 62.3%; Pred. No. 3.8e-179;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

QY 23 TDSLKNETDIELQNH-----EDCLKMSEYENVEPFFVSASTIQTGTGIGIAGKI 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVGTGINAGRI 61
QY 71 LGTLGVPPAGQVASYSLFILGELWPKGNQWEIFMEHVEEIIQNKISTYARNKALTDLKG 130
DB 62 LGVLGVPPAGQVASYSLFILGELWPKGNQWEIFMEHVEEIIQNKISTYARNKALTDLKG 121
QY 131 LGDALAVHDSLESVGNRNTRARSVVKSQVIALELMFVQKLPSPAVSGREVPLPIYA 190
DB 122 LGDSFRAYQQSLEDWLENRDARTSVLHTQVIALELDLFLNAMPFAIRNQEVPLLMVYA 181
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWSYSLGLNLRGNTN 250
DB 182 QAANLHLLLRDASIFGSEFGLTSQEQRYRYERQVTRDYSYCVVWYNTGLNLRGNTN 241
QY 251 AESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAGTGVHPSFT 310
DB 242 AASWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAGTGVHPSFT 299
QY 311 STTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYMMNWGHKLEFRIT 370
DB 300 SMWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYMMNWGHKLEFRIT 359
QY 371 GGTNLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFTQPVN-VPRVDFHFWK 427
DB 360 GGLNTSTHGTATNTSINPVTLPFTSRDYRTESLAGLNLFTQPVN-VPRVDFHFWK 416
QY 428 THP-----IASDNFYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISASH 482
DB 417 TNPQNISRGTANYSQP-YESPGLQKDSSETLPETTERPNYESYSHRLSHIGLISASH 475
QY 483 VKALVYTSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 542
DB 476 VNVFVYTSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 535
QY 543 FGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYKTFX 602
DB 536 FGIIRVTNPGPLTQRYRIGRYASTVDFVFSRGGTANNFRFLRTMNSGDELKYNFV 595
QY 603 TVGFTTTPFSLDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 662
DB 596 RRAFTTTPFTQIQTIDRTSIQSLSGNEVYIDKIEIPIVATFATFEAYDLERAQEAVAL 655
QY 663 FTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 5

US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 59.6%; Score 2236; DB 10; Length 1207;
Best Local Similarity 63.9%; Pred. No. 4.6e-178;
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;
40 EDCLKMSEYNEVPFVASTQTGTGIGAKILGVLGVPFAGQVASYLSFILGELWPKGN 99
10 EDLCLAEAGNNIDPFVASTVQTGINAGILGVLGVPFAGQVASYLSFILGELWPKGRD 69
100 QWEIFMEHVEEIIINOKISTYARNKALTDLKGDLAVLVYHDSLESVWGNRNTRARVVK 159
70 QWEIFLEHVEQLINQITENARTALARLOGLGDSFRAYQOSLEDWLENRDDARTSVLY 129
160 SOVIAELMFVQKLPSFAVSGEEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEIST 219
130 TOVIAELDFLNAFPLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEFGLTSQIQ 189
220 FYNQVERAGDYSYHCVKWYSTGLNLRGTNAESWVRVYNQFRDMTLMVLDAVALFPSYD 279
190 YYERQVERTRDYSYCVWYNTGLNSLGTNAESWVRVYNQFRDRLTLGLVLDVALFPSYD 249
280 TOMYPIKTAQLTREVTDAIGTVHHPHSFTSTTWNNNAPSFAIEAAVVRNPHLLDFL 339

250 TRYPINTSAQLTREVTDAIGAT--GVNMAWNNYNNAPSFAIEAAAIKPSHLLDFL 307
340 EQVTIYSLLSRWSNTQYMNMGHKLFEFTIGTTLNISTQGSTNTSINPVTLPFTSRDYY 399
308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDYY 367
400 RTESLAGLNL--LTQPVN-VPRVDFHWKEVTHP-----IASDNFYYPGYAGIGTQLQDS 451
368 RTESYAGVLLWGLIYLEPIHGVPTVRENF--TNPQNISDRGTANYSQP-YESPLQLKDS 423
452 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTTIEPNSITQIPL 511
424 ETELPPETTERPNYESYSHRLSHIGLILQSRVNVVYVSWTHRSADRTTIGPNRITQIPM 483
512 VKAFNLSSGAADVVRGPGFTGGDILRRNTGTGDIRVNNPPFAQRYVRIRVASTTDLQ 571
484 VKASELPQGTTVVRGPGFTGGDILRRNTGCGFGPIRVTVNGPLTQRYRIGFRYASTVDFD 543
572 FHTSINGKAINQGNFSATMRGEDLDYKTEXTVGTTPFSLLDVQSTFTTIGAWNFSSGNE 631
544 FFVSRGGTTVANNFRFLRTMNSGDELKYNFVRRAFTTPTFTQIQDIIRTSIOGLSGNGE 603
632 VIIDRIEFVPEVTEAAYDEFAKQKVTALFTSTNPRGLKTDVXDYHIDQVSNLVESLS 691
604 VIDKIELIIPVTATFEAAYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663
692 DEFYLDKRELFEIVKYAKQLHIERNM 718
664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6

US-10-428-961-63
Sequence 63, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201--1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent in version 3.2
SEQ ID NO 63
LENGTH: 1227
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-428-961-63

Query Match 57.5%; Score 2156; DB 15; Length 1227;
Best Local Similarity 58.8%; Pred. No. 2.5e-171;
Matches 420; Conservative 105; Mismatches 175; Indels 14; Gaps 4;

13 SSNAKVDKISTDLSLKN-----ETDIELQINHEDCMKSEYNEVPFVASTTQTGIG 65
7 NENEIINALSIPAVSNHSAQMNLSLDARI-----EDSLCIAEGNNIDPFVASTVQTGIN 61
66 IAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKAL 125
62 IAGRILGVLGVPFAGQVASYLSFILGELWPKGRDPWEIFLEHVEHLIRQQVTENTRDAL 121
126 TDLKGLGDALAVYHDSLESVWGNRNTRARVVKSVQIALELMFVQKLPSFAVSGEVL 185

Db 523 SDKITQIPAVKDMLYLGGSVWQPGFTGGDILKRTNPSILGTFVAVTWNGSLSQRYRVI 582
QY 563 RYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYKTFXTVGTFTTFFSLDLDVQSTFTIG 622
Db 583 RYASTTDFEF-TLYLGDITTEKRNKNTWDNGASLTYTEFKFASFTIDFQFRETQDKILLS 641
QY 623 ANFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKYATLTSTNPRGLKTDVQYHIDQ 682
Db 642 MGDFSSGQEVYIDRIEFVPEVTEYAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700
QY 683 VSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 718
Db 701 AANLVECLSDLLYPNEKRLLFDAVREAKRLSGARNL 736
RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 40.0%; Score 1500.5; DB 13; Length 1206;
Best Local Similarity 44.2%; Pred. No. 2.5e-116;
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;
QY 1 MCLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPFANEPTNALQNM DYKDYKYLKMSAGNASYPGS 59
QY 51 VEPFVSA-STIQTGIGIAGKILGTLGVPPAGQVAVSLYSFILGELWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLSGLGVFPVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQV 119
QY 109 EEINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNNTNRSRVKVSQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNVYQLYLTALAEWEENPNNGSRALRDVNRNFEILDSL 179
QY 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERA 228
Db 180 FTQMPFRVTNFEVFPFLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYDQMKLT 239
QY 229 GDYSVHCVKWYSTGLNNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTQMYPIKTT 288
Db 240 AEYSDHCVKWYETGLAKLGTSKQWVDYNQFRDMTLMVLVDLVALFPSTQMYPIKTT 299
QY 289 AOLTRVYTDAGTVHPHPSFTSTWYNNAPSFAEAAVVRNPHLLDFLEQVITYSL 348
Db 300 AOLTRVYTDPLGAVNVS---SIGSWY-DKAPSGFVIESSVIRPPHVFYDITGLTYVYQS 355
QY 349 SRWNTQYMMWGGHKLFEPTIGTGLNISTQGSTNTSNIPV-TLPFTSRDYRTESLAGL 407
Db 356 RSISSARYIRHWAGHQISYHRVSRGNSLQOMYGTGNQNLHSTSTFTDFTNYDIYKLSKDAV 415

QY 408 NLFLTQP-----VNVPRVDFHMKFVTHPIASDN---FYYPGVAGICTQLQDSENELPPE 458
Db 416 LLDIVYPGVYIIFGMEVEF---FMVNQLNNTKTLKYNPVSKDIIASTRDESELEPPE 472
QY 459 ATGPQNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRNTIENPSITQIPLVKAP 515
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNNTIYSDKITQIPAVKCM 532
QY 516 NLSSGAAVRGPGFTGGDILR-RTNTGTFGDI---RVNINPFAQRYRVRIRYASTTDLQ 571
Db 533 DNLFPVPVVKPGHGTGGDLLQYNRSTGVTGLFLARVGLALEKAGKYRVLRYATDADIV 592
QY 572 FHTSINGKAINQGNFSATMNRGEDLDYKTF-----XTVGFTTTPFSL-----DVQST 618
Db 593 LH--VNDAQI---QMPKTNWPGEDLTSTKTFKVADAIITLNLATDSSLAKHKNLGEDPNST 647
QY 619 FTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKYATLTSTNPRGLKTDVQY 678
Db 648 LS-----GIVYVDRIEFIPVDEYAEQDLEAAKAVNALFTNTKD-GLRPGVTDY 697
QY 679 HIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 718
Db 698 EVNQAANLVECLSDLLYPNEKRLLFDAVREAKRLSEARNL 737
RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 40.0%; Score 1500.5; DB 14; Length 1206;
Best Local Similarity 44.2%; Pred. No. 2.5e-116;
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;
QY 1 MCLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPFANEPTNALQNM DYKDYKYLKMSAGNASYPGS 59
QY 51 VEPFVSA-STIQTGIGIAGKILGTLGVPPAGQVAVSLYSFILGELWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLSGLGVFPVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQV 119
QY 109 EEINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNNTNRSRVKVSQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNVYQLYLTALAEWEENPNNGSRALRDVNRNFEILDSL 179
QY 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERA 228
Db 180 FTQMPFRVTNFEVFPFLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYDQMKLT 239

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds
(without alignments)
4171.616 Million cell updates/sec

Title: US-10-019-823B-55
Perfect score: 3760
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: Pir1:.*
2: Pir2:.*
3: Pir3:.*
4: Pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	2 I39815	insecticidal prote
2	3751	99.8	719	2 S25383	parasporal crystal
3	3743	99.5	719	2 I39814	insecticidal prote
4	3520	93.6	719	2 I40590	crv465 protein -
5	2277.5	60.6	1228	2 S00873	parasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1492	39.7	1157	1 S49247	parasporal crystal
8	1482.5	39.4	1166	2 S32645	parasporal crystal
9	1474	39.2	1155	2 A26513	parasporal crystal
10	1471	39.1	1174	2 S32649	parasporal crystal
11	1467	39.0	1155	2 JD0002	parasporal crystal
12	1467	39.0	1156	2 A29125	parasporal crystal
13	1454.5	38.7	934	2 A22798	parasporal crystal
14	1453.5	38.7	1176	2 JT0241	parasporal crystal
15	1450	38.6	1155	2 S02134	parasporal crystal
16	1449.5	38.6	1181	2 A41052	parasporal crystal
17	1447.5	38.5	1176	2 JC2219	parasporal crystal
18	1446	38.5	1155	2 I39838	parasporal crystal
19	1443.5	38.4	1176	2 A22617	parasporal crystal
20	1443.5	38.4	1176	2 S02215	parasporal crystal
21	1360	36.2	1174	2 A42459	parasporal crystal
22	1353	36.0	1138	2 A48944	parasporal crystal
23	1339.5	35.6	1156	2 A29838	parasporal crystal
24	1331.5	35.4	823	2 S04181	parasporal crystal
25	1322.5	35.2	1189	2 S00944	parasporal crystal
26	1310	34.8	1154	2 S39536	parasporal crystal
27	1272	33.8	1171	2 I40572	parasporal crystal
28	1272	33.8	1171	2 A37829	parasporal crystal
29	1263	33.6	1176	2 A48970	parasporal crystal

30	1234	32.8	1160	2 S32647	parasporal crystal
31	1219.5	32.4	1165	2 S11446	parasporal crystal
32	1209.5	32.2	655	2 JC7140	protoxin - Bacillu
33	1196	31.8	1172	2 S32689	parasporal crystal
34	1186	31.5	1160	2 I40589	parasporal crystal
35	1163.5	30.9	1178	1 USBSXH	parasporal crystal
36	1163	30.9	1177	2 A49785	parasporal crystal
37	1156	30.7	652	2 A27323	parasporal crystal
38	1133	30.1	659	2 S10228	parasporal crystal
39	1100.5	29.3	652	2 I39811	parasporal crystal
40	986	26.2	649	1 JH0261	parasporal crystal
41	935	24.9	618	2 S11445	parasporal crystal
42	886	23.6	1156	2 S19306	parasporal crystal
43	828	22.0	1136	1 USBS81	parasporal crystal
44	694.5	18.5	934	2 B29838	parasporal crystal
45	667	17.7	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I39815
insecticidal protein cryV - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39815
R;Gleave, A.P.; Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1993
A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for iensis subsp. kurstaki.
A;Reference number: I39815; MUID:93298009; PMID:8517758
A;Accession: I39815
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PID:AAA22354.1; PID:G142768
C;Genetics:
A;Gene: cryV
C;Superfamily: parasporal crystal protein

Query Match	100.0%;	Score	3760;	DB	2;	Length	719;
Best Local Similarity	100.0%;	Pred. No.	2.9e-256;				
Matches	719;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MLKNQDKHQSFSNAKVDKISTDLSKNETDIELQNIHEDCLMKSEYENVEPFVSASTI	60				
Db	1	MLKNQDKHQSFSNAKVDKISTDLSKNETDIELQNIHEDCLMKSEYENVEPFVSASTI	60				
Qy	61	QTGIGIAGKILGTLGVPPAGQVASLYSFTLGLWPKGNQWEIFMEHVVEEIIINQKISTYA	120				
Db	61	QTGIGIAGKILGTLGVPPAGQVASLYSFTLGLWPKGNQWEIFMEHVVEEIIINQKISTYA	120				
Qy	121	RNKALTDLKGDLALAVYHDSLESWVGNNRNNTRRSVVKSQYIALELMFVQKLPSPFVSG	180				
Db	121	RNKALTDLKGDLALAVYHDSLESWVGNNRNNTRRSVVKSQYIALELMFVQKLPSPFVSG	180				
Qy	181	EEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFFYNQVERAGDYSCHVKWYS	240				
Db	181	EEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFFYNQVERAGDYSCHVKWYS	240				
Qy	241	TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMPYIKTTAQLTREVYTDAI	300				
Db	241	TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMPYIKTTAQLTREVYTDAI	300				
Qy	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360				
Db	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360				
Qy	361	GGHKLFRITIGTGLNISTQSGTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR	420				
Db	361	GGHKLFRITIGTGLNISTQSGTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR	420				

421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHKALVSWTHRSADRTNTIEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
481 ASHKALVSWTHRSADRTNTIEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
601 TFRVTGFTTTPSFLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
601 TFRVTGFTTTPSFLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 719
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 719

RESULT 2
S25383
parasporal crystal protein cryIIa1 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV
C:Species: Bacillus thuringiensis
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S25383
R:Taylor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin
A:Reference number: S25383; MUID:92269582; PMID:1588820
A:Accession: S25383
A:Molecule type: DNA
A:Residues: 1-719 <TAI>
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290
C:Genetics:
A:Gene: cryV
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 99.8%; Score 3751; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 1.3e-255;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKVSQYIALELMFVKLPSPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKVSQYIALELMFVKLPSPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
DB 241 TGLNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420

421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHKALVSWTHRSADRTNTIEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
481 ASHKALVSWTHRSADRTNTIEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600
601 TFRVTGFTTTPSFLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
601 TFRVTGFTTTPSFLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 719
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 719

RESULT 3
I39814
insecticidal protein cryVI - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C:Accession: I39814
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I39814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: GB:L36338; NID:G540281; PIDN:AAC36999.1; PID:G540282
C:Genetics:
A:Gene: cryVI
C:Superfamily: parasporal crystal protein

Query Match 99.5%; Score 3743; DB 2; Length 719;
Best Local Similarity 99.6%; Pred. No. 4.6e-255;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKVSQYIALELMFVKLPSPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKVSQYIALELMFVKLPSPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
DB 241 TGLNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420

Qy 421 VDFHWKFTVTHPIASDNFFYPGAGIGTQLQDSENELPPEATGPNYESYSHRSLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFFYPGAGIGTQLQDSENELPPEATGPNYESYSHRSLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Qy 541 TGTFGDIRVINPPEAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVINPPEAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDYDEKAQEKV 660
Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDYDEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 4

140590
cryV465 protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40590
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I40590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672
C;Genetics:
A;Gene: cryV465
C;Superfamily: parasporal crystal protein

Query Match 93.6%; Score 3520; DB 2; Length 719;
Best Local Similarity 92.9%; Pred. No. 2.2e-239;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;
Qy 1 MKLKNDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFFVSASTI 60
Db 1 MKLKNDKHQSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHSDIPFFVSASTI 60
Qy 61 QTGIGIAGKILGTLGVPPFAGQIASLYSFLIGELWPKGKQWEIFMEHVVEIINQKILTYA 120
Db 61 QTGIGIAGKILGTLGVPPFAGQIASLYSFLIGELWPKGKQWEIFMEHVVEIINQKILTYA 120
Qy 121 RNKALTDLKGLGDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALSDLRGLGDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSG 180
Qy 181 BEVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEISFTFYNQVERAGDYSCHVCWKYS 240
Db 181 BEVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEISFTFYNQVERTRDYSCHCIKWYN 240
Qy 241 TGLNNLRGTNAESWRYNQPRRDMTLMVLDLVALPSPYDTQMYPIKTTAQLTREVTYDAI 300
Db 241 TGLNNLRGTNAESWRYNQPRRDMTLMVLDLVALPSPYDTQMYPIKTTAQLTREVTYDAI 300
Qy 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360
Db 301 GTVHPNQAFSTTWNNAFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360
Qy 361 GGHKLBFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLLTQPVNGVPR 420
Db 361 GGHRLSRRPIGALNTSTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLLTQPVNGVPR 420

Qy 421 VDFHWKFTVTHPIASDNFFYPGAGIGTQLQDSENELPPEATGPNYESYSHRSLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFFYPGAGIGTQLQDSENELPPEATGPNYESYSHRSLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Qy 541 TGTFGDIRVINPPEAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVINPPEAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDYDEKAQEKV 660
Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDYDEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 5

S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 60.6%; Score 2277.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. No. 1.2e-151;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;
Qy 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPADRIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPFAGQVASLYSFLIGELWPKGKQWEIFMEHVVEIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPFAGQVASLYSFLIGELWPRGRDQWEIFLEHVLEQLNQITENARNATALRQ 121
Qy 131 LGDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSGEVEPLPIYA 190
Db 122 LGDSFRAYQOSLEDWLENRDDARTRSVLTYQYIALELDFLNAMPFLAIRNQEVEPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKEWGLSSSEISFTFYNQVERAGDYSCHVCWKYSTGLNNLRGTN 250
Db 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYYERQVTRDYSYCVWEYNTGLNSLRGTN 241
Qy 251 AESWRYNQPRRDMTLMVLDLVALPSPYDTQMYPIKTTAQLTREVTYDAIGTVHPHPSFT 310
Db 242 AASWRYNQPRRDLTLGLVDLVALPSPYDTRTYPINTSAQLTREVTYDAIGAT - GVNMA 299
Qy 311 STTWYNNNAFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGGHKLFRPTI 370
Db 300 SMWYNNNAFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGGHKLFRPTI 359
Qy 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLF--LTQPVNGVPRVDFHWK 428
Db 360 GGGNTSTHGTATNTSINPVTLPFTSRDVRVYRTESYAGVLLWGIYLEPIHGVPTVRFNF--- 416

Tue Feb 15 10:07:51 2005

S49247
 parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
 N;Alternate names: parasporal crystal protein cryIH
 C;Species: Bacillus thuringiensis
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: A59350; S49247
 R;Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V.
 Appl. Environ. Microbiol. 62, 80-86, 1996
 A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity again
 A;Reference number: A59350; MUID:96141404; PMID:8572715
 A;Accession: A59350
 A;Molecule type: DNA
 A;Residues: 1-1157 <L>
 A;Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:9547554; PIDN:CAA85764.1; PID:95475;
 A;Experimental source: serovar tolworthi
 C;Comment: This parasporal crystal protein, active against corn borer and other insects,
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 39.7%; Score 1492; DB 1; Length 1157;
 Best Local Similarity 43.3%; Pred. No. 1.9e-96;
 Matches 322; Conservative 115; Mismatches 217; Indels 90; Gaps 15;

QY 26 LKNETDIELQINIHEDCLKMEYENVEPVSAS-----TIQTGIGIAGKILGTLPV 78
 Db 29 LASDPAALQNMVYKDYLMQTDSDYTSISGRDAVQATLVVGRILGALGV 88
 QY 79 AGQVASYLSPILGELWPKGNQ-WEIPMEHVEEIIINQKISYARNKALTDLKGLDALAV 137
 Db 89 SGQIVSYFQELNLTLPVNDTAEAFNRQVEELVNOQITFARNQALRLQGLGDSFNV 148
 QY 138 YHDSLESVGNRNTRARSVVKSQYIALLEMFVKLPSPFAVSGEVEPLLPPIYAQANLHL 197
 Db 149 YQSLQNLADNRNLSVVRQAFIALDLDFVNAIPLFAVNGQVQVPLLSVYAQVNLHL 208
 QY 198 LLLRDASIFGKELWGLSSSEISTFYNQVERAGDYSDHCVKYSTGLNNLRGTNAESVRY 257
 Db 209 LLLKXASLFGEGWGTQGEISTYDRLQELTAKYNTYCTWTNTGLDRLRGINTESWLRY 268
 QY 258 NQFRDMTLMVLDAVLPSTQMYPIKTAOLTRVYTDATGTHPHPSFTSTTWN 317
 Db 269 HQFRREMTLVLDVVALFPYDRLYPTGNSPQLTREVTDPVFNPPANVGLCRRWGTN 328
 QY 318 NAPSFAIEAAVVRNPHLLDFLEQVTIYSLRSWS-NTQYMMNGGHKLE----- 366
 Db 329 PNTFSELENAFIRPHLFDRLNLSLTSS--NRFPVSNFMFYWSGHTLRRSLYNDLSAVQ 386
 QY 367 -----FRTIGTGLNSTQSTNTSINPVLPTFTSRDVTRESLAGLNLFLTQPVANGVPR 420
 Db 387 EDSYGLITTTTATINPGVDGTR--LESTAVDFRS-----ALIG-----IYGNR 429
 QY 421 VDFHWKEVTHPIASDNFYPGYAGIGT-----QLQDSENELPP-EATGQPNYESYS 470
 Db 430 ASF-----VPGGLFNGTTPSPANGGCRDLYDTNDELPPDESTG-----SST 469
 QY 471 HRLSHIGLIS-----ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSG 521
 Db 470 HRLSHVTFPSFQTNQAGSIANAGSVPTVWTRDVLNNTITPNRITQLPLVKASAPVSG 529
 QY 522 AAVRGPGTGGDILRRNTGTGDIRVNNINPPFAQRYRVRVYASTTDLQFHTSINGKA 581
 Db 530 TTVLKGPGTGGGILRRNTGTGTLRVTVNSPLTQQYRLVRVFASTGNFSIRVLRGGVS 589
 QY 582 INQGNFSAWNRGEDLDYKTRFTVGTFT-----PFSFLDVQSTFTTIGAWNFSGSEVYI 635
 Db 590 IGDVRLGSTWNRGQELTYESFFTRFTTTPFPNPPFTTQAEIILTVNAEGVSTGGEYI 649
 QY 636 DRIEFVPEVYEAEDFEKAQKVATLFTSTNPRGLKTDYKDHIDQVSNLVSLSDEF 695
 Db 650 DRIEIVPVNPAREAEEDLEAKKAVASLFTTRTD-GLQVNVTDYQVDQANLVSCLSDQ 708
 QY 696 YLDEKRELFEIVKYAKQLHIERNM 719

S49247
 parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
 N;Alternate names: parasporal crystal protein cryIH
 C;Species: Bacillus thuringiensis
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: A59350; S49247
 R;Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V.
 Appl. Environ. Microbiol. 62, 80-86, 1996
 A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity again
 A;Reference number: A59350; MUID:96141404; PMID:8572715
 A;Accession: A59350
 A;Molecule type: DNA
 A;Residues: 1-1157 <L>
 A;Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:9547554; PIDN:CAA85764.1; PID:95475;
 A;Experimental source: serovar tolworthi
 C;Comment: This parasporal crystal protein, active against corn borer and other insects,
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 50.5%; Score 1900; DB 2; Length 380;
 Best Local Similarity 95.5%; Pred. No. 6.6e-126;
 Matches 363; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKLKNPKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMEYENVEPVSASTI 60
 Db 1 MKLKNPKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKISEVENVEPVSASTI 60
 QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
 Db 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
 QY 121 RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSQYIALLEMFVKLPSPFAVSG 180
 Db 121 RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSQYIALLEMFVKLPSPFAVSG 180
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKELWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKELWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240
 QY 241 TGLNNLRGTNAESVVRNQFRDMTLMVLDAVLPSTQMYPIKTAOLTRVYTDAT 300
 Db 241 TGLNNLRGTNAESVVRNQFRDMTLMVLDAVLPSTQMYPIKTAOLTRVYTDAT 300
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLRSWSNTQYMMNW 360
 Db 301 GTVHPNASFATTTWNNAAPSFTIESAVVRNPHLLDFLEQVTIYSLRSWSNTQYMMNW 360
 QY 361 GGHKLEFRITGGTLNISTQG 380
 Db 361 GGHKLEFRITGGTLNISTQG 380

RESULT 7

Db 709 YGHDKKMLLEAVRAAKRLSRERNL 732

RESULT 8

S32645

parasporal crystal protein cry1Gal - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S32645

R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32645

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1166 <I>AM>

A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 39.4%; Score 1482.5; DB 2; Length 1166;

Best Local Similarity 46.1%; Pred. No. 8.9e-96;

Matches 325; Conservative 101; Mismatches 204; Indels 75; Gaps 17;

Qy 41 DCLKMSYE---NVEPFVSASTIQGIGIAGKILGTLGVPPFAGQVASLYSFILGELWPK 96

Db 13 NCLNPESEIFNARNNGFLVSQVSSGL---TRFLEAAVPEAGFALGFDIIWGAL--- 66

Qy 97 GKNQWEIFMEHVEEIIQKISTYARNKALTDLKGLDALAVYHDSLESVGNRNTRARS 156

Db 67 GVDQWSLFRQIEQLRQTELEARNRATAITLGLSSYLYVEALREWENDPNPASQE 126

Qy 157 VVKSQYIALELMFVKQLPSFAVSGEEVPLPIYAQAANLHLLLRDAIFGKFWGLSSSE 216

Db 127 RYTRFRLTDDAIVTGLPTLAIRNLEVNLSVYTAQANLHLSLLRDVYFGERWGLTOAN 186

Qy 217 ISTFYNRQVERAGDYSDHCWKYSTGLNLRGTNAESWVRYNQRRDMLVLDLVALFP 276

Db 187 IEDLYRLTNSIQEYSDHCARWYNQGLNEIGGISR---RYLDFQRDLTISVLIDIVALFP 242

Qy 277 SYDTQMYPIKTTAQLTREVTDAI--GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPH 334

Db 243 NYDIRTYPIPTQSLTREIYTPVAVAGNI-----NFGLSIANVLRAHP 285

Qy 335 LLDLFLEQVTIYSLLSWSNTQYMNWGGHKLFRFTIG-GTLN-----ISTQGSTNTS 385

Db 286 LMDFIDRIVITNSVR--STPY--WAGHEVISRRTGQGGNEIRFPLYGVAANAEPVPT 340

Qy 386 INPVTLPFTSRDVRYES-----LAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFY 439

Db 341 IRPTGFTDEQWYRARSRVVSFRSSGQDFSLVDAG-----FLT-IPSAVSIYR 389

Qy 440 PGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVKALVYSWTHR 494

Db 390 NGF-GFNT---DTIDEIPIEGTDP--FTGYSHRLCHVGFSLASSPFIQYARAPIFSWTHR 443

Qy 495 SADRTWTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNNPP 554

Db 444 SATLTNTIAPDVITQIPLVKAFNLHSGATIVKPGFTGGDILRRTNVGSGFDMRVNITAP 503

Qy 555 FAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRTVGFTTTPSFL 614

Db 504 LSQRYRVRIRYASTTDLQFYTNINGTTINGNFSTMDSGDDLOQYGRFRVAGTTPTTFS 563

Qy 615 DVQSTFTIGANWFSSGNEVYIDRIEFPVPEVTYEAEDFEKAQEKVATLFTSTNPRGLKT 674

Db 564 DANSTFTIGAFGFSPPNNEVYIDRIEFPVPAEVTFEAEYDLEKAQKAVNALFTSSNQIGLKT 623

Qy 675 DVKDYTHIDQVSNLVSDEFLDEKRELFEIVKYAKQLHIERNM 719

Db 624 DVTVDYHIDQVSNLVECLSDBEFLDEKRELSEKVKHAKRLSDERNL 668

RESULT 9.

A26513

parasporal crystal protein - Bacillus thuringiensis (strain aizawai)

C:Species: Bacillus thuringiensis

C:Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004

C:Accession: A26513

R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.; Ohkawa, H.

Gene 53, 113-119, 1987

A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis

A:Reference number: A26513; MUID:87248103; PMID:3297927

A:Accession: A26513

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1155 <O>ED>

A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 39.2%; Score 1474; DB 2; Length 1155;

Best Local Similarity 44.4%; Pred. No. 3.5e-95;

Matches 315; Conservative 113; Mismatches 227; Indels 54; Gaps 12;

Qy 36 NINHEDCLKMSEYENVE-PTVSASTIQG-----IGIAGKILGTLGVPPFAGQVASIYS 87

Db 4 NPINNECIPYNCLSNPEVEVLGGERIETGYTPIDISLSTQLLSEF-VPGAGFVLGLVD 62

Qy 88 FILGELMPKQKNQWEIFMEHVEEIIQKISTYARNKALTDLKGLDALAVYHDSLESWVG 147

Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFPARNQALSRLEGLSNLYQIYAESFREWEA 119

Qy 148 NRNTRARSVYKSOYIALBMLFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFG 207

Db 120 DPTNPALREEMRIQPNDMNSALTTAIPLFAVQNVQVPLSVYVQAANLHLSVLRDVSFVG 179

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSDHCWKYSTGLNLRGTNAESWVRYNQRRDMLTM 267

Db 180 QRWGFDAATINSRYNDLTRLIGNYTHDAVRWYNTGLERWGPDSRDRWIRYNQRRRLTLT 239

Qy 268 VLDLVALFPDYDTQMYPIKTTAQLTREVTDAI GTVHPHPSFTSTTWYNNAPSFAIEA 327

Db 240 VLDIVSLFPNVDSTRYPPIRTVSQLTREIYNPV-----LENFDSFRALAAQ 285

Qy 328 AV---VRNPHLLDFLEQVTIYSLLSR----WSNTQYMN---WGGHKLFRFTIGTTLNIS 377

Db 286 GIEGSIIRSPHLMIDLNSITITDAHRGEYWSGHQIMASPVGSGPEFTFPLYGTMGNA 345

Qy 378 TQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDNF 437

Db 346 PQQRIVAQLGGVYRTLSLTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSNL 396

Qy 438 YYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVYS 490

Db 397 PSAVYRKSGT--VDSLDEIIPPQNNVPPRQGFSHRLSHVSMFRSGFSNVSIIRAPMFS 454

Qy 491 WTHRSADRNTWTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVN 550

Db 455 WIHRSABFNIIIPSSQITQIPLTKSTNLCSGTSVVKGPGFTGGDILRRTSPGOISTLRVN 514

Qy 551 INPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRTVGFTTTP 610

Db 515 ITAPLSQRYRVRIRYASTTDLQFHTSIDGRPINQGNFSAATMRGEDLDYKTRTVGFTTTP 574

Qy 611 FSLFDVQSTTTIGANWFSSGNEVYIDRIEFPVPEVTYEAEDFEKAQEKVATLFTSTNPR 670

Db 575 FNFSNGSSVFTLSAHVFNCSGNEVYIDRIEFPVPAEVTFEAEYDLEKAQKAVNELTSSNQI 634

Qy 671 GLKTDVKDYHIDQVSNLVSDEFLDEKRELFEIVKYAKQLHIERNM 719

Db 635 GLKTDVTDYHIDQVSNLVECLSDBEFLDEKRELSEKVKHAKRLSDERNL 683

RESULT 10

S32649

JD00002
parasporal crystal protein cryIAb3 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot
C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from
A;Reference number: A90025
A;Accession: A90025
A;Molecule type: mRNA
A;Residues: 1-1155 <KON>
A;Cross-references: UNIPROT:P06578
A;Experimental source: subsp. kurstaki
R;Geiser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal protei
A;Reference number: A91560; MUID:87163505; PMID:3557124
A;Accession: A91560
A;Molecule type: DNA
A;Residues: 1-1155 <GEI>
A;Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124
A;Experimental source: subsp. kurstaki
R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
A;Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal
A;Reference number: A90955; MUID:86300092; PMID:3743328
A;Accession: A90955
A;Molecule type: DNA
A;Residues: 1-1155 <WAB>
A;Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720
A;Experimental source: subsp. berliner
R;Chak, K.F.; Jen, J.C.
submitted to the EMBL Data Library, October 1990
A;Description: Complete nucleotide sequence and expression in Escherichia coli of a cry
A;Reference number: S14555
A;Accession: S14555
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1155 <CHA>
A;Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273
R;Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerck
Eur. J. Biochem. 161, 273-280, 1986
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thur
A;Reference number: A26461; MUID:87054026; PMID:3023091
A;Accession: A26461
A;Molecule type: DNA
A;Residues: 1-730, 'L', '732-784', 'R', '786-1155 <HOF>
A;Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255
A;Experimental source: strain berliner 1715
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C;Genetics:
A;Gene: cry-1-2; bt2
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
F;82-586/Product: toxic peptide #status predicted <TXP>
F;82-300/Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted

Query Match 39.1%; Score 1471; DB 2; Length 1174;
Best Local Similarity 44.8%; Pred. No. 5.8e-95;
Matches 325; Conservative 103; Mismatches 202; Indels 96; Gaps 17;
36 NINHE---DCLKMEYENVEPVVSASTIQIGIA-GKILGTGLGVPPFAGQVASLYSPIL 90
4 NQOCVPYCNLSNPEVEILSEERSTGRPLDLSILTRFLLSEFVPGVGVAFGLFDLIW 63
91 GELWPKGKNQWEIFMEHVEEIIINQKISFYARKALTDKLGCDALAVYHDSLESWVGKRN 150
64 GFITP---SEWSLFLQIEQLQRIETLERNRAITTLGLADSYEVLEALREWEENPN 120
151 NTRARSVKSOYIALELMFVQKLPFSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW 210
121 NQALREDVRIRFANTDDALITAINFTLTSFEPLLSVYVQAANLHLLLRDASVFGQW 180
211 GLSSSEISFTFNQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDMLTMD 270
181 GLDIATVNNHYNLNLIIHRYTEHCLDYNQGLNLTGNTFQWSPNQFRELTLTVD 240
271 LVALFSDYDQMPYKTTAQLTREYVTDAGTVHPHPSFTSTTYNNNAPS-FSAIEAAV 329
241 IVALFPNYDARAYPIQTSSQLTREITYTSV--IEDSP-----VSANIPGNFRAEFG- 290
330 VRNPHLDLFLEQVITYSLRSWNTQYMMWGGHKLERTIGTGLNLTSTQGSTNTSINPV 389
291 VRPHLMDFMN-----SLFVTAETVRSQTWGGHLV-----SSRNTAGNPI 331
390 TLFP-----TSRDVYRTESLAGLNLFLTPQVNGVPRVDHFWKVFVTHPIAS 434
332 NFPIYGINPGGAIWAIDEDPRFYRT-----LSDPV-----FVRGGFGN 371
435 DNFYYPGAGIGTQLQ-----DSENELPPATGQPNYESYSHRLSHI----- 476
372 PH-YVLGRLGVAFQQTGNTHTFRNSGTIDSLDIPQDNSGAPWNDYSHVLNHTVFR 430
477 --GLISASHV-KALVYSWTHRSADRTNIEPNSITQIPLVKAFLNLSSGAADVVRGPGTGG 533
431 WPGBIAGSDSWRAPMFSWTHRSADRTNIIINPNIITQIPAKAHLNLSGTVVRGPGTGG 490
534 DILRTNTGFGDIRVNINPPFAQRVIRYASVTTDLQFHTSINGKALNQGNFSATNWR 593
491 DLLRTNTGTFADIRVNITGPLSRVIRYASTTDLQFTRINGTSVNOGNFQRTNWR 550
594 GEDLDYKTFRTVGTTPPSFLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDF 653
551 GGNLESGNFTAGTSTPPFSNAQSTFTLTGTQAFSN-QEVYIDRIEFVPAEVTFAESDL 609
654 EKAQBKVTAFTSTNPRGLKTDVKYHIDQVNLVLESLSDFYLDKRELFVVKYAKOL 713
610 BRAQKAVNALFTSISQLGLKNTVGYHIDQVSNLVACLSDDFCLDEKRELSKVKAHKL 669
714 HIERNM 719
670 SDRNL 675

Db 120 DPTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267
Db 180 QRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDRWIRYNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTTAQLTREVTDAIGTVHPPHSFTSTTWNNAAPS- -S 323
Db 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYNPV- - - - -LENFDCSFRGSAQ 285
Qy 324 AIEAAVVRNPHLLDFEQVTIYLSLSR- - - - -WSNTQYMM- - - - -WGGHKLFRFTIGTINI 376
Db 286 GIEGS-IRSPHLMILNSITITDAHRGEYWSGHQIMASPVGSGPFTFPLVGTMGNA 344
Qy 377 STQGSNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPRVDFHWKFVTHPIASDN 436
Db 345 APQQRIVAQGGVYRTLSSTLYRRPFNIGIN- - - - -NQUSVLDGTEPAYG- - - - -TSSN 395
Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI- - - - -SASHVKALVY 489
Db 396 LPSAVYRKSGT- - - - -VDSLDEIPPQNNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTCTGFDIRV 549
Db 454 SWHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSPQISTLRV 513
Qy 550 NINPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTT 609
Db 514 NITAPLSQRYRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFTT 573
Qy 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKVTALFTSTNP 669
Db 574 PFNFSNGSSVFTLSAHVFNSENEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELFTSSNQ 633
Qy 670 RGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 634 IGLKTDVTDYHIDQVSNLVECLSDREFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 12
A29125
parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <PIS>
A:Cross-references: UNIPROT:Q9f296; UNIPROT:Q93T21
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 39.0%; Score 1467; DB 2; Length 1156;
Best Local Similarity 44.5%; Pred. No. 1.1e-94;
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG- - - - -IGTAGKILGTGVPPFAGQVASIYS 87
Db 4 NPNINECIPNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESVWG 147
Db 63 IIWGI- - - - -GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLSNLYQIYAESFREWEA 119
Qy 148 NRNNTARSVVKSVQYIALELMFVQKLPSFAVSGEEVPLPIYAAQANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267
Db 180 QRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDRWIRYNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTTAQLTREVTDAIGTVHPPHSFTSTTWNNAAPS- -S 323
Db 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYNPV- - - - -LENFDCSFRGSAQ 285
Qy 324 AIEAAVVRNPHLLDFEQVTIYLSLSR- - - - -WSNTQYMM- - - - -WGGHKLFRFTIGTINI 376
Db 286 GIEGS-IRSPHLMILNSITITDAHRGEYWSGHQIMASPVGSGPFTFPLVGTMGNA 344
Qy 377 STQGSNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPRVDFHWKFVTHPIASDN 436
Db 345 APQQRIVAQGGVYRTLSSTLYRRPFNIGIN- - - - -NQUSVLDGTEPAYG- - - - -TSSN 395
Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI- - - - -SASHVKALVY 489
Db 396 LPSAVYRKSGT- - - - -VDSLDEIPPQNNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTCTGFDIRV 549
Db 454 SWHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSPQISTLRV 513
Qy 550 NINPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTT 609
Db 514 NITAPLSQRYRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFTT 573
Qy 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKVTALFTSTNP 669
Db 574 PFNFSNGSSVFTLSAHVFNSENEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELFTSSNQ 633
Qy 670 RGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 634 IGLKTDVTDYHIDQVSNLVECLSDREFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 13
A22798
parasporal crystal protein - *Bacillus thuringiensis*
C:Species: *Bacillus thuringiensis*
C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: A22798
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A:Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuring*
A:Reference number: A22798; MUID:85232070; PMID:2989108
A:Accession: A22798
A:Molecule type: DNA
A:Residues: 1-934 <SHI>
A:Cross-references: UNIPROT:Q9S5V8; GB:M10917; NID:gl43100; PIDN:AAA22552.1; PID:G551713
C:Comment: The authors translated the codon ACA for residue 264 as Ser.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.7%; Score 1454.5; DB 2; Length 934;
Best Local Similarity 43.5%; Pred. No. 5.8e-94;
Matches 310; Conservative 119; Mismatches 222; Indels 61; Gaps 12;

Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG- - - - -IGTAGKILGTGVPPFAGQVASIYS 87
Db 4 NPNINECIPNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESVWG 147
Db 63 IIWGI- - - - -GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLSNLYQIYAESFREWEA 119
Qy 148 NRNNTARSVVKSVQYIALELMFVQKLPSFAVSGEEVPLPIYAAQANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267

Tue Feb 15 10:07:51 2005

us-10-019-823b-55.rpr

Db 180 QRMGDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWVYNOFRRELTLT 239
QY 268 VLDLVALPSPDYTMYPKTAQLTREVTDAIGTVHPHPSFTSTTWYNNAPSFSAIEA 327
Db 240 VLDLVALPSPDYTMYPKTAQLTREVTDAIGTVHPHPSFTSTTWYNNAPSFSAIEA 285
QY 328 AV---VRNPPLDLFLEQVITYSLLSRWSNTQYMMWGGHKLKLEFRTIGGT---LNISTQGS 381
Db 286 RIEQNIQPHLMIDLINRITTYDVHVG-----FNWWSGHQITASVFGSGPEFAFPLFGN 340
QY 382 TMTSINPVTLPFTSRDVRTESE-----AGNLFLTPQVNGVPRVDFHWKVFTHPI 432
Db 341 AGNAAPPVLSLGLGIFRTLSPLRYRIILGSGPN---NQELFVLDGTGTFESFASLTNNL 397
QY 433 ASDNFYPCYAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGTGTV-----DSLVDIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFDI 547
Db 451 TFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRNTGTGFDI 510
QY 548 RVNINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 570
QY 608 TTPFSFLDVQSTFTTGAMNFSNGNEVYIDRIEFPVPEVYEAEDFEKAQKVTAFTST 667
Db 571 TTPFNFSNGSVFVLSAHVFNSENGNEVYIDRIEFPVPEVYEAEDFEKAQKVTAFTST 630
QY 668 NPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 631 NQIGLKTDTVTDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 682

RESULT 14
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N:Alternate names: 135K insecticidal protein
C:Species: Bacillus thuringiensis
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0241
R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A:Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A:Reference number: JT0241
A:Accession: JT0241
A:Molecule type: DNA
A:Residues: 1-1176 <SHI>
A:Cross-references: UNIPROT:P02965
A:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins
C:Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.7%; Score 1453.5; DB 2; Length 1176;
Best Local Similarity 43.5%; Pred. No. 9.9e-94;
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps 12;

QY 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPPAGQVVASLYS 87
Db 4 NPINCEIPYCNLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIFEMHVEEIIINOKISTYARNKALTDKGLGDALAVYHDSLESWVG 147
Db 63 IIVGIF---GPSQWDAFLVQIEQLINQRIEFARQNAISRLGSLNLYQIYAESFREWEA 119
QY 148 NRNNTTRSVKQYQYIALELMFVQKLPSPFVSGEVEPLPIYAOANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTATPFLFAVQNYQVPELLSVYVQAANLHLSVLVDVSVFG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKYSTGLNNLACTNAESWVRYNQFRDMLTLM 267

Db 180 QRMGDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWVYNOFRRELTLT 239
QY 268 VLDLVALPSPDYTMYPKTAQLTREVTDAIGTVHPHPSFTSTTWYNNAPSFSAIEA 327
Db 240 VLDLVALPSPDYTMYPKTAQLTREVTDAIGTVHPHPSFTSTTWYNNAPSFSAIEA 285
QY 328 AV---VRNPPLDLFLEQVITYSLLSRWSNTQYMMWGGHKLKLEFRTIGGT---LNISTQGS 381
Db 286 RIEQNIQPHLMIDLINRITTYDVHVG-----FNWWSGHQITASVFGSGPEFAFPLFGN 340
QY 382 TMTSINPVTLPFTSRDVRTESE-----AGNLFLTPQVNGVPRVDFHWKVFTHPI 432
Db 341 AGNAAPPVLSLGLGIFRTLSPLRYRIILGSGPN---NQELFVLDGTGTFESFASLTNNL 397
QY 433 ASDNFYPCYAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGTGTV-----DSLVDIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFDI 547
Db 451 TFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRNTGTGFDI 510
QY 548 RVNINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 570
QY 608 TTPFSFLDVQSTFTTGAMNFSNGNEVYIDRIEFPVPEVYEAEDFEKAQKVTAFTST 667
Db 571 TTPFNFSNGSVFVLSAHVFNSENGNEVYIDRIEFPVPEVYEAEDFEKAQKVTAFTST 630
QY 668 NPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 631 NQIGLKTDTVTDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 682

RESULT 15
S02134
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai ICI)
N:Alternate names: delta-endotoxin ICI; entomocidal crystal protein
C:Species: Bacillus thuringiensis
A:Variety: strain aizawai ICI
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S02134; S04994
R:Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A:Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICI entomocidal crystal
A:Reference number: S02134; MUID:89083518; PMID:3205732
A:Accession: S02134
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1155 <HAI>
A:Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278
A:Experimental source: strain aizawai ICI
R:Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes
A:Reference number: S04994; MUID:89362455; PMID:2769751
A:Accession: S04994
A:Molecule type: DNA
A:Residues: 429-449, 'A', 451-724 <HAW>
A:Cross-references: EMBL:X16315
A:Experimental source: strain aizawai ICI
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.6%; Score 1450; DB 2; Length 1155;
Best Local Similarity 44.1%; Pred. No. 1.7e-93;
Matches 313; Conservative 112; Mismatches 229; Indels 56; Gaps 13;

QY 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPPAGQVVASLYS 87

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds
(without alignments)
4539.261 Million cell updates/sec

Title: US-10-019-823B-55

Perfect score: 3760

Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	1 C1IA_BACTK	Q45752 bacillus th
2	3760	100.0	719	2 Q6X181	Q6x181 bacillus th
3	3755	99.9	719	2 Q93N05	Q93nj5 bacillus th
4	3754	99.8	719	2 Q85796	Q85796 bacillus th
5	3625	96.4	719	2 Q8KY61	Q8ky61 bacillus th
6	3551	94.4	719	2 Q9F0P8	Q9f0p8 bacillus th
7	3520	93.6	719	1 C1IB_BACTE	Q45709 bacillus th
8	3397	90.3	719	1 C1ID_BACTU	Q9xdl1 bacillus th
9	3377	89.8	719	1 C1IC_BACTU	Q87404 bacillus th
10	2446.5	65.1	1229	1 C1BB_BACTU	Q45739 bacillus th
11	2446.5	65.1	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2278.5	60.6	1228	2 Q93T75	Q93t75 bacillus th
13	2277.5	60.6	1228	2 Q93NM5	P05517 bacillus th
14	2269.5	60.4	1228	2 Q93NM5	Q93nm5 bacillus th
15	2195.5	58.4	849	2 Q6PYW8	Q6pyw8 bacillus th
16	2195.5	58.4	1227	1 C1BE_BACTU	Q85805 bacillus th
17	2112.5	56.2	1231	2 Q8KNY2	Q8kny2 bacillus th
18	2107.5	56.1	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
19	1988.5	52.9	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1904	50.6	381	2 Q45740	Q45740 bacillus th
21	1670.5	44.4	1157	1 C8AA_BACUK	Q45704 bacillus th
22	1658	44.1	1144	2 Q8KZL7	Q8kz17 bacillus th
23	1492	39.7	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1486.5	39.5	1169	1 C8BA_BACUK	Q45705 bacillus th
25	1482.5	39.4	1166	1 C1GA_BACTU	Q45746 bacillus th
26	1478	39.3	1167	1 C1JA_BACTU	Q45738 bacillus th
27	1477	39.3	1169	1 C1FB_BACTM	Q66377 bacillus th
28	1471	39.1	1174	2 Q45749	Q45749 bacillus th
29	1467	39.0	1155	1 C1AB_BACTK	P06578 bacillus th
30	1467	39.0	1155	2 Q7BE98	Q7be98 bacillus th
31	1467	39.0	1155	2 Q9F296	Q9f296 bacillus th

RESULT 1-

C1IA_BACTK

ID	C1IA_BACTK	STANDARD;	PRT;	719 AA.
AC	Q45752; P71092; Q45750; Q45751; Q45756;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin			
DE	CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
GN	Names=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryVI;			
OS	Bacillus thuringiensis (subsp. kurstaki).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=29339;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSIR732;			
RX	MEDLINE=93298009; PubMed=8517758;			
RA	Gleave A.P., Williams R., Hedges R.J.;			
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis			
RT	serotypes for the presence of cryV-like insecticidal protein genes and			
RT	characterization of a cryV gene cloned from B. thuringiensis subsp.			
RT	kurstaki.";			
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=JHCC4835;			
RX	MEDLINE=92269582; PubMed=1588820;			
RA	Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RT	"Identification and characterization of a novel Bacillus thuringiensis			
RT	delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."			
RL	Mol. Microbiol. 6:1211-1217(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HD-1;			
RX	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus			
RT	thuringiensis and cloning of cryV-type genes from Bacillus			
RT	thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.			
RT	entomocidus.";			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AB88;			
RX	MEDLINE=96178985; PubMed=8606196;			
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,			
RA	Craig J.A., Koziel M.G., Estruch J.J.;			
RT	"Cloning of a cryV-type insecticidal protein gene from Bacillus			
RT	thuringiensis: the cryV-encoded protein is expressed early in			
RT	stationary phase.";			
RL	J. Bacteriol. 178:2141-2144(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=61;			

ALIGNMENTS

RA Selvapandiyan A., Bhatnagar R.K.;
RT "Isolation, cloning and expression of cryV gene.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC
CC Active on Plutella xylostella and Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to licenses@isb-sib.ch).
CC
CC -----
CC EMBL; M98544; AAA22354.1; -
CC EMBL; X62821; CAA44633.1; -
CC EMBL; L36338; AAC36999.1; -
CC EMBL; L49391; AAB00958.1; -
CC EMBL; Y08920; CAA70124.1; -
CC PIR; I39815; I39815.
CC PIR; S25383; S25383.
CC HSSP; P02965; IC1Y.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
KW VARIANT 159 159 K -> R (in strain 61).
FT D -> Y (in strain JHCC4835 and strain HD-
FT VARIANT 233 233 1).
FT
FT
FT VARIANT 443 443 A -> V (in strain AB88).
FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 100.0%; Score 3760; DB 1; Length 719;
Best Local Similarity 100.0%; Pred. No. 3e-251;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNINHEDCMKSEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNINHEDCMKSEYENVEPFSASTI 60

QY 61 QTGIGIAGKILGTLGVPPAGQVASIYSLFGLWPKGNQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTLGVPPAGQVASIYSLFGLWPKGNQWEIFMEHVEEIIINOKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGNGRNNTRARSVVKVSKQYIALELMFVKLPFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWGNGRNNTRARSVVKVSKQYIALELMFVKLPFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240

QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDFALPSPYDTQMPYIKTAQLTREVYDAI 300
DB 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDFALPSPYDTQMPYIKTAQLTREVYDAI 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAAEEAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAAEEAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLTPQVNGVPR 420

DB 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLTPQVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFFYPGYAGIGITQLODSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFFYPGYAGIGITQLODSNELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTIENSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTIENSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVINPFPAAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600
DB 541 TGTFGDIRVINPFPAAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600
QY 601 TERTVGTTFPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAEYDFEKAQEKV 660
DB 601 TERTVGTTFPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 2
QX181
ID Q6X181 PRELIMINARY; PRT; 719 AA.
AC O6X181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CryII.
GN Name=cryII;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;
SQ

Query Match 100.0%; Score 3760; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3e-251;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNINHEDCMKSEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNINHEDCMKSEYENVEPFSASTI 60

QY 61 QTGIGIAGKILGTLGVPPAGQVASIYSLFGLWPKGNQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTLGVPPAGQVASIYSLFGLWPKGNQWEIFMEHVEEIIINOKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGNGRNNTRARSVVKVSKQYIALELMFVKLPFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWGNGRNNTRARSVVKVSKQYIALELMFVKLPFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240


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QY 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
Db 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMNW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTTTPSFQDVGSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
Db 601 TFRVGTFTTTPSFQDVGSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Crylia.
GN Name=crylia;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.9%; Score 3755; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 6.6e-251;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQNINHEDECLMSEYENVEPVASATI 60
Db 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQNINHEDECLMSEYENVEPVASATI 60
QY 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
```

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Db 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGIGDALAVYHDSLESWVGNNRNRTRARSVVKSYQYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLESWVGNNRNRTRARSVVKSYQYIALELMFVQKLPFAVSG 180
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISSTFYNRQVERAGDYSCHCVKWS 240
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISSTFYNRQVERAGDYSCHCVKWS 240
QY 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
Db 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMMNW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGICTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTTTPSFQDVGSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
Db 601 TFRVGTFTTTPSFQDVGSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
O85796 PRELIMINARY; PRT; 719 AA.
ID O85796;
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryI01;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S101;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
```



```
DE GN Name=cryII;
OS Bacillus thuringiensis.
OC Plasmid pBTC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007;
RX MEDLINE=22837682; PubMed=12957903;
RA DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
RA Hu Y., Li G., Huang D.;
RT "Identification of cryII-type genes from Bacillus thuringiensis
RT strains and characterization of a novel cryII-type gene.";
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; ICIY.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_N; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid.
SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 94.4%; Score 3551; DB 2; Length 719;
Best Local Similarity 93.6%; Pred. No. 8.5e-237;
Matches 673; Conservative 26; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNQKHQSFSNAKVDKISTDSLKNETDIELQINHEHDLCKMSEYENVEPVFSASTI 60
DB |||||
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120
DB |||||
QY 61 QTGIGIAGKILGTGVFPAGQIASLSYFILGELWPKGKSQWEIFMEHVBEIINQKISTYA 120
DB |||||
QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNTRRSVKSQYIALELMFVKQLPSFAVSG 180
DB |||||
QY 121 RNIALADLKLGDALAVYHDSLESWGNRNTRRSVKSQYIALELMFVKQLPSFAVSG 180
DB |||||
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKGLSSSEISTFYNRQVERAGDYSHCVKWYS 240
DB |||||
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKGLSSNSISTFYNRQVERTSDYSHCVKWYS 240
DB |||||
QY 241 TGLNLRGTNAESWVRNQFRDMLMVLVDLVALFPSTQMYPIKTTAQLTREVTYDAI 300
DB |||||
QY 241 TGLNLRGTNAESWVRNQFRDMLMVLVDLVALFPSTQMYPIKTTAQLTREVTYDAI 300
DB |||||
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLGRWSNTQYMNW 360
DB |||||
QY 301 GTVHPNASFASTWYNNAPSAIESAVVRNPHLLDFLEQVTIYSLGRWSNTQYMNW 360
DB |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGNLFLTPQVNGVPR 420
DB |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGNLFLTPQVNGVPR 420
DB |||||
QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB |||||
QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB |||||
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
DB |||||
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
DB |||||
QY 541 TGTFGDIRVNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB |||||

Db 541 TGTFGDIRVNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TERTVGTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
DB |||||
QY 601 TERTVGTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
DB |||||
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719
DB |||||
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719
DB |||||

RESULT 7
CLIB_BACTE STANDARD; PRT; 719 AA.
ID Q45709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pestigical crystal protein cryIIB (Insecticidal delta-endotoxin
DE CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIB; Synonyms=cryII(b), cryv, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S.; Park S.-H.; Choi S.-K.; Koo B.T.; Lee S.T.; Kim J.I.;
RT "Distribution of cryv-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryv-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; U07642; AAA82114.1; -.
CC PIR; I40590; I40590.
CC HSSP; P02965; ICIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

Query Match 93.6%; Score 3520; DB 1; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.2e-234;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNQKHQSFSNAKVDKISTDSLKNETDIELQINHEHDLCKMSEYENVEPVFSASTI 60
DB |||||
QY 1 MKLKNQKHQSLSNAKVDKIATDSLKNETDIELKNMNEHDLCKMSEHESIDPFVSASTI 60
DB |||||
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QY 61 QTGIGIAGKILGTLGVPFAGQVAVSLYFGLGELWPKGKQWEIEMHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVPFAGQVAVSLYFGLGELWPKGKQWEIEMHVEEIIINQKISTYA 120
QY 121 RNKALTDLGLDALAVYHDSLESWGNNRNRTRARVSVKSOYIALELMFVKQLPSFAVSG 180
Db 121 RNKALSDRLGLDALAVYHDSLESWGNNRNRTRARVSVKSOYIALELMFVKQLPSFAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPYDTOMYPIKTTAQLTREVYTDAL 300
Db 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPYDTOMYPIKTTAQLTREVYTDAL 300
QY 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
Db 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
QY 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEBDLYK 600
Db 541 TGTFGDIRVNINPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEBDLYK 600
QY 601 TPTVGTFTTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TPTVGTFTTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 8
CILD_BACTU STANDARD; PRT; 719 AA.
ID CILD_BACTU STANDARD; PRT; 719 AA.
AC Q9XLLI;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin
DE CryII(d)) (crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryII; Synonyms=cryII(d), NRCryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RX MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
RT gene".
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae. Active on Plutella
CC xylostella and on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

terminus.
-!- SIMILARITY: Belongs to the delta endotoxin family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AF047579; AAD44366.1; -.
DR HSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
Query Match 90.3%; Score 3397; DB 1; Length 719;
Best Local Similarity 89.8%; Pred. No. 3.8e-226;
Matches 646; Conservative 35; Mismatches 38; Indels 0; Gaps 0;
QY 1 MKLKNQKHQSFSSNAKVDKISTSLKNETDIELQNIHEDCLKMSYENVEFVSASTI 60
Db 1 MKSKQNNYRSFSSNATVDKFTDPLEHNTNMLQNSHEDCLKMSYEVESVEFVSASTI 60
QY 61 QTGIGIAGKILGTLGVPFAGQVAVSLYFGLGELWPKGKQWEIEMHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVPFAGQVAVSLYFGLGELWPKGKQWEIEMHVEEIIINQKISTYA 120
QY 121 RNKALTDLGLDALAVYHDSLESWGNNRNRTRARVSVKSOYIALELMFVKQLPSFAVSG 180
Db 121 RNKALADLGLDALAVYHDSLESWGNNRNRTRARVSVKSOYIALELMFVKQLPSFAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPYDTOMYPIKTTAQLTREVYTDAL 300
Db 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPYDTOMYPIKTTAQLTREVYTDAL 300
QY 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
Db 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
QY 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEBDLYK 600
Db 541 TGTFGDIRVNINPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEBDLYK 600
QY 601 TPTVGTFTTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TPTVGTFTTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719


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Db 661 TAMFTSTNLRLKTNVTDCHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLNIERNM 719
RESULT 9
CLIC_BACTU
ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC -----
DR EMBL; AF056933; AAC62933.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_N.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid; Sporulation; Toxin.
KW SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;
Query Match 89.8%; Score 3377; DB 1; Length 719;
Best Local Similarity 89.8%; Pred. No. 9.1e-225;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MKLKNQDKHOFSSNAKVDKISTSLKNETDIELQINHEDECLKMSEYENVPFVSASTI 60
Db 1 MKLKNPDKHQTLSSNAKVDKIATSLKNETDIELKNMNEDEYLRMSEHESIDPFVSASTI 60
Qy 61 QTGIGTAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGTAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGLDALAVYHDSLESWGVRNTRNRSVVKQSYQYIALELMFVKQLPSFAVSG 180
Db 121 RNKALTDLKGLDALAVYHDSLESWGVRNTRNRSVVKQSYQYIALELMFVKQLPSFAVSG 180
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNRQVERAGDYSDHCVKWYS 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNRQVERAGDYSDHCVKWYS 240
Qy 241 TGLNLRGTNAESWRYNQRRDMLVLDLVALFPSPYDTQMPYIKTAQLTRVYTDAL 300
Db 241 TGLNLRGTNAESWRYNQRRDMLVLDLVALFPSPYDTQMPYIKTAQLTRVYTDAL 300
Db 241 TGLNLRGTNAESWRYNQRRDMLVLDLVALFPSPYDTQMPYIKTAQLTRVYTDAL 300
Qy 301 GTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMMNM 360
Db 301 GTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMMNM 360
Qy 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHKKFVTHPIASDNFYYPGYAGITQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHKKFVTHPIASDNFYYPGYAGITQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSGAAVVRGFGTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSGAAVVRGFGTGGDILRTN 540
Qy 541 TGTGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TERTVGTTPFSELDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660
Db 601 TERTVGTTPFSELDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLNIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLNIERNM 719
RESULT 10
C1BB_BACTU
ID C1BB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbB (Insecticidal delta-endotoxin
DE CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbB; Synonyms=cryET5, cryIb(b);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RL "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects."
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC -----
DR EMBL; L32020; AAA22344.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
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Qy 543 TFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMNRGDLDTKTF 602
Db 541 TFGDIRVNINPVSQRYRIRYASTTDLQFHTSINGKAINQNFSAATMNRGDLDTKTF 600
Qy 603 RTVGFTTTPFSLDVOSTFTTGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662
Db 601 RTAGFTTTPFSLDVOSTFTTGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 659
Qy 663 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEDEFYLDKRELFLVYKAKQLHIERNM 719
Db 660 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEDEFYLDKRELFLVYKAKQLHIERNM 716

RESULT 12
ID Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Names-cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defence response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.6%; Score 2278.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred No. 1.8e-148;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNH-----EDCLKMSEVENVEPVFVASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLDPDARIEDSLCIAEGNNIDPFVASTVQTGINIAGRI 61
Qy 71 LGTLGVPPFAGQVASYLFIQELWPKQKQWEIPEHVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPFAGQLASFYSLVGLWPRGRDQWEIPEHVEEIIINQKISTYARNKALTDLKG 121
Qy 131 LGDALAVYHDSLESVGNRNTRARSVKSQYIALFELMPVQKLPFSFAVSGEEVPLLPYA 190
Db 122 LGDSFRAYQOQSLDLEWNRDARTSVLHTQYIALFELMPVQKLPFSFAVSGEEVPLLPYA 181
Qy 191 QAANLHLLLRDASIFGKWEGLSSSEISTPYNROVERAGDYSCHVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYERQVTRDRSDYCVENYNTGLNLRGTN 241
Qy 251 AESWRYNQPRDMLVLDLVALPSPDYQMPYIKTTAQLTREVTDAIGTVHPHSFT 310
Db 242 AASWRYNQPRDMLVLDLVALPSPDYQMPYIKTTAQLTREVTDAIGTVHPHSFT 299
Qy 311 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNMGHKLFRPTI 370
Db 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNMGHKLFRPTI 359
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Qy 371 GGTLMNSTOGSTNTSINPVTLPSTRDVRVYTESLAGLNLF--LTPVNGVPRVDFHMKFV 428
Db 360 GGGLNTSTHGATNTSINPVTLPSTRDVRVYTESLAGLNLF--LTPVNGVPRVDFHMKFV 416
Qy 429 THP-----TASDNFYYPGAGIGTQLODSENELPPEATQPNYSEYSHRLSHIGLISASH 483
Db 417 TNPQINISDRGTANYSQP-YESPGIQLKDSSETLPPTTERPNYSEYSHRLSHIGLISASH 475
Qy 484 VKALVYSWTHRSADRTNTIENPSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGT 543
Db 476 VNPVYSWTHRSADRTNTIENPSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGT 535
Qy 544 FGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMNRGDLDTKTF 603
Db 536 FGIIRVTNGLTORIGRIFRYASTVDFFVSRGGTIVNNFRFLRTWNSGDELKYNFV 595
Qy 604 TVGFTTTPFSLDVOSTFTTGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 663
Db 596 RRAFTTTPFTQIQDIIRTSIQGLSGNGEVYIDKIEIPVTATFEAYDLEAQAQVNA 655
Qy 664 FTSTNPRGLKTDVQYHIDQVSNLVESLSEDEFYLDKRELFLVYKAKQLHIERNM 719
Db 656 FTNTNPRGLKTDVQYHIDQVSNLVESLSEDEFYLDKRELFLVYKAKQLHIERNM 711

RESULT 13
C1BA BACTK
ID C1BA BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry1Ba (Insecticidal delta-endotoxin).
DE Cry1B(a) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Names-cry1Ba; Synonyms=cryA4, cryIB(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis."
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -
CC EMBL; X95704; CAA65003.1; -
CC PIR; S00873; S00873.
CC HSP; P07130; 1DLC.
```



```
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 60.6%; Score 2277.5; DB 1; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2.1e-148;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFVSASTIQTGTGIAGKI 70
Db 2 TSNRKNEEINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQ 121

QY 131 LGDALAVYHDSLESWGVRNNTNRARSVVKVQYIALELMFVQKLPFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQOSLEWLENRDDARTSRVLYTQYIALELDFLAMPFLFAIRNQEVPLLMVYA 181

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGTN 250
Db 182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSYCVWYNTGLNSLRGTN 241

QY 251 AESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAITGVHPHPSFT 310
Db 242 AASWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAITGVHPHPSFT 310

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMMGKHLEFRTI 370
Db 300 SMWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSSASRWSTNRTMYRGHTTQSRPI 359

QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRYSAGLNLNLF--LTQPVNGVPRVDHFKVF 428
Db 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRYSAGLNLNLF--LTQPVNGVPRVDHFKVF 428

QY 429 THP-----IASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPQNISDRGTANYSQP--YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISASH 475

QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 543
Db 476 VNPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 543

QY 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTFR 603
Db 536 FGPVRTVNGPLTQRYRIGFRYASTVDFFVSRGGTTVNNFRFLRTMNSGDELKYGNEV 595

QY 604 TVGFTTPEFLDVQSTFTIGAWNFSSGNEVDRIEFVPEVTEAEYDEPEKAQKVTAL 663
Db 596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVKYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 656 FTNINPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 14
Q93NM5 PRELIMINARY; PRT; 1228 AA.
AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry1Ba.
GN Name=cry1Ba;
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OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match 60.4%; Score 2269.5; DB 2; Length 1228;
Best Local Similarity 62.6%; Pred. No. 7.7e-148;
Matches 448; Conservative 80; Mismatches 163; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFVSASTIQTGTGIAGKI 70
Db 2 TSNRKNEEINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQ 121

QY 131 LGDALAVYHDSLESWGVRNNTNRARSVVKVQYIALELMFVQKLPFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQOSLEWLENRDDARTSRVLYTQYIALELDFLAMPFLFAIRNQEVPLLMVYA 181

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGTN 250
Db 182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSYCVWYNTGLNSLRGTN 241

QY 251 AESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAITGVHPHPSFT 310
Db 242 AASWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAITGVHPHPSFT 310

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMMGKHLEFRTI 370
Db 300 SMWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSSASRWSTNRTMYRGHTTQSRPI 359

QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRYSAGLNLNLF--LTQPVNGVPRVDHFKVF 428
Db 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRYSAGLNLNLF--LTQPVNGVPRVDHFKVF 428

QY 429 THP-----IASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPQNISDRGTANYSQP--YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISASH 475

QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 543
Db 476 VNPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 543

QY 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTFR 603
Db 536 FGPVRTVNGPLTQRYRIGFRYASTVDFFVSRGGTTVNNFRFLRTMNSGDELKYGNEV 595

QY 604 TVGFTTPEFLDVQSTFTIGAWNFSSGNEVDRIEFVPEVTEAEYDEPEKAQKVTAL 663
Db 596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVKYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 656 FTNINPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
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RESULT 15
Q6PYW8 PRELIMINARY; PRT; 849 AA.
AC Q6PYW8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CryiB type crystal protein (Fragment).
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RA Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570734; AAS93797.1; -;
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON TER 849
SQ SEQUENCE 849 AA; 95886 MW; FCB98495787CF763 CRC64;

Query Match 58.4%; Score 2195.5; DB 2; Length 849;
Best Local Similarity 59.4%; Pred. No. 5.9e-143;
Matches 424; Conservative 106; Mismatches 171; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTSLKN-----ETDIELQINIHEDCLMKSEYENVEPVASITQIG 65
DB 7 NENEINALSIPAVSHSAQNMLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGLTGVFPAGQVAVSLYFILGELWPKGNQWEIFMEHVEEIIINQKISTVARNKAL 125
DB 62 IAGRIILGVLPVFPAGQVAVSLYFILGELWPKGRDPWEIFLEHVEQLIRQOVTENTRTAL 121
QY 126 TDLKGLDALAVYHDSLESVGNRNNTARSVKSQYIALLELMFVQKLPSPAVSGEEVPL 185
DB 122 ARQLGLGNSFRAYQQSLEDWLENRDDARTSVLYTQYIALEDFLNAMELFAIRNQEVPL 181
QY 186 LPIYQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSDHCWKYSTGLNN 245
DB 182 LMVYQAANLHLLLRDASLFGSEFGLTSQEIORYYERQVEKTRYSYDCARWYNTGLNN 241
QY 246 LRGTNAESWRYNQFRDRMTLMVLVLPSPSYDTQMPYIKTTAQLTRVYTDAGTVHP 305
DB 242 LRGTNAESWLYNQFRDRDLTLGLVLDLVALFPSTYTRVYPMNTSAQLTRIIYDPIGRNA 301
QY 306 HPSFTSTWYNNAPPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKL 365
DB 302 PSGFASINWNNAPPSAIEAAVIRPPHLLDFPEQLTIPSVLSRWSNTQYMNWVGHRL 361
QY 366 EPTTIGTLNISTQGSTNTSINPVLPTSRDVRATESLAGNLFLTPQVNGVPRVDFHW 425
DB 362 ERTIRSLSTSTHGTNTSINPVLQFTSRDVRATESFAGINILLTTPVNGVPRVDFHW 421
QY 426 KFTVHTIASDNFYPYAGIGTQLODSENELPPEATQPNYESYSHRSLHIGLISASHVK 485
DB 422 RNPLNSLRGSLTYTIGYTGVTGQQLFQSETELPETTERPNYESYSHRSLNIRLSGNTLR 481
QY 486 ALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDLRRNTGTGFG 545
DB 482 APVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDLRRNTGTGFG 541
QY 546 DIRVNIINPPAQRYRVRIRYASTTDLQFTSINGKAINQCNFSATMNRGEDLDYKTFRTV 605

Db 542 SMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGPSTMSANESLTSQSFRFA 601
QY 606 GFTTTPESFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQKVTALFT 665
Db 602 EFPVGISASGSQ-TAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQAVNALFT 660
QY 666 STNPRGLKTDVKDYHIDQVSNLVBESLSDBFYLDEKRELPEIVKYAKQLHIERNM 719
Db 661 NTNPRRLKTGVTDYHIDEVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 714

Search completed: February 14, 2005, 20:40:24
Job time : 85.1112 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds
(without alignments)
3909.384 Million cell updates/sec

Title: US-10-019-823B-55
Perfect score: 3760
Sequence: 1 MKLKNQDKHQSFSSNAKVCK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	16	US-10-782-020-10
2	3760	100.0	719	16	US-10-782-141-8
3	3476.5	92.5	710	15	US-10-428-961-42
4	2278.5	60.6	1228	16	US-10-809-953-10
5	2265.5	60.3	1207	10	US-09-988-462-7
6	2186.5	58.2	1227	15	US-10-428-961-63
7	2171.5	57.8	1186	9	US-09-826-660-23
8	2116	56.3	1228	15	US-10-428-961-38
9	2116	56.3	1228	15	US-10-614-524-2
10	1932.5	51.4	643	9	US-09-826-660-25
11	1722.5	45.8	1167	14	US-10-089-678-1
12	1681.5	44.7	653	15	US-10-428-961-6
13	1670.5	44.4	1157	16	US-10-782-141-16

14	1511	40.2	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1511	40.2	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1511	40.2	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1495	39.8	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1495	39.8	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1495	39.8	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1485.5	39.5	1156	14	US-10-099-285-72	Sequence 72, Appli
21	1485.5	39.5	1156	15	US-10-428-961-28	Sequence 28, Appli
22	1467	39.0	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1467	39.0	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1467	39.0	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1467	39.0	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1467	39.0	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1467	39.0	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1467	39.0	1181	10	US-09-988-462-15	Sequence 15, Appli
29	1467	39.0	1181	10	US-09-988-462-17	Sequence 17, Appli
30	1467	39.0	1181	10	US-09-988-462-28	Sequence 28, Appli
31	1467	39.0	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1467	39.0	1181	15	US-10-136-998A-10	Sequence 10, Appli
33	1467	39.0	1181	15	US-10-136-998A-12	Sequence 12, Appli
34	1467	39.0	1177	14	US-10-035-060-2	Sequence 2, Appli
35	1462	38.9	1177	14	US-10-035-060-8	Sequence 8, Appli
36	1460	38.8	1177	14	US-10-102-469-24	Sequence 24, Appli
37	1459	38.8	1177	14	US-10-782-141-6	Sequence 6, Appli
38	1443.5	38.4	1176	16	US-09-837-961-2	Sequence 2, Appli
39	1420.5	37.8	1176	11	US-10-825-751-2	Sequence 2, Appli
40	1420.5	37.8	1176	16	US-10-428-961-40	Sequence 40, Appli
41	1400	37.2	1167	15	US-09-873-873-26	Sequence 26, Appli
42	1379	36.7	1177	9	US-09-916-956A-26	Sequence 26, Appli
43	1379	36.7	1177	10	US-09-997-914-26	Sequence 26, Appli
44	1379	36.7	1177	10	US-10-365-645-26	Sequence 26, Appli
45	1379	36.7	1177	14		

ALIGNMENTS

RESULT 1
US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match	100.0%	Score	3760;	DB	16;	Length	719;
Best Local Similarity	100.0%	Pred. No.	7.2e-310;				
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Gaps	0;						
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Db	1	MKLKNQDKHQSFSSNAKVCKISTDSLKNETDIEIQNHEDCLKMSEYENVEPVASATI	60				
Qy	61	QTGIGIAGKILGTGLGVFPAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120				
Db	61	QTGIGIAGKILGTGLGVFPAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120				

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DB 121 RNKALTDKGLDALAVVHDSLESWGNRNTRRSVVKSQYIALELMFVQKLPSPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600
QY 601 TERTVGTTPSFSDVQSTFTIGAWNFSSGNEVYDRIEFVPEVTEAEYDPEKAQEKV 660
DB 601 TERTVGTTPSFSDVQSTFTIGAWNFSSGNEVYDRIEFVPEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2
US-10-782-141-8

; Sequence 8, Application US/10782141
; Publication No. US20040197917A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274143

; CURRENT APPLICATION NUMBER: US/10/782,141

; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,632

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 719

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-782-141-8

Query Match 100.0%; Score 3760; DB 16; Length 719;

Best Local Similarity 100.0%; Pred. No. 7.2e-310;

Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60

DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
QY 121 RNKALTDKGLDALAVVHDSLESWGNRNTRRSVVKSQYIALELMFVQKLPSPFAVSG 180
DB 121 RNKALTDKGLDALAVVHDSLESWGNRNTRRSVVKSQYIALELMFVQKLPSPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600
QY 601 TERTVGTTPSFSDVQSTFTIGAWNFSSGNEVYDRIEFVPEVTEAEYDPEKAQEKV 660
DB 601 TERTVGTTPSFSDVQSTFTIGAWNFSSGNEVYDRIEFVPEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3

US-10-428-961-42

; Sequence 42, Application US/10428961

; Publication No. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Ruper, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; FILE REFERENCE: MECO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 42

; LENGTH: 710

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

; FEATURE:

NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 92.5%; Score 3476.5; DB 15; Length 710;
Best Local Similarity 92.5%; Pred. No. 8.3e-286;
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;
QY 1 MRLKQKHQSPSSNAKVDKISTDSLKNETDIELQNKWEIEMFHEVVEEIIINOKISTVARNKALDILKG 60
DB 1 MRSKNQNHQSLSNATVDKNFTGSLNNTNTELFNFH-----EGIEPFVSVSTI 51
QY 61 QTGIGIAGKIILGLVFPAGQVASYLSFILGELWPKGNQWEIEMFHEVVEEIIINOKISTVARNKALDILKG 120
DB 52 QTGIGIAGKIILGLVFPAGQVASYLSFILGELWPKGNQWEIEMFHEVVEEIIINOKISTVARNKALDILKG 111
QY 121 RNKALDILKGLDALAVYHDSLESWGNRNTRARSVKSYQYIALELMFVQKLPSPFAVSG 180
DB 112 RNKALDILKGLDALAVYHDSLESWGNRNTRARSVKSYQYIALELMFVQKLPSPFAVSG 171
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISFYNNQVERAGDYSHCVKWYS 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISFYNNQVERAGDYSHCVKWYS 231
QY 241 TGLNRLGCTNAESWVRNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVYTDAL 300
DB 232 TGLNRLGCTNAESWVRNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVYTDAL 291
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360
DB 292 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 351
QY 361 GGHKLEPRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420
DB 352 GGHKLEPRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 411
QY 421 VDFHMKFVTHPTASDNFYYPGAGICTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 412 VDFHMKFVTHPTASDNFYYPGAGICTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 471
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 472 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531
QY 541 TGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 532 TGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 591
QY 601 TTRTVGTTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
DB 592 TTRTVGTTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 651
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 652 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING BT INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 60.6%; Score 2278.5; DB 16; Length 1228;
Best Local Similarity 62.7%; Pred. No. 9.7e-184;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;
QY 23 TDSLKNETDIELQNKWEIEMFHEVVEEIIINOKISTVARNKALDILKG 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
QY 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIEMFHEVVEEIIINOKISTVARNKALDILKG 130
DB 62 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIEMFHEVVEEIIINOKISTVARNKALDILKG 121
QY 131 LGDALAVYHDSLESWGNRNTRARSVKSYQYIALELMFVQKLPSPFAVSGEVEPLPIYA 190
DB 122 LGDSFRAYQOSLEDWLENRDARTSVLHTQYIALELDLFLNAMPFLAIRNQEVPLLMVYA 181
QY 191 QAANLHLLLRDASIFGKXWGLSDSEISFYNNQVERAGDYSHCVKWYSTGLNLRGTN 250
DB 182 QAANLHLLLRDASIFGKXWGLSDSEISFYNNQVERAGDYSHCVKWYSTGLNLRGTN 241
QY 251 AESWVRNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVYTDALGTVHPHPSFT 310
DB 242 AASWVRNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVYTDALGTVHPHPSFT 299
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGHHKLEPRTI 370
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGHHKLEPRTI 359
QY 371 GGTNLSTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPRVDFHMKFV 428
DB 360 GGLNTSTHGTATNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPRVDFHMKFV 416
QY 429 THP-----IASDNFYYPGAGICTQLQDSNELPPEATQPNYESYSHRLSHIGLISASH 483
DB 417 TNPQNTSDRGRTANYSQP-YESPGQLKQSETELPETTERPNYESYSHRLSHIGLISASH 475
QY 484 VKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 543
DB 476 VNVVYVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 535
QY 544 FGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 603
DB 536 FGPRTVNGPLTQRYRIGFRYASTVDFEVSRRGTTVNNFRFLRTMNSGDELKYGNFV 595
QY 604 TVGTTTPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 663
DB 596 RRAFTTPTFTTQIIDIIRTSIQGLSGNGEYVYIDKIEIIPVTATPEAEYDLERAEAVNAL 655
QY 664 FTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 656 FTNTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 44.7%; Score 1681.5; DB 15; Length 653;
Best Local Similarity 51.5%; Pred. No. 1.7e-133;
Matches 346; Conservative 106; Mismatches 173; Indels 47; Gaps 14;

QY 13 SSNAKVDKISTSLKN---ETDIELONINHEDCMKSEYENVEPFSASTTQTGIGIAGK 69
DB 2 NENEINALSIPAVNSHNSQMDLSL-DARIEDSLCIAAGNNINPLVSASTVQTGINIAG 60

QY 70 ILGTGVPFAGQVSLSYFILGELPKQKQWEIFEMHVEEIIINOKISTYARNKALTDLK 129
DB 61 ILGLVGPVAGQVSLSYFILGELPKQKQWEIFEMHVEEIIINOKISTYARNKALTDLK 120

QY 130 GLGDALAVYHDSLSWVGNRNTRARSVVKVQVIAELMFLVQKLPFAVSGEEVPLPIY 189
DB 121 GLGRGVSRYQALETWLDNRNDARSRIILERYVALELDITTAIPLFIRNEEVLLMVY 180

QY 190 AQANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGYSDHCVKWTSTGLNNLRT 249
DB 181 AQANLHLLLRDASIFGSEWGMASDYNQYQEQRYTEESNHCQWNTGLNNLRT 240

QY 250 NAEWSVRYNQFRDRMTLMVLDLVALFPSTYDQYPIKTTAOLTRVYVTDAGTVPHPSP 309
DB 241 NAEWSVRYNQFRDRMTLMVLDLVALFPSTYDQYPIKTTAOLTRVYVTDAGTVPHPSP 300

QY 310 TSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYLLSRNNTQYNNMGGHLEFRT 369
DB 301 ASTNWFNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRNNTQYNNMGGHLEFRT 360

QY 370 IGGTINISTQGST-NTSINPVLPP-TSRDVRVYTESLAGNLFLLTPQVNGVPRVDFHWKF 427
DB 361 IGGTINISTQGST-NTSINPVLPP-TSRDVRVYTESLAGNLFLLTPQVNGVPRVDFHWKF 418

QY 428 VTHPIASDNFYPP-----GYAGIGTQLODSENELPPEATGQPNVESYSHRSHIG-- 477
DB 419 ITLRFMKAPLPTVNRRELGENLYIKLNYHQK-----QQNDQIMNHVIDISYR 470

QY 478 LISASHVKALVSWTHRSADRNTIENPSITQIPVKAFNLSSGAAVVRGPGFTGDIILR 537
DB 471 LIIGTLRAPVYSWTHRSADRNTIENPSITQIPVKAFNLSSGAAVVRGPGFTGDIILR 529

QY 538 -RTNVTGTF---GDIRVNIIN-PPFAQVRVIRYASITDLOPHTSINGKALNQNFSAWN 592
DB 530 LNRNNGNIQNGYIEVPTQFTSTSTRYVRVRYASVTSIELNVNLGNSSTFTNTLPATAA 589

QY 593 RGEDLDYKTRFTVGFTTFFSLDVQSTFT-----ICAWNFSSGNEVYIDRIEFVPEVFT 646
DB 590 SLDLNQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAEVVIDRFEFIPVTAT 640

QY 647 YEAYDFEKAQE 658
DB 641 FEVEYDLERAQK 652

RESULT 13
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match 44.4%; Score 1670.5; DB 16; Length 1157;
Best Local Similarity 49.1%; Pred. No. 3.6e-132;
Matches 371; Conservative 98; Mismatches 230; Indels 57; Gaps 18;

QY 1 MKLNQDKHQSFSSNAKVDKISTDS---LKNETDIELQININHEDCMKSEYE-----N 50
DB 1 MSPNNQNEYEIIDATPST-SVSSDSNRYPANEPDALTALQNMNYKDYLNKSGGENPELPGN 59

QY 51 VEPFVSASTIQTGIGIAGKILGTGVPFAGQVSLSYFILGELWP-KGKNQWEIFMEHVE 109
DB 60 PETFISSTIQTGIGIAGKILGTGVPFAGQVSLSYFILGELWP-KGKNQWEIFMEHVE 119

QY 110 EIIINOKISTYARNKALTDLKGLGDALAVYHDSLSWVGNRNTRARSVVKVQVIAELMFL 169
DB 120 ELVDQKIEKYVKDKALAEKGLGNALDVYQOSLEDWLENRNDARTSRVSVNQFIALDLNF 179

QY 170 VQKLPFAVSGEEVPLPIYAAQANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAG 229
DB 180 VSSIPSAVSGHEVLLAVYAQAVNLHLLLRDASIFGHEWGTTPGEISRFYNRQVQLTA 239

QY 230 DYSDHCVKWYSTGLNNLRGTNAESVVRYNQFRDRMTLMVLDLVALFPSTYDQYPIKTTA 289
DB 240 EYSDYCVKWKYKIGLDKLGTTKSWLNHYQFRREMTLLVLDLVALFPNYDTHMYPIETTA 299

QY 290 QLTREVYTDAGTVPHPSPFTST---TWNNNAAPSFAIEAAVVRNPHLLDFLEQVITY 345
DB 300 QLTREVYTDAGTVPHPSPFTST---TWNNNAAPSFAIEAAVVRNPHLLDFLEQVITY 355

QY 346 SLLSR-----WSNTQYNNMGGHLEFRT-----TIGGTINISTQGSTNTSINPVLPPFTSR 396
DB 356 T--SRGGITLNDAYINYSWGHLLKYRRRTADSTVYTYTANVGRITSEKNS-----FALEDR 408

QY 397 DVYRTESLAGNLFLLTPQVNGVPRVDFHWKFVTHPIASDNFY-----YPGAGIGTQLOD 451
DB 409 DIFEINSTVANLANYQKAYVPGSWFH--MVKRTSSSTAYLYSKTHALTALQGC-TQYVE 465

QY 452 SENELPPEATGQPNVESYSHRSLHI-----GLISASHVKALVSWTHRSADRNTIET 503
DB 466 SDEIPLDRT-VPVAESYSHRSLHITSHSFSKNG--SAYYGSFVFWVTHTSADLNNTIY 522

QY 504 PMSITQIPVKAFNLSSGAAVVRGPGFTGDIILRTNTGTFGDIRVNIINPPFAQVRVRI 563
DB 590 SLDLNQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAEVVIDRFEFIPVTAT 640

Db 523 SDKITQIPAVKGDMLYLGSSVVGPGFTGGDILKRTNPSILGTFAVTNGSLSQRYRRI 582
QY 564 RYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTRTVGTTTPPSFLDVQSTFTIG 623
Db 593 RYASTTDFEF-TLYLGTIERKRNFKMTDNGASLTETFKFASFTTDFQFRETDKILLS 641
QY 624 AMNFSNGEVYIDRIEFVPEVVEYEAEDFEKAQKVTALFTSTNPRGLKTDVKDYHIDQ 683
Db 642 MGFSSSGEVYIDRIEFIPVDEYEAEDLEAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700
QY 684 VSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719
Db 701 AANLVECLSDDDLYPNEKRLFLDAVREAKRLSGARNL 736
RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2
Query Match 40.2%; Score 1511; DB 13; Length 1206;
Best Local Similarity 44.3%; Pred. No. 1.3e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQININHEDECLM-----SEVE-N 50
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASEYPGS 59
QY 51 VEPFVSA-STIQTGIGIAGKILGTGLGVPFAGQVASLYSFTLGLWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVPFVPGPIVSLYTLQIDILWPSEKSSQWEIFMEQV 119
QY 109 EEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELM 168
Db 120 EEIINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNPNSGRALRDVRNFEILDLSL 179
QY 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNNRQVERA 228
Db 180 FTQYMPFRVTNFEVPLFTVYAMAANLHLLLRDASIFGEEWGSTTTTNNYDRQMKLT 239
QY 229 GDYSDHCWKWYSTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTT 288
Db 240 AEYSDDHCWKWYETGLAKLGTSAKQWVDYNOFRRENTLAVLDVVALFPNYDTRTPMETK 299
QY 289 AQLTREVYTDALGTVHPHPSFTSTTWNNAAPSFAIEAAVVRPHLLDFLEQVITYILL 348
Db 300 AQLTREVYTDPLGAVNVS---SIGSWY-DKAPSGFVIESSVIRPPHVFYITGLTVYVTS 355
QY 349 SRWSNTQYNNMGGHKLFRITGGTINISTQSTNTSINPV-TLPFTSRDVRVRESLAGL 407
Db 356 RSISSARYIRHWAGHQISYHRVSRGSLNQMYGTQNLHSTSTFDFTNYDIYKLSKDAV 415

QY 408 NLFLTQP-----VNGVPRVDFHMKFVTHPIASDN---FYYPGYAGIGTQLQDSENELEPPE 459
Db 416 LLDIVYPGYTYIFFGQMEVEF---FMVQNLNTRKTLKYNPVSKDIIASTRDSLELEPPE 472
QY 460 ATGQPNVESYSHRLSHIGLISAS-HVKAL--VYSWTHESADRTNTIEPNSITQIPLVKAF 516
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPFVSWSHRSADLNNTIYSDKITQIPAVKCM 532
QY 517 NLSSGAUVRGPGFTGGDILR-RYNTGTFGDI---RVNINPPFAQRYRVRIRYASTTDLQ 572
Db 533 DNLFPVVKPGHTGGDLQYNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIV 592
QY 573 FHTSINGKAINQGNFSATMNRGEDLDYKTR-----TVGFTTTPFSFL-----DVQST 619
Db 593 LH--VNDAAQI---QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGCDPNST 647
QY 620 FTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQKVTALFTSTNPRGLKTDVKDY 679
Db 648 LS-----GIVYVDRIEFIPVDEYEAEDLEAAKAVNALFTNTKD-GLRPGVTDY 697
QY 680 HIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719
Db 698 EVNQAAANLVECLSDDDLYPNEKRLFLDAVREAKRLSEARNL 737
RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2
Query Match 40.2%; Score 1511; DB 14; Length 1206;
Best Local Similarity 44.3%; Pred. No. 1.3e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQININHEDECLM-----SEVE-N 50
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASEYPGS 59
QY 51 VEPFVSA-STIQTGIGIAGKILGTGLGVPFAGQVASLYSFTLGLWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVPFVPGPIVSLYTLQIDILWPSEKSSQWEIFMEQV 119
QY 109 EEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELM 168
Db 120 EEIINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNPNSGRALRDVRNFEILDLSL 179
QY 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNNRQVERA 228
Db 180 FTQYMPFRVTNFEVPLFTVYAMAANLHLLLRDASIFGEEWGSTTTTNNYDRQMKLT 239

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds
(without alignments)
2403.590 Million cell updates/sec

Title: US-10-019-823B-55
Perfect score: 3760
Sequence: 1 MKLKNDKQKSPSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	3	US-08-286-870A-8
2	3476.5	92.5	710	4	US-09-661-322A-42
3	3398	90.4	648	3	US-08-286-870A-4
4	3377	89.8	719	2	US-09-003-217-2
5	3372	89.7	719	3	US-09-218-942-2
6	2804	74.6	535	3	US-08-286-870A-6
7	2446.5	65.1	1229	1	US-08-100-709-4
8	2446.5	65.1	1229	1	US-08-176-865-4
9	2446.5	65.1	1229	1	US-08-474-038-4
10	2446.5	65.1	1229	2	US-08-779-046-4
11	2446.5	65.1	1229	2	US-08-881-340-4
12	2344.5	62.4	488	1	US-08-448-170-10
13	2344.5	62.4	488	1	US-08-961-803-10
14	2265.5	60.3	1207	1	US-07-951-715A-7
15	2265.5	60.3	1207	2	US-08-459-448A-7
16	2265.5	60.3	1207	3	US-08-459-595A-7
17	2265.5	60.3	1207	3	US-08-459-504B-7
18	2265.5	60.3	1207	3	US-08-459-444-7
19	2265.5	60.3	1207	3	US-09-053-549-8
20	2265.5	60.3	1207	3	US-09-547-422-7
21	2265.5	60.3	1207	4	US-09-988-462-7
22	2264.5	60.2	1227	3	US-09-053-549-2
23	2195.5	58.4	1227	1	US-08-448-170-8
24	2195.5	58.4	1227	3	US-08-961-803-9
25	2186.5	58.2	1227	4	US-09-661-322A-63
26	2171.5	57.8	1186	3	US-09-178-252-23
27	2171.5	57.8	1186	4	US-09-826-660-23

28	2116	56.3	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1932.5	51.4	643	3	US-09-178-252-25	Sequence 25, Appl
30	1932.5	51.4	643	4	US-09-826-660-25	Sequence 25, Appl
31	1900	50.5	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1681.5	44.7	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1670.5	44.4	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1670.5	44.4	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1670.5	44.4	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1670.5	44.4	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1507.5	40.1	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1492	39.7	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1492	39.7	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1492	39.7	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1492	39.7	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1492	39.7	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1492	39.7	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1486.5	39.5	1169	1	US-08-315-468-4	Sequence 4, Appl
45	1485.5	39.5	1156	3	US-09-002-285-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Query Match	99.9%;	Score 3756;	DB 3;	Length 719;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 718;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI	60	
DB	1	MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI	60	
QY	61	QTGIGIAGKILGTIGVFPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120	
DB	61	QTGIGIAGKILGTIGVFPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120	
QY	121	RNKALTDLGLGDALAVYHDSLSBWGNRNNTARSVVKSOYIALELWFKLPSFAVSG	180	
DB	121	RNKALTDLGLGDALAVYHDSLSBWGNRNNTARSVVKSOYIALELWFKLPSFAVSG	180	
QY	181	EEVPLLPPIYAQAANLHLLLRDASIIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCVKWS	240	
DB	181	EEVPLLPPIYAQAANLHLLLRDASIIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCVKWS	240	
QY	241	TGLNLRGTNAESWVRYNQFRDRMTLWLDLVALFPSYDTQWYPIKTTAQLTREYVTDAI	300	
DB	241	TGLNLRGTNAESWVRYNQFRDRMTLWLDLVALFPSYDTQWYPIKTTAQLTREYVTDAI	300	
QY	301	GTVHPHPSFTSTTWYNNNAPSFSIAEAAVVRNPHLLDPLEQVTIYSLLSRWSNTQYMMW	360	
DB	301	GTVHPHPSFTSTTWYNNNAPSFSIAEAAVVRNPHLLDPLEQVTIYSLLSRWSNTQYMMW	360	
QY	361	GGHKLFEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVTRSLAGNLFLTQPVNGVPR	420	
DB	361	GGHKLFEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVTRSLAGNLFLTQPVNGVPR	420	
QY	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS	480	
DB	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS	480	
QY	481	ASHVKALVYSWTHRSADRNTNTEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540	
DB	481	ASHVKALVYSWTHRSADRNTNTEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540	
QY	541	TGTFGDIRVNIINPPAQRVVRIRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600	
DB	541	TGTFGDIRVNIINPPAQRVVRIRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600	
QY	601	TFRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVTEAAYDFEKAQEKV	660	
DB	601	TFRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVTEAAYDFEKAQEKV	660	
QY	661	TALFSTNPRGLKTDVKDHYHIDOVSNLVESLSDSEFYLDKRELFPEIKVKAKOLHIERNM	719	
DB	661	TALFSTNPRGLKTDVKDHYHIDOVSNLVESLSDSEFYLDKRELFPEIKVKAKOLHIERNM	719	

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; ORGANISM: Bacillus thuringiensis
;
; FEATURE:
; NAME/KEY: misc feature
;
; LOCATION: (200)..(200)
;
; OTHER INFORMATION: No. 6593293-Coding
US-09-6661-322A-42

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Query Match	92.5%;	Score 3476.5;	DB 4;	Length 710;
Best Local Similarity	92.5%;	Pred. No. 5.5e-303;		
Matches 665;	Conservative	15;	Mismatches 30;	Indels 9;

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 90.4%; Score 3398; DB 3; Length 648;
Best Local Similarity 100.0%; Pred. No. 5.3e-296;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVASATI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVASATI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRNTRARSVKSKQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRNTRARSVKSKQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKGLSSEISSTPNRQVERAGDYSHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKGLSSEISSTPNRQVERAGDYSHCVKWYS 240
QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDAI 300
DB 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDAI 300
QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWNSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWNSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVRATESLAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVRATESLAGLNFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSSENLPEATGPQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSSENLPEATGPQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAIINQGNFSATMNRGEDLDYK 600
DB 541 TGTGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAIINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTTPSFSLDVQSTTTIGAMNFFSGNEVYIDRIEFVPEVETYE 648
DB 601 TFRVTGFTTTPSFSLDVQSTTTIGAMNFFSGNEVYIDRIEFVPEVETYE 648

RESULT 4

US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.8%; Score 3377; DB 2; Length 719;
Best Local Similarity 89.8%; Pred. No. 4.8e-294;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVASATI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVASATI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRNTRARSVKSKQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRNTRARSVKSKQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKGLSSEISSTPNRQVERAGDYSHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKGLSSEISSTPNRQVERAGDYSHCVKWYS 240

Tue Feb 15 10:07:50 2005

181 EEVPLPIYAQAANLHLLLRDASIFGKNGLSASEISTFYNQVERTRDYSYHCVKWN 240
241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPSPYDTQMPYIKTTAQLTREVYTDI 300
241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPSPYDTQMPYIKTTAQLTREVYTDI 300
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYNNMW 360
301 GTVDPNQALRSITWYNNAPSAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYNNMW 360
361 GGHKLEFRITIGTILNI STQGSNTSINPVTLPFTSRDVTESLAGLNLFLTQPVNGVPR 420
361 GGHRLSRPIGGALNTSTQGSNTSINPVTLPFTSRDVTESLAGLNLFLTQPVNGVPR 420
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
481 GSHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
541 SGTFGHIRVNIINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
601 TPTVGTFTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
601 TPTVGTFTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDELKRELFEIVKYAKQIHIERNM 719
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDELKRELFEIVKYAKQIHIERNM 719

RESULT 5

US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; TITLE OF INVENTION: Activity
; FILE REFERENCE: Cry1I
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

Query Match 89.7%; Score 3372; DB 3; Length 719;
Best Local Similarity 89.8%; Pred. No. 1.3e-293;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDLCKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQTLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPVSASTI 60
Qy 61 QTGIGTAGKILGTLPVFPAGQVASYSLFTLGLWPKCKNWEIFMEHVEIINOKISTYA 120
Db 61 QTGIGTAGKILGTLPVFPQCIASLYSLFTLGLWPKCKSQWEIFMEHVEIINOKISTYA 120
Qy 121 RNKALTDLKGIGDALAVYHDSLESWGVNNTARSVVKVQSVIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLESWGVNNTARSVVKVQSVIALELMFVQKLPFAVSG 180

181 EEVPLPIYAQAANLHLLLRDASIFGKNGLSASEISTFYNQVERAGDYSYHCVKWN 240
181 EEVPLPIYAQAANLHLLLRDASIFGKNGLSASEISTFYNQVERTRDYSYHCVKWN 240
241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPSPYDTQMPYIKTTAQLTREVYTDI 300
241 TGLNLRGTNAESWVRNQFRDMLTMDLVALPSPYDTQMPYIKTTAQLTREVYTDI 300
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYNNMW 360
301 GTVDPNQALRSITWYNNAPSAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYNNMW 360
361 GGHKLEFRITIGTILNI STQGSNTSINPVTLPFTSRDVTESLAGLNLFLTQPVNGVPR 420
361 GGHRLSRPIGGALNTSTQGSNTSINPVTLPFTSRDVTESLAGLNLFLTQPVNGVPR 420
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
541 SGTFGHIRVNIINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
601 TPTVGTFTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
601 TPTVGTFTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDELKRELFEIVKYAKQIHIERNM 719
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDELKRELFEIVKYAKQIHIERNM 719

RESULT 6

US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.6%; Score 2804; DB 3; Length 535;
Best Local Similarity 100.0%; Pred. No. 8.1e-243; Indels 0; Gaps 0;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQININHEDECKMSEYENVEPVFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQININHEDECKMSEYENVEPVFSASTI 60

QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSPILGELWPKGNQWEIPEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLSPILGELWPKGNQWEIPEHVEEIIINQKISTYA 120

QY 121 RNKALTDKGLGDALAVYHDSLESWGNRNNTARSVKSQYIALELMFVQKLPSPFAVSG 180
DB 121 RNKALTDKGLGDALAVYHDSLESWGNRNNTARSVKSQYIALELMFVQKLPSPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWYS 240

QY 241 TGLNLRGNTNAESWRYNQPRDMLMVLDLVALPSPYDTQMYPIKTTAQLTREVTDAI 300
DB 241 TGLNLRGNTNAESWRYNQPRDMLMVLDLVALPSPYDTQMYPIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360

QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVHTPIASDNFYYPGYAGICTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVHTPIASDNFYYPGYAGICTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jan, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLNK-ETDIELQ-NINHEDECKMSEYENVEPVFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEANNIDPPVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSPILGELWPKGNQWEIPEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQVASYLSPILGELWPKGNQWEIPEHVEEIIINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESWGNRNNTARSVKSQYIALELMFVQKLPSPFAVSGEVPLLPIYA 190
DB 127 LGRGYSYQALETWLDNRNDARSIIILERYVALELDITTAFLFRIRNEEVPLLMYA 186

QY 191 QAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGNTN 250
DB 187 QAANLHLLLRDASIFGSEWGMASDVNQYQEOIRYTEESYSHVQVNTGLNLRGNTN 246

QY 251 AESWRYNQPRDMLMVLDLVALPSPYDTQMYPIKTTAQLTREVTDAIGTVHPHPSFT 310
DB 247 AESWRYNQPRDMLMVLDLVALPSPYDTQMYPIKTTAQLTREVTDAIGTVHPHPSFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNWGGHKLFPRTI 370
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNWGGHKLFPRTI 366

QY 371 GGTGLNISTQGST-NTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPRVDFHWKFT 429
DB 367 GGTGLNISTQGST-NTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPRVDFHWKFT 422

QY 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPETTERPNYESYSHRLSHIGLIIGN 480

QY 483 HVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRRTWG 542
DB 481 TLRAPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRRTWG 540

QY 543 TFGDIRNVNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGBDLDTYKTF 602
DB 541 TFGDIRNVNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGBDLDTYKTF 600

QY 603 RTVGFTTTPFSLDVQSTFTIGAMNFFSSGNEVYIDRIEYFVPEVTEYAEYDFEKAQEKVTA 662
DB 601 RTAGFTTTPFSLDVQSTFTIGAMNFFSSGNEVYIDRIEYFVPEVTEYAEYDFEKAQEKVTA 659


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVKISTSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLFIKELWPKGKQWEIFMEHVBEIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQLASFYSFLVGLWPSGRDPWEIFLEHVQELIROQVTRNTAIAARLEG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVKSYIALELMFVQKLPFAVSGEVEPLPIYA 190
Db 127 LGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVA 186

QY 191 QAAHLHLLLRDASIFGKELWGLSSSEISFYNNQVERAGDYSCHVKWYSTGLNLRGTN 250
Db 127 LGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVA 186

QY 187 QAAHLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEYSNHCYQWYNTGLNLRGTN 246
Db 251 AESSWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTRVYTDAGTVHPHPSFT 310

QY 247 AESSWLRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRNAPSFA 306
Db 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNMGHKLERTI 370

QY 307 STNWFNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNVVGHRLNFRPI 366
Db 371 GGTNLNSTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTPQVNGVPRVDFHWKFT 429

QY 367 GGTNLNSTQGLTNTSINPVTLPFTSRDVYRTESNAGTNILFTTPVNGVPRWARFNF 422
Db 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS 482

QY 423 --INPQNIYERGATTYSQPYQGVGIQLFDSSETLPETTERPNYESYSHRLSHIGLIIGN 480
Db 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 542

QY 481 TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRNTG 540
Db 543 TFGDIRVNINPFPFAQRYRIRYASTDQLQHTSINGKAINQGNFSAWNRGDDLYKTF 602

QY 541 TFGDIRLNINVLSQLRYRIRYASTDQLQFTTRINGTIVNIGNFSRTWNRGDNLEYSF 600
Db 603 RTVGFTTTPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662

QY 601 RTAGFSPTPFNLAQSTFTLGAQSFN-QEVIIDRVFVPAEVTFEAEYDLERAQKAVNA 659
Db 663 LFTSTNPRGLKTDVKYHIDQVNLVESLSDEFYLDKRELFETVKYAKQLHIERNM 719

QY 660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFETVKYAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

```

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; ADDRESSES: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSES: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      65.1%; Score 2446.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVKISTSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLFIKELWPKGKQWEIFMEHVBEIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQLASFYSFLVGLWPSGRDPWEIFLEHVQELIROQVTRNTAIAARLEG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVKSYIALELMFVQKLPFAVSGEVEPLPIYA 190
Db 127 LGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVA 186

QY 191 QAAHLHLLLRDASIFGKELWGLSSSEISFYNNQVERAGDYSCHVKWYSTGLNLRGTN 250
Db 187 QAAHLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEYSNHCYQWYNTGLNLRGTN 246

QY 251 AESSWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTRVYTDAGTVHPHPSFT 310
Db 247 AESSWLRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRNAPSFA 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNMGHKLERTI 370
Db 307 STNWFNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNVVGHRLNFRPI 366

QY 371 GGTNLNSTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTPQVNGVPRVDFHWKFT 429
Db 367 GGTNLNSTQGLTNTSINPVTLPFTSRDVYRTESNAGTNILFTTPVNGVPRWARFNF 422

QY 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQPYQGVGIQLFDSSETLPETTERPNYESYSHRLSHIGLIIGN 480

QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNINPFPFAQRYRIRYASTDQLQHTSINGKAINQGNFSAWNRGDDLYKTF 602
Db 541 TFGDIRLNINVLSQLRYRIRYASTDQLQFTTRINGTIVNIGNFSRTWNRGDNLEYSF 600

QY 603 RTVGFTTTPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662
Db 601 RTAGFSPTPFNLAQSTFTLGAQSFN-QEVIIDRVFVPAEVTFEAEYDLERAQKAVNA 659

QY 663 LFTSTNPRGLKTDVKYHIDQVNLVESLSDEFYLDKRELFETVKYAKQLHIERNM 719
Db 660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFETVKYAKRLSDERNL 716

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127 LGRGYSYQALLETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEYVPLLMVYA 186
191 QANLHLLLRASIFGKEWGLSSSEISTFVNROVERAGDYSDHCVKWYSTGLNNLRGTN 250
187 QANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEYSNHCQVQWYNTGLNNLRGTN 246
251 AESWVRYNQFRDMTMLVLDLVALFPFSDYDQMPYPIKTAQLTREYVYTDAGTVHPHPSFT 310
247 AESWVRYNQFRDLTLGLVLDLVALFPFSDYDQMPYPIKTAQLTREYVYTDAGTVHPHPSFT 306
311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVYTIYLLSWSNTQYMMWGGHKLFRFI 370
307 STWNNNAPSFAIEAAVVRNPHLLDFLEQVYTIYLLSWSNTQYMMWGGHKLFRFI 366
371 GGTNLNSTOYST-NTSINPVTLPFTSRDVRTESELAGNLFLTPQVNGVPRVDHFKFT 429
367 GGTNLNSTOYST-NTSINPVTLPFTSRDVRTESELAGNLFLTPQVNGVPRVDHFKFT 422
430 HPIASDNFYYPG-----YAGIGTLOQDSENELPPEATGQPNYESYSHRSLHGLISAS 482
423 --INPQNIYERGATTYSQYQGVQIQLFDFSETLPETTERPNYESYSHRSLHGLIIGN 480
483 HVKALVYSWTHRSADRTNTEPNSTIOTPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
481 TLAPVYSWTHRSADRTNTEPNSTIOTPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540
543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDDLYKTF 602
541 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDDLYKTF 600
603 RTVGFTTFFSFLDVOSTFTIGAMNFSNGEYVYDRIEFPVPEVTEYAEYDEKAEKAVTA 662
601 RTAGFSTPFNFNAOSTFTILGAQSFN-QEYVIDRVEFPVPAEVTFEAEYDLERAQAVNA 659
663 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719
660 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 716

RESULT 12
US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424

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543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDDLYKTF 602
541 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDDLYKTF 600
603 RTVGFTTFFSFLDVOSTFTIGAMNFSNGEYVYDRIEFPVPEVTEYAEYDEKAEKAVTA 662
601 RTAGFSTPFNFNAOSTFTILGAQSFN-QEYVIDRVEFPVPAEVTFEAEYDLERAQAVNA 659
663 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719
660 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESS: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-881-340-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMSYENVEPVSASTIQTGTGIAGKI 70
7 NENEINALSIPTVSNPSTOMNLSPDARIEDSLCVAEWNIDPFVSASITVQTGINAGRI 66
71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
67 LGVLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126
131 LGDALAVYHDSLESWVGNNRNRARSVVKSKQYIALELMFVQKLPSFAVSGREVPLLPIYA 190

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.4%; Score 2344.5; DB 1; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSIKNETDIELQINHEHEDCLKMSEYENVEPVSASTI 60
Db 1 MKSKQNMHQSLSNNAVDKNTGSLNNTNTLQNFNH-----EGIEPFVSVSTI 51

Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKQWEIFMEHVEELINQKISTYA 111

Qy 121 RNKALTDLKGIDALAVYHDSLEWVGNRNNTTRARSVVKSOYIALELMFVKQLPSPFAVSG 180
Db 112 RNKALADLKGIDALAVYHESLESWIENRNTRTRSVVKSOYITLMLFVQSLPSPFAVSG 171

Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNQVERAGDYSCHVKWYS 240
Db 172 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNQSGKSKESYSDHCWKYN 231

Qy 241 TGLNNLRGTNAESWVRYNQFRDMLTLMVLDLVALFPSPYDTQMPYPIKTTAQLTREYVTDI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMLTLMVLDLVALFPSPYDTQMPYPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 351

Qy 361 GGHKLEPRTIGTGLNTSGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
Db 352 GGHKLEPRTIGTGLNTSGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 411

Qy 421 VDFHWKFTVTHPIASDNFYPCYAGIGCTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKFTVTHPIASDNFYPCYAGIGCTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 471

Qy 481 ASHVKALVYSWTHRSAD 497
Db 472 ASHVKALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 62.4%; Score 2344.5; DB 3; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSIKNETDIELQINHEHEDCLKMSEYENVEPVSASTI 60
Db 1 MKSKQNMHQSLSNNAVDKNTGSLNNTNTLQNFNH-----EGIEPFVSVSTI 51

Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKQWEIFMEHVEELINQKISTYA 111

Qy 121 RNKALTDLKGIDALAVYHDSLEWVGNRNNTTRARSVVKSOYIALELMFVKQLPSPFAVSG 180
Db 112 RNKALADLKGIDALAVYHESLESWIENRNTRTRSVVKSOYITLMLFVQSLPSPFAVSG 171

Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNQVERAGDYSCHVKWYS 240
Db 172 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNQSGKSKESYSDHCWKYN 231

Qy 241 TGLNNLRGTNAESWVRYNQFRDMLTLMVLDLVALFPSPYDTQMPYPIKTTAQLTREYVTDI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMLTLMVLDLVALFPSPYDTQMPYPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 351
```


Best Local Similarity 64.3%; Pred. No. 6.7e-194;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;
40 EDCLKMEYENVEPFVSASTIQTGIGIAGKILGTGVFPAGQVAVSLYFSLGELWPKGN 99
10 EDSLCAEGNIDPFVSASTVQTGINIAGKILGTGVFPAGQVAVSLYFSLGELWPKGRD 69
100 QWEIFMHEVEEINQKISTVARNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVK 159
70 QWEIFLEHVEQLINQITENARNALTALRQLGDSFRAYQQSLEDWLNDRDARTSRVLY 129
160 SQYIALELMFVQKLPSPAVSGEEVPLPIYAQAANLHLLRLDASIFGKEWGLSSSEIST 219
130 TQYIALELDFLNAMPFAIRNQEVPLLMVYAQAANLHLLRLDASIFGSEFGTSEIQR 189
220 FYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRRDMLMVLDLVALFPSYD 279
190 YYERQVERTRDYSYCVWEYNTGLNSLRGTNAESWVRYNQFRRDMLMVLDLVALFPSYD 249
280 TOMYPIKTAQLTREVTDAIGTVHHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFL 339
250 TRTPINTSAQLTREVTDAIGAT--GVNMAAMWYNNNAPSFAIEAAAIRSPHLLDFL 307
340 EQVTYISLSRWSNTQYNNMGGHLEFRTIGGTINISTQGSTNTSINPVTLPFTSRDYY 399
308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLATSTHGTATNTSINPVTLPFTSRDYY 367
400 RTESLAGLNLFP--LTPVNGVPRVDFHWKFVTHP----IASDNFYYPGYAGIGTQLODS 452
368 RTESYAGVLLWGIYLEPIHGVPTVRFNF--TNPQNISDRGTANYSQP--YESPGQLKDS 423
453 ENELPPEATQOPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRNTTIEPNSITQIPL 512
424 ETELPETTERPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRNTTIEPNSITQIPL 483
513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPFAQVRVRYASTDLQ 572
484 VKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNNINPFAQVRVRYASTDLQ 543
573 EHTSINGKAINQGNFSATMNRGDLDTFTFTVGTFTTTPSFDFLDVQSTFTIGAWNFSSGNE 632
544 FFVSRGGTTVANNFRFLRTMNSGDELKYNFVRAFTTFTTQIQTIRTSIQLSGNGE 603
633 VYIDRIEFVPVEVTEAEYDEKAEQKVATLFTSTNPRGLKTDVKYHIDQVSNLVESLS 692
604 VYIDKIEIIPVTATFEAYDLEAQAENALFTNTNPRKLTVDYHIDQVSNLVACL 663
693 DEFVLDEKRELFVIVKAKQLHIERNM 719
664 DEFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dawson, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

361 GGKLEFRTIGTGLNTSTGNTSINPVTLPFTSRDVRSTESLAGLNLFTQPVNGVPR 420
352 GGKLEFRTIGTGLNTSTGNTSINPVTLPFTSRDVRSTESLAGLNLFTQPVNGVPR 411
421 VDFHWKFVTHPTASDNFYYPGYAGIGTQLODSNELPPEATGPNYESYSHRLSHIGLIS 480
412 VDFHWKFVTHPTASDNFYYPGYAGIGTQLODSNELPPEATGPNYESYSHRLSHIGLIS 471
481 ASHVKALVYSWTHRSAD 497
472 ASHVKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dawson, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprull, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-951-715A-7
Query Match 60.3%; Score 2265.5; DB 1; Length 1207;

;; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
;; NUMBER OF SEQUENCES: 94
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 585933gartis Corporation
;; STREET: Patent & Trademark Dept., 520 White Plains
;; STREET: Rd., POB 2005
;; CITY: Tarrytown
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10591-9005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,448A
;; FILING DATE: 02-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/951,715
;; FILING DATE: 25-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/772,027
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pace, Gary M.
;; REGISTRATION NUMBER: 40403
;; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8582
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1207 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-459-448A-7

Query Match 60.3%; Score 2265.5; DB 2; Length 1207;
Best Local Similarity 64.3%; Pred. No. 6.7e-194;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

QY 40 EDCMKSEYENVEPVSASTIQTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGN 99
Db 10 EDSLCIAEGNNIDPFVSASTVQTGINAGRIILGVLPFAGQVASYLSFILGELWPKGRD 69
QY 100 QWEIFMEHVEELINOKISTYARNKALTDLKGGLDALAVVHDSLSWGVGNNTNRARSVVK 159
Db 70 QWEIFLEHVEQLINQITENARNTALARLQGLGDSFRAYQOQSLDLENRDRDARTSVLY 129
QY 160 SQVIALELMFVOKLPSFAVSGEEVPLPIYAAANLHLLLRDASIFGKEWGLSSSEIST 219
Db 130 TQVIALELDLFLNAPLFAIRNQEVPLLMVYAAANLHLLLRDASLFGSEFGLTSQEIQR 189
QY 220 FYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWRYNQFRDRMTLMVLDLVALFPSYD 279
Db 190 YVERQVERTRDYSYCVYEWYNTGLNSLRGTNAASWRYNQFRDRMTLMVLDLVALFPSYD 249
QY 280 TQWYPIKTTAQLTREVTDAIGTVHPHPSFTSTTYNNNAPSFSIAEAAVVRNPHLLDPL 339
Db 250 TRTPYINTSAQLTREVTDAIGAT--GVNMAAMNMYNNNAPSFSIAEAAIRSPHLLDPL 307
QY 340 EQVTIYLLSRWSNTQYMMWCGHKLFPRTIGGTINISTOGSTNTSINPVTLPFTRSDVY 399
Db 308 EQLTIFSASSRWSNTRHTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTRSDVY 367
QY 400 RTESLAGLNLFP--LTQPVNGVRVDFHWKVFVTHP-----IASDNFYYPGVAGIGTQLODS 452
Db 368 RTESYAGVLLWGLIYLEPIHGVTFRVNF---TNPQNISDRGTANYSQP--YESPGLQLKDS 423

QY 453 ENELPPEATGQPNVESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512
Db 424 ETELPPEATERPNVESYSHRLSHIGIILQSRVNVVPVYSWTHRSADRTNTIGPNRITQIPM 483
QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGCTFGDIRVAINPPPAQRYRVRIRYASTTDLQ 572
Db 484 VKASELPQGTTVVRGPGFTGGDILRRNTGCTFGDIRVAINPPPAQRYRVRIRYASTTDLQ 543
QY 573 FHTSINGKAINQGNFSATMNRGDELDTKPTFTVGTFTTTPSFSDVQSTTTIGAWNFFSGNE 632
Db 544 FFVSRGCTTVNNFRFLRTWNSGDELKYGNFVRRRAFTTPTFTTQIIDIIRTSIQGLSGNGE 603
QY 633 VYIDRIEFVPEVTEAEYDFEKAQEKVTALFTSTNPRGLKTDVYHIDQVSNLVESLS 692
Db 604 VYIDKLEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663
QY 693 DEFYLDKRELFEIVKYAKOLHIERNM 719
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

Search completed: February 14, 2005, 20:59:01
Job time : 25.3302 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds
(without alignments)
2827.419 Million cell updates/sec

Title: US-10-019-823B-55

Perfect score: 3760

Sequence: 1 MCLKNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	4	AAB66908 Insectici
2	3760	100.0	719	6	Aae36272 B. thurin
3	3760	100.0	719	8	Adr89421 crylla. 1
4	3756	99.9	719	4	AAB66910 Insectici
5	3756	99.9	719	6	Aae36274 B. thurin
6	3751	99.8	719	4	Aau02095 Bacillus
7	3749	99.7	719	4	AAB66911 Insectici
8	3749	99.7	719	6	Aae36275 B. thurin
9	3743	99.5	719	4	AAB66909 Insectici
10	3743	99.5	719	6	Aae36273 B. thurin
11	3739	99.4	719	2	AAR08041 81 kD end
12	3728.5	99.2	718	6	Aae36271 B. thurin
13	3722.5	99.0	718	4	AAB66907 Insectici
14	3551	94.4	719	7	Adm74717 B. thurin
15	3520	93.6	719	4	AAB66912 Insectici
16	3520	93.6	719	6	Aae36276 B. thurin
17	3476.5	92.5	710	4	Aau02041 B. thurin
18	3397	90.3	719	3	Abb07073 Bacillus
19	3377	89.8	719	2	Aaw49089 Bacillus
20	3291	87.5	1217	4	Aau02092 Bacillus
21	2734	72.7	1208	4	Aau02093 Bacillus
22	2448	65.1	1230	8	Adk98484 B thuring
23	2448	65.1	1230	8	Adk98489 B thuring
24	2448	65.1	1230	8	Adk98481 B thuring
25	2448	65.1	1230	8	Adk98491 B thuring

26	2448	65.1	1230	8	ADK98487
27	2446.5	65.1	1229	2	AAR54074
28	2446.5	65.1	1229	2	AAW35259
29	2446.5	65.1	1229	2	AAW17699
30	2446.5	65.1	1229	2	AAW87633
31	2446.5	65.1	1229	2	AAW30923
32	2446.5	65.1	1229	8	ADK98479
33	2344.5	62.4	488	4	AAW44322
34	2344.5	62.4	488	4	AAW19947
35	2278.5	60.6	1228	2	AAR50955
36	2273.5	60.5	1209	4	AAU02094
37	2264.5	60.2	1227	2	AAW31990
38	2195.5	58.4	1227	2	AAW44321
39	2195.5	58.4	1227	4	AAW19950
40	2186.5	58.2	1227	4	AAU02046
41	2171.5	57.8	1186	2	AAW16796
42	2156.5	57.4	1221	4	AAU00421
43	2142.5	57.0	1221	4	AAU00420
44	2116	56.3	1228	4	AAB84628
45	2116	56.3	1228	4	AAU02039

ALIGNMENTS

RESULT 1
AAB66908
ID AAB66908 standard; protein; 719 AA.
XX
AC AAB66908;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa2.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
(ZENE) ZENECA LTD.
PA Griffing J, Carlile AJ, Cayley RJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
controlling insects, and for insect-resistant transgenic plant
production.
XX
PS Claim 14; Page 55-57; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
insecticidal proteins can be used to produce transgenic plants, which are
insect-resistant. Also, the insecticidal proteins are useful for
controlling insects by providing them at a locus where insects feed
Sequence 719 AA;
Query Match 100.0%; Score 3760; DB 4; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-293;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Feb 15 10:07:50 2005

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFFVSASTI 60
Db |||||
QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFFVSASTI 60
Db |||||
QY 61 QTGIGIAGKILGTLGVPAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
Db |||||
QY 61 QTGIGIAGKILGTLGVPAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
Db |||||
QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVKQYIALELMFVQKLPSPFVAVG 180
Db |||||
QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVKQYIALELMFVQKLPSPFVAVG 180
Db |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVCWKYS 240
Db |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVCWKYS 240
Db |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
Db |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
Db |||||
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
Db |||||
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
Db |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLFITQPVNGVPR 420
Db |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLFITQPVNGVPR 420
Db |||||
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db |||||
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIPIVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIPIVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db |||||
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db |||||
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db |||||
QY 601 TERTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db |||||
QY 601 TERTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db |||||
QY 661 TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db |||||
QY 661 TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db |||||

RESULT 2
AAE36272
ID AAE36272 standard; protein; 719 AA.
AC AAE36272;
XX

26-JUN-2003 (first entry)
B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

Bacillus thuringiensis.
WO200298911-A2.
12-DEC-2002.
30-MAY-2002; 2002WO-GB002666.
07-JUN-2001; 2001GB-00013900.
XX
PR
XX
PA (SYGN) SYNGENTA LTD.
XX

PI Vincent JL, Viner R;
XX WPI; 2003-175137/17.
DR
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT
XX
PS Claim 12; Page 44-47; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
CC
XX
SQ Sequence 719 AA;

Query Match 100.0%; Score 3760; DB 6; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-293;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFFVSASTI 60
Db |||||
QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFFVSASTI 60
Db |||||
QY 61 QTGIGIAGKILGTLGVPAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
Db |||||
QY 61 QTGIGIAGKILGTLGVPAGQVASYLIFGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
Db |||||
QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVKQYIALELMFVQKLPSPFVAVG 180
Db |||||
QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNTARSVKQYIALELMFVQKLPSPFVAVG 180
Db |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVCWKYS 240
Db |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVCWKYS 240
Db |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
Db |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
Db |||||
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
Db |||||
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
Db |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLFITQPVNGVPR 420
Db |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLFITQPVNGVPR 420
Db |||||
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db |||||
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIPIVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIPIVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db |||||
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db |||||
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db |||||
QY 601 TERTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db |||||
QY 601 TERTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db |||||
QY 661 TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db |||||
QY 661 TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db |||||

RESULT 3
ADR89421
ID ADR89421 standard; protein; 719 AA.
XX
AC ADR89421;
XX
DT 18-NOV-2004 (first entry)
XX
DE cryIIa.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.

OS Bacillus thuringiensis.
XX
XX WO2004074462-A2.
PN
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
PI WPI; 2004-635574/61.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Example 6; SEQ ID NO 33; 178pp; English.

XX This sequence represents a delta-endotoxin crystal protein. This protein
CC was included in the scope of the invention as a comparison to the delta-
CC endotoxins of the invention. Some of the delta-endotoxin coding sequences
CC of the invention have alternative start codons, producing more than one
CC protein from a single open reading frame. The nucleic acid sequences of
CC the invention are useful in DNA constructs or expression cassettes for
CC transformation and expression in plants and bacteria. The nucleic acids
CC and corresponding polypeptides are useful for killing lepidopteran or
CC coleopteran pests. Compositions containing the delta-endotoxins of the
CC invention, and methods for their production, are useful for the
CC production of organisms with pesticide resistance, specifically bacteria
CC and plants. These organisms are useful for generating altered or improved
CC delta-endotoxin or delta-endotoxin-associated proteins that have
CC pesticidal activity, or for detecting the presence of delta-endotoxin or
CC delta-endotoxin-associated proteins or nucleic acids in products or
CC organisms.

XX Sequence 719 AA;
SQ
Query Match 100.0%; Score 3760; DB 8; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-293;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDCLKMSEYENVEPFSASTI 60

Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDCLKMSEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGLWPKGKNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGLWPKGKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSG 180
QY 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVCWYS 240
Db 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVCWYS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMYPIKTTAQLTREVYTDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMYPIKTTAQLTREVYTDAI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPPTSVDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPPTSVDVYRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600
Db 541 TGTFGDIRVNINPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600
QY 601 TFRVTGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 660
Db 601 TFRVTGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDBFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDBFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
AAB66910
ID AAB66910 standard; protein; 719 AA.
XX
AC AAB66910;
XX 12-APR-2001 (first entry)
DT Insecticidal protein cryIIa4.
DE Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX WO200100841-A1.
PN 04-JAN-2001.
PD
XX 23-JUN-2000; 2000WO-GB002457.
PF
XX 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE) ZENECA LTD.
XX

PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX Claim 14; Page 60-62; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;
SQ
Query Match 99.9%; Score 3756; DB 4; Length 719;
Best Local Similarity 99.9%; Pred. No. 2.4e-293;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPFVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPFAVSG 180
Db 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSTOIPLVKAPNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSTOIPLVKAPNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVGTFTTFFSLDQVSTFTTGAWNSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Db 601 TFRVGTFTTFFSLDQVSTFTTGAWNSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLDSDEFYLDKEKRELFEIVKAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLDSDEFYLDKEKRELFEIVKAKQLHIERNM 719

AAE36274
ID AAE36274 standard; protein; 719 AA.
XX AC
AC AAE36274;
XX DT
DT 26-JUN-2003 (first entry)
XX DE
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.
XX KW
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX OS
OS Bacillus thuringiensis.
XX PN
PN WO200298911-A2.
XX PD
PD 12-DEC-2002.
XX PF
PF 30-MAY-2002; 2002WO-GB002666.
XX PR
PR 07-JUN-2001; 2001GB-00013900.
XX PA
PA (SYGN) SYNGENTA LTD.
XX PI
PI Vincent JL, Viner R;
XX XX
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Claim 12; Page 50-53; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX Sequence 719 AA;
SQ
Query Match 99.9%; Score 3756; DB 6; Length 719;
Best Local Similarity 99.9%; Pred. No. 2.4e-293;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPFVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPFAVSG 180
Db 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPR 420

Db 361 GGHKLEFRTIGTGLNLTSTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
RESULT 6
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX
AC AAU02095;
XX
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.
XX
KW Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;
KW mutant; mutcin.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= signal_peptide
FT Protein 20..719 /label= Mature_CryIIa
XX
PN EP1099760-A1.
XX
PD 16-MAY-2001.
XX
PF 09-NOV-1999; 99EP-00203723.
XX
PR 09-NOV-1999; 99EP-00203723.
XX
PA (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.
XX
PI De Maagd RA, Bosch HJ;
XX
DR WPI; 2001-337141/36.
DR N-PSDB; AAS04855.
XX
XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT domains derived from at least 2 different crystal proteins, such as
PT CryIIa and CryIIb, and having insecticidal activity, useful for combating
PT insects.
XX
PS Example; Page 30-32; 43pp; English.
XX
CC The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
CC encoding which was mutated to allow cloning of domain III or domains I
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins
CC of the invention, having structural domains I, II and III in this order
CC starting from the N-terminal derived from at least 2 different crystal
CC proteins, are useful for protecting plants against pest insects, e.g.

CC moths, butterflies and Colorado potato beetle or for combating insects
SQ Sequence 719 AA;
Query Match 99.8%; Score 3751; DB 4; Length 719;
Best Local Similarity 99.9%; Pred. No. 6.1e-293;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLVNEDTDLQINNHEDCLKMSYENVEPFSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLVNEDTDLQINNHEDCLKMSYENVEPFSASTI 60
Qy 61 QTGIGIAGKILGTILGVPFAGQVASYLSYFGLGELWPKGKNQWEIFMEHVEEINQKISTYA 120
Db 61 QTGIGIAGKILGTILGVPFAGQVASYLSYFGLGELWPKGKNQWEIFMEHVEEINQKISTYA 120
Qy 121 RNKALTDLKGLGDALAVVHDSLSWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGLGDALAVVHDSLSWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSG 180
Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
Qy 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLVALFPPSYDTQMPYIKTKAQLTREVYTDAL 300
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLVALFPPSYDTQMPYIKTKAQLTREVYTDAL 300
Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIAAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIAAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNLTSTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420
Db 361 GGHKLEFRTIGTGLNLTSTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
RESULT 7
AAB66911
ID AAB66911 standard; protein; 719 AA.
XX
AC AAB66911;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa5.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX

Tue Feb 15 10:07:50 2005

PD	04-JAN-2001.	Db	601	TFTVTGFTTPTSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVFPVEVTEAEYDFEKAQEKV	660
XX	23-JUN-2000; 200WO-GB002457.	QY	661	TALFTSTNPRGLKTDVYHIDQVSNLVSLSDFYLDEKRELFEIVKYAKQLHIERNM	719
PF	29-JUN-1999; 99GB-00015215.	Db	661	TALFTSTNPRGLKTDVYHIDQVSNLVSLSDFYLDEKRELFEIVKYANELHIERNM	719
XX	23-DEC-1999; 99GB-00030536.				
XX	(ZENE) ZENECA LTD.				
PA	Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;				
XX	Vincent JL, Lee MD;				
PI	WPI; 2001-123015/13.				
XX	Novel insecticidal protein obtained from species of Paecilomyces for				
XX	controlling insects, and for insect-resistant transgenic plant				
XX	production.				
XX	Claim 14; Page 62-64; 72pp; English.				
PS	The present invention relates to novel insecticidal proteins obtained				
XX	from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The				
CC	insecticidal proteins can be used to produce transgenic plants, which are				
CC	insect-resistant. Also, the insecticidal proteins are useful for				
CC	controlling insects by providing them at a locus where insects feed				
CC					
XX	Sequence 719 AA;				
SQ					
Query Match	99.7%; Score 3749; DB 4; Length 719;				
Best Local Similarity	99.6%; Pred. No. 8.8e-293;				
Matches	716; Conservative				
QY	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFSASTI	60			
Db	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFSASTI	60			
QY	61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120			
Db	61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120			
QY	121 RNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVQKLPFAVSG	180			
Db	121 RNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVQKLPFAVSG	180			
QY	181 EYVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS	240			
Db	181 EYVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS	240			
QY	241 TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSTQMYPIKTTAQLTRVYTDAL	300			
Db	241 TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSTQMYPIKTTAQLTRVYTDAL	300			
QY	301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMMNW	360			
Db	301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMMNW	360			
QY	361 GGHKLEFRITGGTINISQGSNTSINPVTLPFTSRDVYTESLAGLNLFTQPVNGVPR	420			
Db	361 GGHKLEFRITGGTINISQGSNTSINPVTLPFTSRDVYTESLAGLNLFTQPVNGVPR	420			
QY	421 VDFHKNFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480			
Db	421 VDFHKNFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480			
QY	481 ASHVKALVYSWTHRSADRNTIENSIITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN	540			
Db	481 ASHVKALVYSWTHRSADRNTIENSIITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN	540			
QY	541 TGTFGDIRVININPPAQVRVIRYASTTDLOPHTSINGKAINQGNFSATMNRGSDLDYK	600			
Db	541 TGTFGDIRVININPPAQVRVIRYASTTDLOPHTSINGKAINQGNFSATMNRGSDLDYK	600			
QY	601 TERTVTGFTTPTSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVFPVEVTEAEYDFEKAQEKV	660			

QY 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALPSPYDQMYPIKTTAQLTREYVYDAI 300
DB 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALPSPYDQMYPIKTTAQLTREYVYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
QY 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAITMNRGEDLDYK 600
DB 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAITMNRGEDLDYK 600
QY 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQSKV 660
DB 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQSKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYDIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 9

AAB66909 standard; protein; 719 AA.

AC AAB66909;
XX
DT 12-APR-2001 (first entry)
DE Insecticidal protein cryIIa3.
XX
KW Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.
XX WO200100841-A1.

XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
XX 29-JUN-1999; 99GB-00015215.
XX 23-DEC-1999; 99GB-00030536.

PA (ZENE) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.

XX Claim 14; Page 57-59; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;
SQ

Query Match 99.5%; Score 3743; DB 4; Length 719;
Best Local Similarity 99.6%; Pred. No. 2.7e-292;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDLSKNETDIELQNIHEDCLKMSYENVEFPVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDLSKNETDIELQNIHEDCLKMSYENVEFPVSASTI 60

QY 61 QTGIGIAGKILGTGLVPFAGQVASLYSFLIGELMPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGLVPFAGQVASLYSFLIGELMPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKIGLDALAVYHDSLESWVGNRNTRARSVVKSOYIALELMFVKLPFAVSG 180
DB 121 RNKALTDLKIGLDALAVYHDSLESWVGNRNTRARSVVKSOYIALELMFVKLPFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALPSPYDQMYPIKTTAQLTREYVYDAI 300
DB 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALPSPYDQMYPIKTTAQLTREYVYDAI 300

QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAITMNRGEDLDYK 600
DB 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAITMNRGEDLDYK 600

QY 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQSKV 660
DB 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQSKV 660

QY 661 TALFTSTNPRGLKTDVKDHYDIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYDIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 10

AAE36273 standard; protein; 719 AA.

AC AAE36273;

XX 26-JUN-2003 (first entry)

XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

OS Bacillus thuringiensis.

XX WO200298911-A2.

Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNQVERAGDYSYHCVKWS 240
Qy 241 TGLNLRGTAESWVRNQFRDMLMVLVLDVALPSPYDQMPYIKTTAQLTREVVYDAI 300
Db 241 TGLNLRGTAESWVRNQFRDMLMVLVLDVALPSPYDQMPYIKTTAQLTREVVYDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTVISLRSWNTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTVISLRSWNTQYMNW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLKY 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLKY 600
Qy 601 TERTVGFTTTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TERTVGFTTTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12

AAE36271
ID AAE36271 standard; protein; 718 AA.
XX
AC AAE36271;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT
XX
PS Claim 12; Page 42-44; 67pp; English.
XX
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as

CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 718 AA;

Query Match 99.2%; Score 3728.5; DB 6; Length 718;
Best Local Similarity 99.6%; Pred. No. 3.9e-291;
Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEVENPEFVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEVENPEFVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEIFMEHVVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEIFMEHVVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGLGDALAVYHDSLSRWGNRNTRARSVVKSQYIALELMFVKLPSFAVSG 180
Db 121 RNKALTDLKGLGDALAVYHDSLSRWGNRNTRARSVVKSQYIALELMFVKLPSFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNQVERAGDYSYHCVKWS 240
Qy 241 TGLNLRGTAESWVRNQFRDMLMVLVLDVALPSPYDQMPYIKTTAQLTREVVYDAI 300
Db 241 TGLNLRGTAESWVRNQFRDMLMVLVLDVALPSPYDQMPYIKTTAQLTREVVYDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTVISLRSWNTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTVISLRSWNTQYMNW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLKY 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLKY 600
Qy 601 TERTVGFTTTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TERTVGFTTTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 13

AAE66907
ID AAE66907 standard; protein; 718 AA.
XX
AC AAE66907;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa1.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX

Db 540 TGTGDIIRVNINPPFAQRYRVRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
Qy 601 TERTVGTTPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDEKAEKV 660
Db 600 TERTVGTTPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDEKAEKV 659
Qy 661 TALTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 TALTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 14

ADM74717
ID ADM74717 standard; protein; 719 AA.
XX
AC ADM74717;
XX
DT 03-JUN-2004 (first entry)
XX
DE B. thuringiensis cryIIel SEQ ID NO:2.
XX
KW cryI; toxicity; lepidoptera; cryIaB; cryIbA; coleoptera; diptera;
KW cryIIel.
XX
OS Bacillus thuringiensis.
XX
PN CN1401772-A.
XX
PD 12-MAR-2003.
XX
PF 20-AUG-2001; 2001CN-00124163.
XX
PR 20-AUG-2001; 2001CN-00124163.
XX
PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.
XX
PI Song F, Zhang J, Huang D;
XX
XX WPI; 2003-442339/42.
XX N-PSDB; ADM74716.

Qy 1 MCLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
Db 1 MCLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120
Db 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120
Qy 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARVSVKQSYIAELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARVSVKQSYIAELMFVQKLPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFVNQVERAGDYSVHCVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFVNQVERAGDYSVHCVKWYS 240
Qy 241 TGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTRVYTTDAI 300
Db 241 TGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTRVYTTDAI 300
Qy 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSWSNTQYMNW 360
Db 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSWSNTQYMNW 360
Qy 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFITQPNVGR 420
Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFITQPNVGR 419
Qy 421 VDFHWKFTVTHIASDNFYYPGYAGIGTQLQDSENLPEATGQPNYESYSHRLSHGLIS 480
Db 420 VDFHWKFTVTHIASDNFYYPGYAGIGTQLQDSENLPEATGQPNYESYSHRLSHGLIS 479
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
Qy 541 TGTGDIIRVNINPPFAQRYRVRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600

Query Match 99.0%; Score 3722.5; DB 4; Length 718;
Best Local Similarity 99.4%; Pred. No. 1.2e-290;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OS Paecilomyces sp.
XX WO200100841-A1.
PN
XX
XX
PD 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-GB002457.
XX
XX 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
PR
XX
XX (ZENE) ZENECA LTD.
XX
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
XX WPI; 2001-123015/13.
DR
XX
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
XX Claim 14; Page 53-55; 72pp; English.
PS
XX
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB6901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
XX Sequence 718 AA;

Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence with high-toxicity to lepidoptera pests, encoded protein, primer sequences and the shuttle vector pSKY422b, useful as a pesticide.
Example 3; SEQ ID NO 2; 29pp; Chinese.
The invention relates to a novel Bacillus thuringiensis cryI gene, gene combination, expression vector, nucleotide sequence of the B thuringiensis cryI gene with high-toxicity to lepidoptera pests and the amino acid sequence of the protein encoded by it, cooperative use of the cryI gene with the expression product of cryIaB or cryIbA, primer sequences for expressing the genes, and the constructed shuttle vector pSKY422b. The gene in combination with the cryIaB or cryIbA genes displays high toxicity to the lepidoptera, coleoptera and diptera pests. The present sequence represents the cryIIel protein.

Sequence 719 AA;

Query Match 94.4%; Score 3551; DB 7; Length 719;
Best Local Similarity 93.6%; Pred. No. 7.9e-277;
Matches 673; Conservative 26; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MCLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
Db 1 MCLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120
Db 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120
Qy 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARVSVKQSYIAELMFVQKLPFAVSG 180

Db 121 RNIALADLKGDLALAYHESLESWKRNARATSVKQYIALELLFVQKLPSPAVSG 180
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSRHCWKYS 240
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QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDLEQVTIYLLSRWSNTQYMNW 360
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QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
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QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 15

AAB66912
ID AAB66912 standard; protein; 719 AA.

XX AC AAB66912;

XX DT 12-APR-2001 (first entry)

XX DE Insecticidal protein cry11b1.

XX KW Insecticide; transgenic plant; insect-resistance.

XX OS Paecilomyces sp.

XX PN WO200100841-A1.

XX PD 04-JAN-2001.

XX PF 23-JUN-2000; 2000WO-GB002457.

XX PR 29-JUN-1999; 99GB-00015215.

XX PR 23-DEC-1999; 99GB-00030536.

XX PA (ZENE) ZENECA LTD.

XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX PI Vincent JL, Lee MD;

XX DR WPI; 2001-123015/13.

XX PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.

XX PS

XX Claim 14; Page 64-66; 72pp; English.

XX CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed

XX SQ Sequence 719 AA;

Query Match 93.6%; Score 3520; DB 4; Length 719;
Best Local Similarity 92.9%; Pred. NO. 2.5e-274;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

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Search completed: February 14, 2005, 20:50:27
Job time : 101.351 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.6029 Seconds
(without alignments)
3350.901 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su

Database : Published Applications AA:**

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4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp:
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20:	/cgn2_6/ptodata/1/pubpaa/US360_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Match	Score	Length		
1	100.0	3760	719	16	US-10-782-020-10 Sequence 10, Appl
2	100.0	3760	719	16	US-10-782-141-8 Sequence 8, Appl
3	92.5	3476.5	710	15	US-10-428-961-42 Sequence 42, Appl
4	60.6	2278.5	1228	16	US-10-809-953-10 Sequence 10, Appl
5	60.3	2278.5	1207	10	US-09-988-463-7 Sequence 7, Appl
6	58.2	2186.5	1227	15	US-10-428-961-63 Sequence 63, Appl
7	57.8	2171.5	1186	9	US-09-826-660-23 Sequence 23, Appl
8	56.3	2116	1228	15	US-10-428-961-38 Sequence 38, Appl
9	56.3	2116	1228	15	US-10-614-524-2 Sequence 2, Appl
10	51.4	1932.5	643	9	US-09-826-660-25 Sequence 25, Appl
11	45.8	1722.5	1167	14	US-10-089-678-1 Sequence 1, Appl
12	44.7	1681.5	653	15	US-10-428-961-6 Sequence 6, Appl
13	44.4	1670.5	1157	16	US-10-782-141-16 Sequence 16, Appl

1511	40.2	1206	13	US-10-032-717-2	Sequence 2, Appl	
14	40.2	1206	14	US-10-416-637-2	Sequence 2, Appl	
1511	40.2	1206	15	US-10-606-320-2	Sequence 2, Appl	
1511	40.2	1206	15	US-10-606-320-2	Sequence 2, Appl	
1495	39.8	1210	13	US-10-032-717-4	Sequence 4, Appl	
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20	39.5	1156	14	US-10-099-285-72	Sequence 72, Appl	
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22	1467	39.0	1155	10	US-09-988-462-9	Sequence 9, Appl
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27	1467	39.0	1181	10	US-09-988-462-15	Sequence 15, Appl
28	1467	39.0	1181	10	US-09-988-462-17	Sequence 17, Appl
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31	1467	39.0	1181	15	US-10-136-998A-8	Sequence 8, Appl
32	1467	39.0	1181	15	US-10-136-998A-10	Sequence 10, Appl
33	1467	39.0	1181	15	US-10-136-998A-12	Sequence 12, Appl
34	1467	39.0	1177	14	US-10-035-060-2	Sequence 2, Appl
35	1462	38.9	1177	14	US-10-035-060-8	Sequence 8, Appl
36	1460	38.8	1177	14	US-10-102-469-24	Sequence 24, Appl
37	1459	38.8	1177	14	US-10-782-141-6	Sequence 6, Appl
38	1443.5	38.4	1176	16	US-09-837-961-2	Sequence 2, Appl
39	1420.5	37.8	1176	11	US-10-825-751-2	Sequence 2, Appl
40	1420.5	37.8	1176	16	US-10-428-961-40	Sequence 40, Appl
41	1400	37.2	1167	15	US-09-873-873-26	Sequence 26, Appl
42	1379	36.7	1177	9	US-09-916-956A-26	Sequence 26, Appl
43	1379	36.7	1177	10	US-09-997-914-26	Sequence 26, Appl
44	1379	36.7	1177	14	US-10-365-645-26	Sequence 26, Appl
45	1379	36.7	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

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RESULT 1
US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197316A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

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Db	181	EEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISFYNRQVERAGDYSCHVKWYS	240
QY	241	TGLNLRGTNAESWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL	300
Db	241	TGLNLRGTNAESWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL	300
QY	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW	360
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QY	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVNGVPR	420
Db	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVNGVPR	420
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Db	601	TFTVTGFTTTPSFVLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
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; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Cartz, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; METHODS OF INVENTION: Methods for its Use			
; FILE REFERENCE: 045600/274143			
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; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
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Db	121	RNKALTDLKGGLDALAVYHDSLESWGNRNTRARVSVKSYIALELMFVQKLPFAVSG	180
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; Publication No. US2003023711A1			
; GENERAL INFORMATION:			
; APPLICANT: Baum, James A.			
; APPLICANT: Chu, Chih-Rei			
; APPLICANT: Donovan, William P.			
; APPLICANT: Gilmer, Amy J.			
; APPLICANT: Ruper, Mark J.			
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin			
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)			
; FILE REFERENCE: MECO201--1			
; CURRENT APPLICATION NUMBER: US/10/428,961			
; CURRENT FILING DATE: 2003-05-02			
; PRIOR APPLICATION NUMBER: 09/661,322			
; PRIOR FILING DATE: 2000-09-13			
; PRIOR APPLICATION NUMBER: 60/153,995			
; PRIOR FILING DATE: 1999-09-15			
; NUMBER OF SEQ ID NOS: 63			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 42			
; LENGTH: 710			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
; FEATURE:			

NAME/KEY: misc feature
LOCATION: (200) (200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 92.5%; Score 3476.5; DB 15; Length 710;
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Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;

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DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKESYSDHCVKWN 231
QY 241 TGLNLRGTMNAESVRYNQFRDMLVLDLVALFSPYDTQYPIKTAQLTREVTDAI 300
DB 232 TGLNLRGTMNAESVRYNQFRDMLVLDLVALFSPYDTQYPIKTAQLTREVTDAI 291
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DB 292 GTVPHPSFTSTWYNNAPSPFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 351
QY 361 GGHKLEFRITIGTLNISTQSTNTSINPVTLPTSDRVYRTESLAGLNFLTPQVNGVPR 420
DB 352 GGHKLEFRITIGTLNISTQSTNTSINPVTLPTSDRVYRTESLAGLNFLTPQVNGVPR 411
QY 421 VDFHFWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
DB 412 VDFHFWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 471
QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 472 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531
QY 541 TGTGDIRVNPFPFAQRYRIRYASTTDLPHTSINGKAINQGNFSAATMNRGEBDLYK 600
DB 532 TGTGDIRVNPFPFAQRYRIRYASTTDLPHTSINGKAINQGNFSAATMNRGEBDLYK 591
QY 601 TFRVTGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 660
DB 592 TFRVTGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 651
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719
DB 652 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 710

RESULT 4

US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Van Mellaert, Herman
APPLICANT: Boterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 60.6%; Score 2278.5; DB 16; Length 1228;
Best Local Similarity 62.7%; Pred. No. 8.6e-184;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNH-----EDCLKMEYENVEPPFVSASTIQTGIGIAGKI 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
QY 71 LGTLGVPPAGQVAVSLYSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 62 LGVLGVPPAGQVAVSLYSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121
QY 131 LGDALAVHDSLESVGNRNTRARSVVKSVQVIALELMFVQKLPSPAVSGEVPVLLPIYA 190
DB 122 LGDSFRAYQQLSDLEWLENRDARTSRVLHTQYIALELDLFLNAMPLEFAIRNOQEVPLLMVYA 181
QY 191 QAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVRAGDYSCHCVKWSYSLGLNLRGTN 250
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYRYRQVTRDYSDYCVEMWYNTGLNSLRGTN 241
QY 251 AESWRYNQFRDMLVLDLVALFSPYDTQYPIKTAQLTREVTDAIGTWHVHPSFT 310
DB 242 AASWRYNQFRDMLVLDLVALFSPYDTQYPIKTAQLTREVTDAIGTWHVHPSFT 299
QY 311 STWYNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLERTI 370
DB 300 SMWYNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLERTI 359
QY 371 GGTNLNISTQSTNTSINPVTLPTSDRVYRTESLAGLNFLTPQVNGVPRVDFHFWK 428
DB 360 GGTNLNISTQSTNTSINPVTLPTSDRVYRTESLAGLNFLTPQVNGVPRVDFHFWK 416
QY 429 THP-----IASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISASH 483
DB 417 TNPQNIISRGATANYSQP-YESPGLQKQDSETELPPETTERPNYESYSHRSLHIGLISQSR 475
QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 543
DB 476 VNVFVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 535
QY 544 FGDIRVNINPFPFAQRYRIRYASTTDLPHTSINGKAINQGNFSAATMNRGEBDLYKTFR 603
DB 536 FGPVIRVTNPGPLTQRYRIGFRYASTVDFVFSRGGTNNFRFLRTMNSGDELKYNFV 595
QY 604 TVGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEVKTAL 663
DB 596 RRAFTTFFFTQIQDIIRTSIQGLSGNEVYIDKIEIIPVATFATFAYDLERAQEAVAL 655
QY 664 FTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 711

RESULT 5

US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sygenta Biotechnology, Inc.

STREET: 3054 Cornwalis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 60.3%; Score 2265.5; DB 10; Length 1207;

Best Local Similarity 64.3%; Pred. No. 1.1e-182;

Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

40 EDCLKMEYENVEPVASASTIQTGIGAKILGTGVFPAGOVASLYSFTLGLMWPCKGN 99

10 EDSLCAEAGNIDPPFASASTVQGINIAGRILVGLVFPAGQLASFYFLVGLMWPGRGD 69

100 QWEIFMEHVEEIIINOKISTYARNKALTDLKGDLAVYHDSLESWVGNNRNRARSVVK 159

70 QWEIFLEHVEQLINQOITENARNALARLQGLGDSFRAYQQSLDWMLENRDARTSVLY 129

160 SQVIALELMFVQKLPSEFVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST 219

130 TOVIALELDLFNAMPPLFAIRNOEVPPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189

220 FYNQOVERAGDYSCHVCWYSTGLNLRGTNAESWVRNQFRDMLTLMVLVLPFSSYD 279

190 YVERQVERTRDYSYCVWEWYNTGLNSLRGTNAESWVRNQFRDMLTLMVLVLPFSSYD 249

280 TOMYPIKTAQLTREVTDAIGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFL 339

Db 250 TRTYPINTSAQLTREVTDAIGAT--GVNWSMWNWNNNAPSFAIEAAAIRSPHLLDFL 307

Qy 340 EQVTIYLLSRWSNTQYMMWGGHKLFRITGIGTLNISTGGSTNTSINPVTLPFTSRDVS 399

Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQRPIGGGLNTSTHGATNTSINPVTLPFASRDVS 367

Qy 400 RTESLAGLNL--LTQVNGVPRVDFHWKFWTHP-----IASDNFYFPGYAGIGTQLQDS 452

Db 368 RTESYAGVLLWGIYLEPIHGVFTVRNF---TNPQWISDRGTANYSQP--YESPQLQLKDS 423

Qy 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNIEPNSITQIPL 512

Db 424 ETELPPEPPERPNYESYSHRLSHIGLILQSRVNVVYSWTHRSADRTNIEPNSITQIPL 483

Qy 513 VKAFNLSSGAAVVRGPGTGGDILRRNTGTGDIRVNIWPPFAQRYRVRIRYASTTDLQ 572

Db 484 VKASELPQGTTVVRGPGTGGDILRRNTGTGDIRVNIWPPFAQRYRVRIRYASTTDLQ 543

Qy 573 FHTSINGKAINQGNFSATMNRGDLVDYKTRTVGFTTFFSFLDVOSTFTTGAMNPFSSGNE 632

Db 544 FFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFITPTFTQIIDIIRTSIQGLSGNGE 603

Qy 633 VYIDRIEFVPEVYEAEDFEKAQEKYALTFTSTNPRGLTDDYDHYHIDQVSNLVESLS 692

Db 604 VYIDKIEIIPVTATPEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663

Qy 693 DEFYLDKRELFEIVKYAKQLHIERNM 719

Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6

US-10-428-961-63

Sequence 63, Application US/10428961

Publication No. US2003023711A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Donovan, William P.

APPLICANT: Gilmer, Amy J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201--1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patent in version 3.2

SEQ ID NO 63

LENGTH: 1227

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 15; Length 1227;

Best Local Similarity 59.2%; Pred. No. 5.6e-176;

Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;

13 SSNAKVDKISTDSLKN-----ETDIELQNINHEDCMKSEYENVEPVFASASTIQTGIG 65

7 NENEIINALSIPAVSNHSAQMLNSTDARI-----EDSLCIAEGNIDPPFVSASTVQTGIN 61

66 IAGKILGTLPFPAGOVASLYSFTLGLMWPCKGNQWEIFMEHVEEIIINQKISTYARNKAL 125

62 IAGRILGVLPFPAGQIASFSYFLVGLMWPGRDPPWEIFLEHVEHLIRQOVTENTRTAL 121

126 TDLKGLGDALAVYHDSLESWVGNNRNRARSVVKSOYIALELMFVQKLPSEFVSGEEVPL 185

[illegible]

RESULT 10
US-09-826-660-25
; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
;

Query Match	56.3%	Score 2116;	DB 15;	Length 1228;							
Best Local Similarity	59.5%;	Pred. No. 5.4e-170;									
Matches 424;	Conservative	98;	Mismatches 181;	Indels 10;	Gaps 7;						
QY	13	SSNAVKD	KISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSA	SIQTGIGIAGKI	70						
DB	7	NENEIINALS	IPAVSNHSTOMDLSPOARIEDSLCIAEGNNINPLVSA	SVTQTGINIAGRI	66						
QY	71	LGTLVGP	PAGQVAVLSYFII	LGELWPKGKNQWEIFMEHV	EIIINOKISTYARNKALTDLKG	130					
DB	67	LGVLVGP	PAGQIASFYFSLV	GLWPRGRDQWEIFLEHVEQ	LIINOQITENARNNTALARLOG	126					
QY	131	LGDALAV	YVHDSLESVGN	RNNTRPVSUVK	SQYIALELMFVQKLP	SAVSGSEEVPLLP	190				
DB	127	LGDSFRA	YQQOSLEDWLEN	RDDARTSRVLYTQ	YIALELDLFNAMPLFAIRN	QEVPLLMVYA	186				
QY	191	QAANLH	LLLLLDASIFGKE	WGLSSSETSTFYN	RQVRAGDYS	DHCVKWTSTGLNLRGTN	250				
DB	187	QAANLH	LLLLLDASLFGSE	FGLTSQEI	QRYERYERQVEQ	TRDYSYDCEVWYNTGLNSLRGTN	246				
QY	251	AESVRY	YNQFRDDMTL	VLVDLVALFP	SYDTOMYP	PIKTTAQLTREV	YTDALGTVHPHPSPFT	310			
DB	247	AASWRY	YNQFRDDMTL	GVLDLVALFP	SYDTRYP	INTSAQLTREV	YTDALIGAT--GVNMA	304			
QY	311	STTWYNN	NAPSFSAIEAAV	VRNPHLLDLEQ	VTIYSLLSR	NSNTQYNNM	GGHKLFRFTI	370			
DB	305	SMWYNN	NAPSFSAIEAT	VI	RSRPHLLDLEQ	LTI	FSTSSRWSATRHTYWRGHTIQSRPI	364			
QY	371	GGTLN	ISTQGSTNTS	INPYTL	PFTSRD	VYRTESLAGLNL	F--LTQPVNGVPRVD	PHKVFV	428		
DB	365	GGGLNT	STHGSTNTS	INPVRLS	FFSRD	VYWTESYAGVLL	WGYYLEP	THGVTYVRFNRNP	424		
QY	429	--THPI	ASDNFYPY	PYAGIGTQ	LDSENELP	PEATGQPN	YESYSHRLSHIGLISASHVKA	486			
DB	425	QNTFER	GTANYSQP--YES	PGLQKDS	ETELP	PETTERPEN	YESYSHRLSHIGLISQSRHVH	483			
QY	487	LWYSW	THRSADRTNTEP	NSITQ	PLVKA	PNLSSGAAV	VRGPGFTGGDIL	RRNTNTGFGD	546		
DB	484	PVYSW	THRSADRTNTEP	SSDITQ	PLVKS	ENLNSGT	SVVSGPGFTGGDI	IRTNVNGSVLS	543		
QY	547	IRVNI	NPFPFAQRYR	IRYR	ASTTD	LQFHTS	INGKAINQ	NFSA	TNMRGEDLDYKTFRTVG	606	
DB	544	MGLNF	NNTSLOR	YRVR	YRYAASQ	TWVL	RVTVGGSTTFDQ	GFPS	TMSANESLTSQSFRFAE	603	
QY	607	FITP	FSFLDVQSTFT	ICAMN	ESSGNEV	YIDRIE	FVP	VEVTEYAEYD	FEKAEKVTA	666	
DB	604	FPVGIS	ASGSQ--TAGIS	ISNNAG	RTQTFH	FDKIE	FIPITATFEA	EYD	LERAEQA	EVNALFTN	662
QY	667	TNPRGL	KTDVKDYHID	OVSNL	VESLS	DEFLVD	EKREL	FEIV	KYAKQLHI	ERNM	719
DB	663	TNPR	LKTDVTDYHID	QVSNL	VACL	SDEF	CLDEK	RELLEK	VKYAKRL	SDERNL	715

RESULT 9

US-10-614-524-2

; Sequence 2, Application US/10614524

```

; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWETSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

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; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match      51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 7.5e-155;
Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTDSLN-----ETDIELQNHEDCLKMSYENVEPFVSASTIQTGIG 65
DB 7 NENEIINALSIPAVNSHSAQMLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVAVSLYFSLGELWPKGNQWIFMEHVEEINQKISTYARNKAL 125
DB 62 IAGRILGVLPFAGQIASFYSLVGEWLPGRDPPWEIFLEHVEQLRQVTESTRDALTAL 121
QY 126 TDLKGLGDALAVHDSLESWVGNNRNRTRARSVVKSOYIALELMFVOKLPSFAVSGEEVPL 185
DB 122 ARLOGLGNFRAYQOQSLDLENRDADRTRSVLYTQYIALELDLFNAMPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKWYSTGLNN 245
DB 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRYERQVEKTRSYDYCARWYNTGLNN 241
QY 246 LRGTHAESWRYNQFRDRMTLMVLVDLVALFPSSYDTQYPIKTAQITREVYTDAGTVHP 305
DB 242 LRGTHAESWRYNQFRDRMTLMVLVDLVALFPSSYDTQYPIKTAQITREVYTDAGTVHP 301
QY 306 HPSFTSTTWNNAAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSTNTQYNNMGGHKL 365
DB 302 PSGFASTNWNNAAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSTNTQYNNMGGHKL 361
QY 366 EFRIGTGUNISTOGSTNTSINPVLPTPSRQVYRTSSLAGLNLFLTPQVNGVPRVDFHW 425
DB 362 ESRTIRGLSTSTHGNTSINPVLPTPSRQVYRTSSLAGLNLFLTPQVNGVPRVDFHW 421
QY 426 KFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHLIGLSASHVK 485
DB 422 RNPILNSLRGSLLYTIGYGVGTQLFDSSETLPPTTERPNYESYSHRLSNIRLISGNTLR 481
QY 486 ALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRNTGTFG 545
DB 482 APVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRNTGTFG 541
QY 546 DIRVNPFPFAQRYRVRIRYASTDQLQHTSINGKALNOGNFSATMNRGEDLDYKTFRTV 605
DB 542 SMGLNFNNTSLQRYRVRIRYAASTQMLVLRVTVGSTTFDQGFPSSTANESLTSQSFRFA 601
QY 606 GFTTTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTYVE 648
DB 602 EFPVGISASGSQ-TAGISISNAGRQTFHFDKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

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; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; OTHER INFORMATION: US-10-089-678-1

Query Match      45.8%; Score 1722.5; DB 14; Length 1167;
Best Local Similarity 47.9%; Pred. No. 1.3e-136;
Matches 361; Conservative 126; Mismatches 218; Indels 49; Gaps 12;

QY 1 MCLKNQDKHQ---SFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYE-----NV 51
DB 1 MSPNNQNEYEILDASSSTVSVDNSRYPLANDQTTTLQNNMYKDYLRMSEGENPELFGNP 60
QY 52 EPPFVSASTIQTGIGIAGKILGTGVPFAGQVAVSLYFSLGELWPKCK-NQWEIFMEHVEE 110
DB 61 ETPFSSSTVQTGIGIVGVLPFAGQIASFYSLVGEWLPSSSTVSVWEMIMKQVED 120
QY 111 IINQKISTYARNKALTDLKGDLGDLAVYHDSLESWVGNNRNRTRARSVVKSOYIALELMFV 170
DB 121 LIDOKITSVRKALAGLQGLDGLDYQKSLKNWLENRNDTRARSVVVTQYIALELDV 180
QY 171 QKLPFSFVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGD 230
DB 181 AKIPSFASISGQEVPLLSVYAQAANLHLLLRDASIFGAEWGTPEGEISTFYDRQVTRTAQ 240
QY 231 YSDHCWKWYSTGLNLRGTHAESWRYNQFRDRMTLMVLVDLVALFPSSYDTQYPIKTAQ 290
DB 241 YSDYCVKWYNTGLDKGTNAASWLVKHQFRREMTLLVLDLVALFPNYDTRTYPIETTAQ 300
QY 291 LTRVYTDAGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDPLEQVTIYSLLS- 349
DB 301 LTRVYTDAGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDPLEQVTIYSLLS- 360
QY 350 -RWSNTQYNNMGGHKLFRFTIGTGLTSTQGSTNTSINPVLPTPSRQVYRTSSLAGL 407
DB 361 LPLNNTLEYWVGHISIKYKNTNASSALERNYGTITSNKIKYDLANKIDIFQVRSGLADL 420
QY 408 NLFLTQPVNGVPRVDFHWKFTVTHPIASDNFYYPGYAGIG-----TQLQDSE 453
DB 421 ANYYAQ-VYGVPIYASF-----TLDDQN---TSGSVGSGFTYKPHHTTMQVCTQVNTI 469
QY 454 NELPPEATQPNYESYSHRLSHLIGLS-----ASHVKALVYSWTHRSADRTNTIEPN 505
DB 470 DEIPPE--NEPLSRGYSHRLSHLITSYSPSKNASSPARYGNLVPFAWTHRSADVTNTVYSD 527
QY 506 SITQIPLVKAENLSSGAAVVRGPGFTGGDILRRNTGTFGDIRVNPFPFAQRYRVRIRY 565
DB 528 KITQIPVKAHTLVSGTIVKPGFTGGDILRRNTGTFGDIRVNPFPFAQRYRVRIRY 587
QY 566 ASITDQLQHTSINGKALNOGNFSATMNRGEDLDYKTFRTVGTFTTTPFSLDVQSTFTIGAW 625
DB 588 ASTTNLRFPVTISGTRIYSINVNKTMKGGDLTFTNTPDLATIGTATFTFSNYSDSLTVGAD 647
QY 626 NFSSGNEVYIDRIEFVPEVTYVEAEYFEKAQEKVTLFTSTNPRGLKTDVKDYHIDQVS 685
DB 648 SFASGGEVYVDKFEILIPVNTATFEAEEDLDVAKAVNGLFTSKKD-ALQTSVTDYQVNOQA 706
QY 686 NLVESLSDEFYLDKELFEIVKVAQQLHIERNM 719
DB 707 NLVECLSDLYPNEKRLMDVAKEAKRLVQARNL 740

RESULT 12

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Thu Mar 10 14:26:04 2005

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US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 44.7%; Score 1681.5; DB 15; Length 653;
Best Local Similarity 51.5%; Pred. No. 1.6e-133;
Matches 346; Conservative 106; Mismatches 173; Indels 47; Gaps 14;

QY 13 SSNAKVDKISTSLKN---ETDIELQINHHEDCLKMSYENVEPPFVSASTIQTGIGIAGK 69
DB 2 NENEIINALSPAVNSHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINIAGR 60

QY 70 ILGTLGVPPFAGOVASLYSFLIGELMPKGNQWELFMEHVEEINQKISTYARNKALTDLK 129
DB 61 ILGVLGVPPFAGQLASYSFLVIGELMPKGNQWELFMEHVEEINQKISTYARNKALTDLK 120

QY 130 GLGDALAVYHDSLESVGNRNTRARSVVKVSKQYLAELMFLVQKLPFAVSGEVPLLPIY 189
DB 121 GLGRGYRSYQALETWLDNRNDARSIIILERYVALELDITTAIPLRINEEVPLLMVY 180

QY 190 AQANLHLLLDASIFGKWLSSSEISTFYNRQVERAGDYSDHCVKWKYSTGLNNLRGT 249
DB 181 AQANLHLLLDASIFGSEWGMASDVQYQEQIRYTEYSNHCWQYNTGLNNLRGT 240

QY 250 NAEWSVRYNQFRDMLTMDLVLPSPSYDTOMYPIKTTAQLTREVTYDAIGTVHPHPSF 309
DB 241 NAEWSLRYNQFRDMLTMDLVLPSPSYDTOMYPIKTTAQLTREVTYDAIGTVHPHPSF 300

QY 310 TSTTWYNNNAPSFAIAAANVRNPHLLDFLEQVTTYSLLSRWSNTQYMNWGGHKLPRPT 369
DB 301 ASTWNNNAPSFAIAAANVRNPHLLDFLEQVTTYSLLSRWSNTQYMNWGGHKLPRPT 360

QY 370 IGGTLNISTQGST-NTSINPVTLPF-TSRDVRRTESLAGNLFQVNVGVPRVDFHKKF 427
DB 361 IGGTLNISTQGLTNTSINPVTLPF-LHYVSSRDVYRTESNAGNLFQVNVGVPRVDFHKKF 418

QY 428 VTHPIASDNFYPP-----GYAGIGTQLODSENELPPEATQPNYESYSHRLSHIG-- 477
DB 419 ITRIFMKEAPLPVNRIRLGFNYLQKLNHYQK-----QONDQIMNHIVIDISYR 470

QY 478 LISASHVKALVSWTHRSADRTNTIENSIITQIPLVKAFNLSGGAANVRGPGFTGGDILR 537
DB 471 LIIGNTLAPVSWTHRSADRTNTIENSIITQIPLVKAFNLSGGAANVRGPGFTGGDILR 529

QY 538 -RTNRTGTF---GDIRVWIN-PPFAQRYVRIRYASITDQLQHTSINGKAINQGNFSATWN 592
DB 530 LNRNNGNIQNRGYLEVPIQFTSTSTRYVRVYASVTSIELNVNLGNSSIFTNTLPATAA 589

QY 593 RGEDLDYKTRFTVGTFTPFSLDVQSTFT-----IGANFSSGNEVYIDRIEFPVPEVT 646
DB 590 SLDNLQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAEEVIDRFEFIPVTAT 640

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QY 647 YEAEYDFEKAQE 658
DB 641 FEVEYDLERAQK 652

RESULT 13
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Haigiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match 44.4%; Score 1670.5; DB 16; Length 1157;
Best Local Similarity 49.1%; Pred. No. 3.3e-132;
Matches 371; Conservative 98; Mismatches 230; Indels 57; Gaps 18;

QY 1 MCLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQINHHEDCLKMSYENVEPPFVSASTIQTGIGIAGK 50
DB 1 MSPNNQNEYEIIDATPST-SVSSDSNRYPPANEPTDALQNMVYKDYLMKSGGENPELFGN 59

QY 51 VEPFVSASTIQTGIGIAGKILGTGVPPFAGOVASLYSFLIGELMP-KGNQWELFMEHVE 109
DB 60 PETFISSTIQTGIGIAGKILGTGVPPFAGOVASLYSFLIGELMP-KGNQWELFMEHVE 119

QY 110 EITNQKISTYARNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKVSKQYLAELMFL 169
DB 120 ELVDQKIEKYVKDQKALAEKGLGNALDVYQOSLEWLNENRDARTSRVSVNQFIALDLNF 179

QY 170 VQKLPFAVSGEVPLLPIYQAANLHLLLDASIFGKWLSSSEISTFYNRQVERAG 229
DB 180 VSSIPFAVSGEVPLLPIYQAANLHLLLDASIFGKWLSSSEISTFYNRQVERAG 239

QY 230 DYSCHCVKWKYSTGLNNLRGTNAESVVRYNQFRDMLTMDLVLPSPSYDTOMYPIKTTA 289
DB 240 EYSDYCVKWKYSTGLNNLRGTNAESVVRYNQFRDMLTMDLVLPSPSYDTOMYPIKTTA 299

QY 290 QLTREVTYDAIGTVHPHPSFTST---TWYNNNAPSFAIAAANVRNPHLLDFLEQVTTIY 345
DB 300 QLTREVTYDAIGTVHPHPSFTST---FNIVTSTGFCNPNWSTHSGILFYEVENNVRPPLFDILLSVEIN 355

QY 346 SLLSR-----WSNTQYMNWGGHKLPRPT-----TIGGTNLNISTQGSTNTSINPVTLPFTSR 396
DB 356 T--SRGITLNDADYINWWSGHTLKRYRTADSTVYTYANYGRITSEKNS-----PALEDR 408

QY 397 DVYRTESLAGNLFQVNVGVPRVDFHKKFVTHPIASDNFY-----YPGYAGIGTQLOD 451
DB 409 DIFEINSTVANLANVYQKAYGVPGSWFH--MVKRGTSSTAYLYSKHTALQGC-TQVYE 465

QY 452 SENELPPEATQPNYESYSHRLSHI-----GLISASHVKALVSWTHRSADRTNTIE 503
DB 466 SSDEIFLDRIT-VPVAESYSHRLSHITSHSFSKNG--SAYYGSFPFVFWVWTHTSADLNTIY 522

QY 504 PNSTIQTPLVKAFNLSGGAANVRGPGFTGGDILRRTNTGTFTGDIRVWINPPEAQRVRI 563
DB 504 PNSTIQTPLVKAFNLSGGAANVRGPGFTGGDILRRTNTGTFTGDIRVWINPPEAQRVRI 563

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Db 523 SDKITQIPAVKDMLYLGGSVVQPGFTGGDILKRTNPSILGTFVAVTVNGSLSQRXRVRI 582
QY 564 RYASTTDLOFHTSINGKAINQGNFSATNWRGEDLDYKTRTGVGFTTPPSFLDVQSTFTIG 623
Db 583 RYASTTDFEF-TLYLGDTEIKRNFKNKMDNGASLTYTEFFKFASTITDFQFRETQDKILLS 641
QY 624 AWFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFTSTNPRGLKTDVVDYHIDQ 683
Db 642 MGDSSGQEVYIDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTYEVNQ 700
QY 684 VSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 701 AANLVECLSDLLYPNEKRLFLDAVREAKRLSGARNL 736

RESULT 14

US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 40.2%; Score 1511; DB 13; Length 1206;
Best Local Similarity 44.3%; Pred. No. 1.2e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIBLQNIHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRPFFANEPTNALQNDYKYDKLMSAGNASSEYPGS 59
QY 51 VEPFVSA-STIQTGIGIAGKILGTGLVPPAGQVAVSLYSFILGELWPKG-KNQEWFMEHV 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGSEKQWEIFMEQV 119
QY 109 EEIINQKISTYARKNALTDLKGLGDALAVYHDSLESWSVGNRNTRARSVVKSQYIALELM 168
Db 120 EELINQKIAEYARKNALSLEGLGNVYQLYLTALAEENPNPNSRRLRDVRNRFELDLSL 179
QY 169 FVQKLPSFAVSGBEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 228
Db 180 FTQYMPFRVTNFEVPFLTVYAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 239
QY 229 GDYSDHCVKWYSTGLNNLRGTNAESWRYNQFRDWTLMVLVDLVALFPSPYDTQMYPIKTT 288
Db 240 AEYSDHCVKWYETGLAKLKGTSKQWVDYNQFRREMTLAVLDVVALFPNVDTRTPMETK 299
QY 289 AQLTREYVTDAGTVHPHPSFTSTTWNNAPSAEAAVVRNPHLLDFLEQVITYSL 348
Db 300 AQLTREYVTDPLGAVNVS---SIGSWY-DKAPSGFVIESSVIRPPHVFDTYITGLTYVTQS 355
QY 349 SRWNTQYNNMGWGHKLEFRRTIGTGLNISTQGSTNTSNIPV-TLPFTSRDYRTESLAGL 407
Db 356 RSISARYIRHWAGHQISYHRVSRGSLNQOMYGTGNQNLHSTSTFDFTNYDIYKTLKSDAV 415

QY 408 NLFLTQP-----VNGVPRVDFHMKFVTHPIASDN---FYYPGYAGIGTQLODSENELPPE 459
Db 416 LLDIVYPGVTYIIFGMEPEVEF---FMVQLNNTRKTLKYNPVSODIIASTRDSLELEPPE 472
QY 460 ATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRNTTIEPNSITQIPLVKAF 516
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNNTIYSDKITQIPAVKCM 532
QY 517 NLSSGAAVVPGPGTGGDILR-RNTGTGFDI---RVNINPPPAQRYRVRIRYASTTDLQ 572
Db 533 DNLFPVVPVVGPGHTGGDLQYNRSTGSGTFLARYGLALEKAGKYRVRRLRYATDADIV 592
QY 573 FHTSINGKAINQGNFSATNWRGEDLDYKTR-----TVGFTTTPFSFL-----DVQST 619
Db 593 LH--VNDQI---QMPKTNWPGEDLTSKTFKVADAIITLNLATDSSALKKNLGEDDNST 647
QY 620 FTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFTSTNPRGLKTDVVDY 679
Db 648 LS-----GIVYVDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDY 697
QY 680 HIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 698 EVNQAANLVECLSDLLYPNEKRLFLDAVREAKRLSEARNL 737

RESULT 15

US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 40.2%; Score 1511; DB 14; Length 1206;
Best Local Similarity 44.3%; Pred. No. 1.2e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIBLQNIHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRPFFANEPTNALQNDYKYDKLMSAGNASSEYPGS 59
QY 51 VEPFVSA-STIQTGIGIAGKILGTGLVPPAGQVAVSLYSFILGELWPKG-KNQEWFMEHV 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGSEKQWEIFMEQV 119
QY 109 EEIINQKISTYARKNALTDLKGLGDALAVYHDSLESWSVGNRNTRARSVVKSQYIALELM 168
Db 120 EELINQKIAEYARKNALSLEGLGNVYQLYLTALAEENPNPNSRRLRDVRNRFELDLSL 179
QY 169 FVQKLPSFAVSGBEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 228
Db 180 FTQYMPFRVTNFEVPFLTVYAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 239

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds
(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-55
Perfect score: 3760
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	3 US-08-286-870A-8	Sequence 8, Appli
2	3476.5	92.5	710	4 US-09-661-322A-42	Sequence 42, Appl
3	3398	90.4	648	3 US-08-286-870A-4	Sequence 4, Appli
4	3377	89.8	719	2 US-09-003-217-2	Sequence 2, Appli
5	3372	89.7	719	3 US-09-218-942-2	Sequence 2, Appli
6	2804	74.6	535	3 US-08-286-870A-6	Sequence 6, Appli
7	2446.5	65.1	1229	1 US-08-100-709-4	Sequence 4, Appli
8	2446.5	65.1	1229	1 US-08-176-865-4	Sequence 4, Appli
9	2446.5	65.1	1229	1 US-08-474-038-4	Sequence 4, Appli
10	2446.5	65.1	1229	2 US-08-779-046-4	Sequence 4, Appli
11	2446.5	65.1	1229	2 US-08-881-340-4	Sequence 4, Appli
12	2344.5	62.4	488	3 US-08-448-170-10	Sequence 10, Appl
13	2344.5	62.4	488	3 US-08-961-803-10	Sequence 10, Appl
14	2265.5	60.3	1207	1 US-07-951-715A-7	Sequence 7, Appli
15	2265.5	60.3	1207	2 US-08-459-448A-7	Sequence 7, Appli
16	2265.5	60.3	1207	3 US-08-459-595A-7	Sequence 7, Appli
17	2265.5	60.3	1207	3 US-08-459-504B-7	Sequence 7, Appli
18	2265.5	60.3	1207	3 US-08-459-444-7	Sequence 7, Appli
19	2265.5	60.3	1207	3 US-09-053-549-8	Sequence 8, Appli
20	2265.5	60.3	1207	3 US-09-547-422-7	Sequence 7, Appli
21	2265.5	60.3	1207	4 US-09-988-462-7	Sequence 7, Appli
22	2264.5	60.2	1227	3 US-09-053-549-2	Sequence 2, Appli
23	2195.5	58.4	1227	1 US-08-448-170-8	Sequence 8, Appli
24	2195.5	58.4	1227	3 US-08-961-803-9	Sequence 9, Appli
25	2186.5	58.2	1227	4 US-09-661-322A-63	Sequence 63, Appl
26	2171.5	57.8	1186	3 US-09-178-252-23	Sequence 23, Appl
27	2171.5	57.8	1186	4 US-09-826-660-23	Sequence 23, Appl

28	2116	56.3	1228	4 US-09-661-322A-38	Sequence 38, Appl
29	1932.5	51.4	643	3 US-09-178-252-25	Sequence 25, Appl
30	1932.5	51.4	643	4 US-09-826-660-25	Sequence 25, Appl
31	1900	50.5	380	5 PCT-US91-02560-4	Sequence 4, Appli
32	1681.5	44.7	653	4 US-09-661-322A-6	Sequence 6, Appli
33	1670.5	44.4	1157	1 US-07-876-280-30	Sequence 30, Appl
34	1670.5	44.4	1157	1 US-07-812-180A-2	Sequence 2, Appli
35	1670.5	44.4	1157	1 US-08-315-468-2	Sequence 2, Appli
36	1670.5	44.4	1157	3 US-07-941-650A-2	Sequence 2, Appli
37	1507.5	40.1	1176	1 US-08-257-999-2	Sequence 5, Appli
38	1492	39.7	1157	2 US-08-532-547-5	Sequence 5, Appli
39	1492	39.7	1157	2 US-08-379-656B-5	Sequence 5, Appli
40	1492	39.7	1157	3 US-08-455-838-5	Sequence 5, Appli
41	1492	39.7	1157	3 US-09-019-803-5	Sequence 5, Appli
42	1492	39.7	1157	4 US-09-471-177-5	Sequence 5, Appli
43	1492	39.7	1157	4 US-09-220-806-5	Sequence 5, Appli
44	1486.5	39.5	1169	1 US-08-315-468-4	Sequence 4, Appli
45	1485.5	39.5	1156	3 US-09-002-285-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Thu Mar 10 14:26:04 2005

us-10-019-823b-55.ra

Query Match 99.9%; Score 3756; DB 3; Length 719;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 718; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
DB 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N O K I S T Y A 120
DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N O K I S T Y A 120
QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
DB 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240
DB 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240
QY 241 T C L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
DB 241 T C L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
QY 301 G T V H P H S F T S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
DB 301 G T V H P H S F T S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
QY 361 G G H K L E P R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
DB 361 G G H K L E P R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
DB 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540
DB 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540
QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N O G N F S A T M R G E D L D Y K 600
DB 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N O G N F S A T M R G E D L D Y K 600
QY 601 T F R T V G F T P P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T E A E Y D F E K A Q E K V 660
DB 601 T F R T V G F T P P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T E A E Y D F E K A Q E K V 660
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719
DB 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 92.5%; Score 3476.5; DB 4; Length 710;
Best Local Similarity 92.5%; Pred. No. 5.5e-303;
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;
QY 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
DB 1 M K S K N Q N H Q S L S N A T V D K N F T G S L E N T N T E L Q N F N H -----EGIEP F V S V S T I 51
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N O K I S T Y A 120
DB 52 Q T G I G I A G K I L G N L G V P F A G Q V A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N O K I S T Y A 111
QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
DB 112 R N K A L A D L K G L G D A L A V H E S L E S W I E N R N N T R T R S V V K S Q Y I T L E L M F V Q S L S F A V S G 171
QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240
DB 172 E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S K S K E Y S D H C V K W Y N 231
QY 241 T C L N N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
DB 232 T C L N R L M G N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 291
QY 301 G T V H P H S F T S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
DB 292 G T V H P H S F T S T T W Y N N A P S F S T E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 351
QY 361 G G H K L E P R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
DB 352 G G H K L E P R T I G T L N T S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 411
QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
DB 412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 471
QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540
DB 472 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R K N 531
QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N O G N F S A T M R G E D L D Y K 600
DB 532 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N O G N F S A T M R G E D L D Y K 591
QY 601 T F R T V G F T P P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T E A E Y D F E K A Q E K V 660
DB 592 T F R T V G F T P P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T E A E Y D F E K A Q E B V 651
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719
DB 652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D K F Y L D E K R E L F E I V K A Q L H I E R N M 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 90.4%; Score 3398; DB 3; Length 648;
Best Local Similarity 100.0%; Pred. No. 5.3e-296;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180
DB 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
QY 241 TGLNLRGTNAESWRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTQAUTREYVTDI 300
DB 241 TGLNLRGTNAESWRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTQAUTREYVTDI 300
QY 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNMW 360
QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPNVGVPR 420
DB 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPNVGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNRGEDLDYK 600
QY 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTYE 648
DB 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTYE 648
RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.8%; Score 3377; DB 2; Length 719;
Best Local Similarity 89.8%; Pred. No. 4.8e-294;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180
DB 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVOKLPSFAVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240

Thu Mar 10 14:26:04 2005

181 EEVPLPIYAQAANLHLLLRDASIFPKXGGLSASEISTFYNRQVTRDYSYHCVKWN 240
241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTQYPIKTTAQLTREVYTD 300
241 TGLNLRATNGQSWVRYNQFRKDIEMVLDLVRFPSTQYPIKTTAQLTREVYTD 300
301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
301 GTVDNQALRSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRFTESLAGLNLFLTQPVNGVPR 420
361 GGHLESRPFGALNTSTQGSTNTSINPVTLPFTSRDVRFTESLAGLNLFLTQPVNGVPR 420
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLOQSDSENELPPEATGQPNYESYSHRSLHIGLIS 480
421 VDFHWKFTPLPIASDNFYYPGYAGIGTQLOQSDSENELPPEATGQPNYESYSHRSLHIGLIS 480
481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540
481 GSHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540
541 TGTFGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
541 STFGHIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
601 TERTVGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
601 TERTVGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
661 TALFTSTNPRGLTKDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 719
661 TALFTSTNPRGLTKDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: Cyt11
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2
Query Match 89.7%; Score 3372; DB 3; Length 719;
Best Local Similarity 89.8%; Pred. No. 1.3e-293;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

1 MKLKNQKHQSFNNAKVDKISTLSKNETDIELQINNHEDCLKMSYENVEPFSASTI 60
1 MKLKNPDKHQTLSSNAKVDKIATDLSKNETDIELKNMNEEDYLRMSHESIDPFSASTI 60
61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIQKISTYA 120
61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIQKISTYA 120
121 RNKALTDLKLGDALAYVHDSLESWVGNNRNNRARSVVKSQYIALELMFVQKLPSFAVSG 180
121 RNKALTDLKLGDALAYVHDSLESWVGNNRNNRARSVVKSQYIALELMFVQKLPSFAVSG 180

181 EEVPLPIYAQAANLHLLLRDASIFPKXGGLSASEISTFYNRQVTRDYSYHCVKWN 240
181 EEVPLPIYAQAANLHLLLRDASIFPKXGGLSASEISTFYNRQVTRDYSYHCVKWN 240
241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTQYPIKTTAQLTREVYTD 300
241 TGLNLRATNGQSWVRYNQFRKDIEMVLDLVRFPSTQYPIKTTAQLTREVYTD 300
301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
301 GTVDNQALRSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRFTESLAGLNLFLTQPVNGVPR 420
361 GGHLESRPFGALNTSTQGSTNTSINPVTLPFTSRDVRFTESLAGLNLFLTQPVNGVPR 420
421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLOQSDSENELPPEATGQPNYESYSHRSLHIGLIS 480
421 VDFHWKFTPLPIASDNFYYPGYAGIGTQLOQSDSENELPPEATGQPNYESYSHRSLHIGLIS 480
481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540
481 GSHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540
541 TGTFGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
541 STFGHIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
601 TERTVGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
601 TERTVGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
661 TALFTSTNPRGLTKDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 719
661 TALFTSTNPRGLTKDVKDYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989


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;
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match      74.6%; Score 2804; DB 3; Length 535;
Best Local Similarity 100.0%; Pred. No. 8.1e-243;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFFVSASTI 60
DB 1 MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFFVSASTI 60

QY 61 QTGIGIAGKILGTIGVPPAGQVASYLSFILGELWPKGNOWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTIGVPPAGQVASYLSFILGELWPKGNOWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGLDALAVYHDSLSWVGNNRNTARSVVKSVQYIALELMFVQKLPSPAVSG 180
DB 121 RNKALTDLKGLDALAVYHDSLSWVGNNRNTARSVVKSVQYIALELMFVQKLPSPAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240

QY 241 TGLNLRGNTNAESWRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
DB 241 TGLNLRGNTNAESWRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360

QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSSENLPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHPIASDNFYYPGYAGIGTQLODSSENLPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHKVAVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 481 ASHKVAVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
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;
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match      65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINNHEDCLKMSYENVEPFFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPVSNPSTQMLSPDARIEDSLCVAEVENIDPFFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNOWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQVASYLSFILGELWPKGNOWEIFMEHVEEIIINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLSWVGNNRNTARSVVKSVQYIALELMFVQKLPSPAVSGEVPVLLPIYA 190
DB 127 LGRGVSRYQALETWLDNRNDARSRSIILRYVALELDITTAIPLFRIRNEEVPLLMVYA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGNTN 250
DB 187 QAANLHLLLRDASIFGSEWGMASDVNQYQOEIRYTEEYSHNCVQWYNTGLNLRGNTN 246

QY 251 AESWRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 310
DB 247 AESWRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 306

QY 311 STTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMWGCHKLEFRTI 370
DB 307 STWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMWVGHRLNFRPI 366

QY 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPRVDFHKKFVT 429
DB 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPRVDFHKKFVT 422

QY 430 HPIASDNFYYPG-----YAGIGTQLODSSENLPEATQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTSYQPYQGVGIQLFDSSETLPPTTERPNYESYSHRLSHIGLIGN 480

QY 483 HVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542
DB 481 TLRAVYVSWTHRSADRTNTIEPNSITQIPLVKALNLSGVTVVGPGFTGGDILRRTNTG 540

QY 543 TFGDIRVNIINPPFAQYRVRIYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYKTF 602
DB 541 TFGDIRVNIINPPFAQYRVRIYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYKTF 600

QY 603 RTVGFTTTPSEFLDVQSTETIGAWNFSGNEVYIDRIEFVPRVETVYAEYDFEKAQSKVTA 662
DB 601 RTAGFSTPFENFLNAQSTFTLGAQSFNS-QEVYIDRVEFVPAEVTFEAEYDLERAQAVNA 659
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QY      663 LFTSTNPRGLKTDVDYHIDOVSNLVESLSDFEYLDEKRELFEVVKVAKQLHIERNM 719
        ||||| ||||| ||||| ||||| : ||||| ||||| ||||| : |||||
        ||||| ||||| ||||| ||||| : ||||| ||||| ||||| : |||||
nb      660 LFTSTNPRRLKTDVTYHIDOVSNMVACLSDFECLDEKRELFEVVKVAKRLSDERNL 716
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RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
INSECTS TOXIC TO LEPIDOPTERAN

	Query Match	65.1%;	Score 2446.5;	DB 1;	Length 1229;
	Best Local Similarity	65.6%;	Pred. No. 3.9e-210;		
	Matches 470;	Conservative	92;	Mismatches 138;	Indels 17; Gaps 16;
QY	13	SSNAKVDKISTDLKN-ETDIEIQ-NINHHEDCLKMSEYENVEPFVSASTTQTGTGIGIAGKI	70		
Db	7	NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGTGINIAGRI	66		
QY	71	LGTGLGVFPFAGQVASLYFTLGEIWPKGKNQWEIFMEHVEEIIINOKISTYARNKALTDLKG	130		
Db	67	LGVLGVFPFAGQLASFYSFLVGEIWPSGRDPWEIFLEHVEQLIRQQVTRNTAARLEG	126		
QY	131	LGDALAVYHDSLESWVGNNRNTNRARSVVKVQSYIALEMFVQKLPSPFVSGSEVPLLPIYA	190		
Db	127	LGRGYSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFIIRNEEVPLLMVYA	186		
QY	191	QAANLHLLLRDASIFGKEWGLSSEISITFYNNRQVERAGDYSDHCVKWKYSTGLNNLRGTN	250		
Db	187	QAANLHLLLRDASLFGSEWGMASDVNOYQEQIRYTEEYNNHCVOYNTGLNNLRGTN	246		
QY					
Db					

	Dd	247	AESLWRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRTNAPSGFA	308
	Qy	311	STTWNNNAPSFAIEAAVVRPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLEFRTI	370
	Dd	307	STWNFNNAAPSFAIEAAIFRPPLHLDFFPEQLTIYSASSRWSSTQHMYVWGHRLNFRPI	366
	Qy	371	GGLINISTQGST-NTSINPVLTLPFTSRDVRYTESLAGNLFLTPQVNGVPVRVDPHWKFTV	429
	Dd	367	GGLTNTSTQGLTNTNISINPVLTLPFTSRDVRYTESNAGTNILFTTPVNGVPWARPNF---	422
	Qy	430	HPIASDNFYYPG-----YAGIGTLODSENELPPEATGOPNYEYSYSHRLSHIGHUISAS	482
	Dd	423	--INPONIERYGATTYSOPYQGVGIOLFDSATELPPPTTERPRNYESYSHRLSHIGHLIGN	480
	Qy	483	HVKALVYSWTHRSADRTWTIEPNSITQTPLKAFNLSSGAAVRGPGFTGGDIILRRNTG	542
	Dd	481	TLRAPVYSWTHRSADRTWTIGPNKRITQTPLKALNLSHGVTVVGPGFTGGDIILRRNTG	540
	Qy	543	TFGDIRVINPPPFAORYRVIRYASTTDLQFHTSINGKAINOGNFESATMNRGEDLYKTF	602
	Dd	541	TFGDIRLINVPVSQRVRYRIYASTTDLQFFTRINGTTVNIGFSRTMNRGDNLERYSF	600
	Qy	603	RTVGFTTPPSFLDVQSFTTGAWNFSSGNNEVIYDRIEFVPVEVTYEAEYDFEKAQEKVTA	662
	Dd	601	RTAGESTPFNFLNAOSTFTFLCAQGSFN-QEVYIDRVFEVPAEVTFEAEYDLERAQAUNA	659
	Qy	663	LFTSTNPRLGTVDKYDHIDQVSNLVSESDEFYLDEKRELFEIVKYAKOLHIERNM	719
	Dd	660	LFTSTNPRLKTVDVTYHDIDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLSDERNL	716

RESULT 9
 US-08-474-038-4
 ; Sequence 4, Application US/08474038
 ; Patent No. 5679343
 ; GENERAL INFORMATION:
 ; APPLICANT: Donovan, William P.
 ; APPLICANT: Tan, Yuping
 ; APPLICANT: Jany, Christine S.
 ; APPLICANT: Gonzalez Jr., Jose M.
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
 ; ADDRESSEE: Nadel
 ; STREET: 1601 Market Street, 36th Floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,038
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/176,865
 ; FILING DATE: 30-DEC-1993
 ; APPLICATION NUMBER: US 08/100,709
 ; FILING DATE: 29-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Egoif, Christopher
 ; REGISTRATION NUMBER: 27633
 ; REFERENCE/DOCKET NUMBER: 7205-49
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-757-1590
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-038-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVPFVSASTIQTGIGIAGKI 70
DB 7 NENEINALSIPTVSNPSTQMNLSPDARIEDSLCAEYNNIDPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPFAGQLASFYSFLVGLWPGSDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126
QY 131 LGDALAVYHDSLESWVGNNRNRARSVVKSYQYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSRIILERYVALELDITTAIFLRINEEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWSYGLNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEWGMASDVNQYQYIRYEEYSNHCVMQYNTGLNLRGTN 246
QY 251 AESWRYNQFRDMTLMVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 310
DB 247 AESWRYNQFRDMLTGLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 306
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWNTQYNNMGHKLFRFTI 370
DB 307 STWFNNAPSFSAIEAAIFRPHLLDFEQVTIYSLLSRWNTQYNNMGHKLFRFTI 366
QY 371 GGTNLISTQGST-NTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHVKFVT 429
DB 367 GGTNLSTQGLTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHVKFVT 422
QY 430 HPIASDNFYYPG-----YAGICTQLQDSSENLPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQGVGIQDFSETELPPETTERPNYESYSHRLSHIGLIIGN 480
QY 483 HVKALVYSWTHRSADRNTNIEPNSITQPLVKAFNLSSGAAVRGGPGFTGGDILRRNTG 542
DB 481 TLRAVPYSWTHRSADRNTNIEPNSITQPLVKALNLHSGTVVGGPGFTGGDILRRNTG 540
QY 543 TFGDIRVNPFPFQRYRIRYASTDLOFHTSINGKAINQGNFSATMNGEDLDYKTF 602
DB 541 TFGDIRLNVPLSQRYRIRYASTDLOFHTSINGKAINQGNFSATMNGEDLDYKTF 600
QY 603 RTVGFTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVYEAEDFEKAQEKVTA 662
DB 601 RTAGSTPFPNLNAQSTFLLCAQSFN-QEYVIDRVEFVPAEVTFEAEYDLERAKAVNA 659
QY 663 LFTSTNPRGLTKTDVYHIDQVSNMVACLUSDEFCLDEKRELFEIVKAKQLHIERNM 719
DB 660 LFTSTNPRGLTKTDVYHIDQVSNMVACLUSDEFCLDEKRELFEIVKAKQLHIERNM 716

RESULT 10

US-08-779-046-4
Sequence 4, Application US/08779046
Patent No. 5854053
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-046-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVPFVSASTIQTGIGIAGKI 70
DB 7 NENEINALSIPTVSNPSTQMNLSPDARIEDSLCAEYNNIDPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPFAGQLASFYSFLVGLWPGSDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126
QY 131 LGDALAVYHDSLESWVGNNRNRARSVVKSYQYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSRIILERYVALELDITTAIFLRINEEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWSYGLNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEWGMASDVNQYQYIRYEEYSNHCVMQYNTGLNLRGTN 246
QY 251 AESWRYNQFRDMTLMVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 310
DB 247 AESWRYNQFRDMLTGLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 306
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWNTQYNNMGHKLFRFTI 370
DB 307 STWFNNAPSFSAIEAAIFRPHLLDFEQVTIYSLLSRWNTQYNNMGHKLFRFTI 366
QY 371 GGTNLISTQGST-NTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHVKFVT 429
DB 367 GGTNLSTQGLTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHVKFVT 422
QY 430 HPIASDNFYYPG-----YAGICTQLQDSSENLPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQGVGIQDFSETELPPETTERPNYESYSHRLSHIGLIIGN 480
QY 483 HVKALVYSWTHRSADRNTNIEPNSITQPLVKAFNLSSGAAVRGGPGFTGGDILRRNTG 542
DB 481 TLRAVPYSWTHRSADRNTNIEPNSITQPLVKALNLHSGTVVGGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNINPPFAQRVVRIRYASTDLOQHTSINGKAINOQNFSAATMNRGDLKYTF 602
DB 541 TFGDIRVNINPFSQRVVRIRYASTDLOQHTSINGKAINOQNFSAATMNRGDLKYTF 600
QY 603 RTVGFTTFFSLDQSTFTIGAMNFFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVT 662
DB 601 RTAGFSTPFLNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFAEYDLERAKAVNA 659
QY 663 LFTSTNPRGLKTDVYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 660 LFTSTNPRRLKTDVYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-881-340-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMSEYENVEPFSASTIQTGTGIAGKI 70
DB 7 NENEINALSIPVSNPSTQMNLSPDARIEDSLCVAEVNNDPFSASTVQTGINAGRI 66
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIQKISTYARNKALTDLKG 126
QY 131 LGDALAVYHDSLSWVGNNRNTARSVVKSQYIALELMFVQKLPSFAVSGEVPPLPIYA 190

DB 127 LGRGYSYQOALETWLDRNDARSRSILERYVALELDITTAIPLFIRNEEVPLLMVYA 186
QY 191 QAAHLHLRLDASIFGKEWGLSSSEISTFYNRQVERAGDYSDCHVKWYSTGLNLRGTN 250
DB 187 QAAHLHLRLDASIFGSEWGMASQVQYQEQIRYTEESNHCVCOWYNTGLNLRGTN 246
QY 251 AEWRYNQFRDRMTLMDLVALFSPYDTQMPYIKTQAQTLREVVYDAIGTVHPHPSFT 310
DB 247 AESWLRYNQFRDRLTGLVLDLVALFSPYDTRTYPINTSAQLTREIYTDPIGRTNAPSGFA 306
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYLLSRWSNTQYNNMGGHKLFEFTI 370
DB 307 STNWFNNAPSFAIEAAIFRPHLLDLEQVTIYLLSRWSNTQYNNMGGHKLFEFTI 366
QY 371 GGTLANISTQGST-NTSINPVTLPFTSRDVRFTESLAGNLFLTQPVNGVPRVDFFHKKFVT 429
DB 367 GGTLANISTQGST-NTSINPVTLPFTSRDVRFTESLAGNLFLTQPVNGVPRVDFFHKKFVT 422
QY 430 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPEPETERPNYESYSHRLSHIGLISAS 480
QY 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRNTG 542
DB 481 TLRAVYVSWTHRSADRTNTEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRNTG 540
QY 543 TFGDIRVNINPPFAQRVVRIRYASTDLOQHTSINGKAINOQNFSAATMNRGDLKYTF 602
DB 541 TFGDIRVNINPFSQRVVRIRYASTDLOQHTSINGKAINOQNFSAATMNRGDLKYTF 600
QY 603 RTVGFTTFFSLDQSTFTIGAMNFFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVT 662
DB 601 RTAGFSTPFLNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFAEYDLERAKAVNA 659
QY 663 LFTSTNPRGLKTDVYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 660 LFTSTNPRRLKTDVYHIDQVSNLVESLDEFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 12
US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 102D.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-170-10

Query Match 62.4%; Score 2344.5; DB 1; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60
D B 1 M K S K N Q N M H Q S L S N N A T V D K N F T G S L E N N T N T E L Q N F N H -----E G I E P F V S V S T I 51
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I N Q I S T Y A 120
D B 52 Q T G I G I V G K I L G N L G V P F A G Q V A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I N Q I S T Y A 111
QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G V G N R N T R A S V V K S Q V I A L E L M F V Q K L P S F A V S G 180
D B 112 R N K A L A D L K G L D A L A V Y H S L E S W I E N R N T R S V V K S Q V I T L E L M F V Q S L P S F A V S G 171
QY 181 E E V P L L P I Y A Q A N L H L L L R D A S I F G K W G L S S S E I S T F Y N R Q V R A G D Y S D H C V K W Y S 240
D B 172 E E V P L L P I Y A Q A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S G K S K E Y S D H C V K W Y N 231
QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
D B 232 T G L N L M G N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 291
QY 301 G T V H P H P S F T S T T Y N N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 360
D B 292 G T V H P H P S F T S T T Y N N N A P S F S T I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 351
QY 361 G G H K L E F R T I G T L N I S T G S T N T S I N P V T L P F T S R D V R Y T E S L A G N L F L T Q P V N G V P R 420
D B 352 G G H K L E F R T I G T L N T S T G S T N T S I N P V T L P F T S R D V R Y T E S L A G N L F L T Q P V N G V P R 411
QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 480
D B 412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 471
QY 481 A S H V K A L V T S W T H R S A D 497
D B 472 A S H V K A L V T S W T H R S A D 488

RESULT 13
US-08-961-803-10
Sequence 10, Application US/08961803
Patent No. 6150589
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. Ps158c2, Active Against Lepidopteran Pests, and Genes

TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: M/S 102DCD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-961-803-10

Query Match 62.4%; Score 2344.5; DB 3; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60
D B 1 M K S K N Q N M H Q S L S N N A T V D K N F T G S L E N N T N T E L Q N F N H -----E G I E P F V S V S T I 51
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I N Q I S T Y A 120
D B 52 Q T G I G I V G K I L G N L G V P F A G Q V A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I N Q I S T Y A 111
QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G V G N R N T R A S V V K S Q V I A L E L M F V Q K L P S F A V S G 180
D B 112 R N K A L A D L K G L D A L A V Y H S L E S W I E N R N T R S V V K S Q V I T L E L M F V Q S L P S F A V S G 171
QY 181 E E V P L L P I Y A Q A N L H L L L R D A S I F G K W G L S S S E I S T F Y N R Q V R A G D Y S D H C V K W Y S 240
D B 172 E E V P L L P I Y A Q A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S G K S K E Y S D H C V K W Y N 231
QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
D B 232 T G L N L M G N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 291
QY 301 G T V H P H P S F T S T T Y N N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 360
D B 292 G T V H P H P S F T S T T Y N N N A P S F S T I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M W 351

Best Local Similarity 64.3%; Pred. No. 6.7e-194; Indels 13; Gaps 5;
Matches 442; Conservative 78; Mismatches 154;
40 EDCMKSEYENVEPVFSASTIQTGTGIGIAGKILGTGVPAGVAVSLYFGLGELWPKGN 99
10 EDSLCIAEGNNIDPFVSASTVQTGINIAGILGLVGPAGVAVSLYFGLGELWPKGRD 69
100 QWEIFMEHVEEINQKISTYARKALTDKGLDALAVYHDSLESWGNRNNTRARSVVK 159
70 QWEIFLEHVEQLNQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTSRVLY 129
160 SQYIALELMFVQKLPSFAVSGEEVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEIST 219
130 TQYIALELDFLNAMPLFAIRNQEVPLLMVYAAQANLHLLLRDASIFGSEFGLTSQEIQ 189
220 FYNROVERAGDYSCHCKVWYSTGLNNLRGTNAESWRYNQFRRDMLVLDLVALFPSYD 279
190 YVERQVTRDYSYCVWYNTGLNSLRGTNAASWRYNQFRRDMLVLDLVALFPSYD 249
280 TOMYPIKTTAQLTREVTDAIGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFL 339
250 TRTYPINTSAQLTREVTDAIGAT--GVNMAWYNNNAPSFAIEAAAIRSPHLLDFL 307
340 EQVTYLSLRWSNTQYNNMGGHKLERTIGTGLNLSQTGSTNTSINPVTLPFTSRDVS 399
308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDVS 367
400 RTESLAGLNF--LTOPVNGVPRVDFHVKFVTHP-----IASDNFYYPGVAGIGTQLQDS 452
368 RTESYAGVLLWGIYLEPIHGVPTVRNF---TNPQNISDRGTANYSQP-YESPGQLQKDS 423
453 ENELPPEATGQPNYESYSHRLSHITGLISASHVKALVYSWTHRSADRNTIENSTIQLPL 512
424 ETELPPETTERPNEPYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRNTIENSTIQLPM 483
513 VKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRVNNPAPPAQVRVRYASTDLQ 572
484 VRASELPQGTTVVRGPGFTGGDILRRTNTGTGDIRVNVGPGPIRTVYRIGFRYASTVDFD 543
573 FHTSINGKAINQGNFSATMNRGDLDTKTRTGTGFTTTPPSFLDVQSTFTIGAWNPFSSGNE 632
544 FVSRGGTTVANNFRFLRTMNSGDELKYNFVRRAFTTPTFTTQIDIRTSIQGLSGNGE 603
633 VYIDRIEFVPEVTEYAEYDEKAEKVTALFTSTNPRGLKTDVYHIDQVSNLVESLS 692
604 VYIDKIEIPVTATFEAEYDLERAQAVNALFTNTNPRUKTDVTDYHIDQVSNLVACLS 663
693 DEFYLDKRELFIEIVKYAKQLHIERNM 719
664 DEFCLDEKRELLKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

361 GGKLEFFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTPQVNGVPR 420
352 GGKLEFFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTPQVNGVPR 411
421 VDFHWKFTVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
412 VDFHWKFTVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 471
481 ASHKALVYSWTHRSAD 497
472 ASHKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-7

Query Match 60.3%; Score 2265.5; DB 2; Length 1207;
Best Local Similarity 64.3%; Pred. No. 6.7e-194;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;
QY 40 EDCIKMSEYENVEPVFVASTIQTGIGIAGKILGTLPVFPAGQVASYSLFGLGELMPKGKN 99
DB 10 EDSLCAEGNNIDPFVASTVQTGINIAGRILGVLGVFPAGQVASYSLFGLGELMPGRGD 69
QY 100 QWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVK 159
DB 70 QWEIFLEHVEQLINQITENARNALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLY 129
QY 160 SQYIALELMPVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST 219
DB 130 TQYIALELDFLNPFLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189
QY 220 FYNQVERAGDYSCHCKWYSTGLNNLRTGNAESWRYNQFRDMLMVLVALFPSPYD 279
DB 190 YERQVERTEDYSYCVENWYNTGLNSLRTGNAESWRYNQFRDMLMVLVALFPSPYD 249
QY 280 TOMYPIKTAQLTRREYTDAGTVHPHPSFTSTWYNNAPSFAIEAAVVRNPHLLDFL 339
DB 250 TRTPINTSAQLTRREYTDAGTAT--GVNMAWMYNNAPSFAIEAAAIRSPHLLDFL 307
QY 340 EQVTIYSLSRWSNTQYMMWGGHKLERTIGTGLNISTQSTNTSINPVTLPFTSRDVS 399
DB 308 EQLTIFSSASSRWSNRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDVS 367
QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFTVHP-----IASDNFYYPYAGIGTQLODS 452
DB 368 RTESYAGVLLWGIYLEPIHGVPVTRFNF---TNPQNSDRGTANYSQP-YESPGLQKDS 423

QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIBPNSITQIPL 512
DB 424 ETELPPEPPERPNYESYSHRLSHIGLILQSRVNVVYVSWTHRSADRTNTIGNRITQIPM 483
QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVYNINPPEAQRVYRIRYASTTDLQ 572
DB 484 VKASELPQGTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGELTQRYRIGRYASTVDFD 543
QY 573 FHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFPTTFFSFLDVQSTFTIGAWNFSNGNE 632
DB 544 FFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRAFTTPTFTQIQDIIRTSIQGLSGNGE 603
QY 633 VYIDRIEFVPEVTYEAEDYFEKAQEKVLTSTNPRGLKTDVKYHIDQVSNLVESLS 692
DB 604 VYIDKIEIIPVTATFEAYDLEAQAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663
QY 693 DEFYLDKRELFEIVKYAKQLHIERNM 719
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

Search completed: March 9, 2005, 17:27:40
Job time : 25.1512 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds
(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-56
Perfect score: 3762
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3739	99.4	719	3 US-08-286-870A-8	Sequence 8, Appli
2	3459.5	92.0	710	4 US-09-661-322A-42	Sequence 42, Appl
3	3389	90.1	648	3 US-08-286-870A-4	Sequence 4, Appli
4	3379	89.8	719	2 US-09-003-217-2	Sequence 2, Appli
5	3374	89.7	719	3 US-09-218-942-2	Sequence 2, Appli
6	2795	74.3	535	3 US-08-286-870A-6	Sequence 6, Appli
7	2437.5	64.8	1229	1 US-08-100-709-4	Sequence 4, Appli
8	2437.5	64.8	1229	1 US-08-176-865-4	Sequence 4, Appli
9	2437.5	64.8	1229	1 US-08-474-038-4	Sequence 4, Appli
10	2437.5	64.8	1229	2 US-08-779-046-4	Sequence 4, Appli
11	2437.5	64.8	1229	2 US-08-881-340-4	Sequence 4, Appli
12	2335.5	62.1	488	1 US-08-448-170-10	Sequence 10, Appl
13	2335.5	62.1	488	3 US-08-961-803-10	Sequence 10, Appl
14	2250.5	59.8	1207	1 US-07-951-715A-7	Sequence 7, Appli
15	2250.5	59.8	1207	2 US-08-459-448A-7	Sequence 7, Appli
16	2250.5	59.8	1207	3 US-08-459-595A-7	Sequence 7, Appli
17	2250.5	59.8	1207	3 US-08-459-504B-7	Sequence 7, Appli
18	2250.5	59.8	1207	3 US-08-459-444-7	Sequence 7, Appli
19	2250.5	59.8	1207	3 US-09-053-549-8	Sequence 8, Appli
20	2250.5	59.8	1207	3 US-09-547-422-7	Sequence 7, Appli
21	2250.5	59.8	1207	3 US-09-988-462-7	Sequence 7, Appli
22	2249.5	59.8	1227	3 US-09-053-549-2	Sequence 2, Appli
23	2180.5	58.0	1227	1 US-08-448-170-8	Sequence 8, Appli
24	2180.5	58.0	1227	3 US-08-961-803-9	Sequence 9, Appli
25	2171.5	57.7	1227	4 US-09-661-322A-63	Sequence 63, Appl
26	2156.5	57.3	1186	3 US-09-178-252-23	Sequence 23, Appl
27	2156.5	57.3	1186	4 US-09-826-660-23	Sequence 23, Appl

28	2101	55.8	1228	4 US-09-661-322A-38	Sequence 38, Appl
29	1923.5	51.1	643	3 US-09-178-252-25	Sequence 25, Appl
30	1923.5	51.1	643	4 US-09-826-660-25	Sequence 25, Appl
31	1891	50.3	380	5 PCT-US91-02560-4	Sequence 4, Appli
32	1678.5	44.6	653	4 US-09-661-322A-6	Sequence 6, Appli
33	1655.5	44.0	1157	1 US-07-876-280-30	Sequence 30, Appl
34	1655.5	44.0	1157	1 US-07-812-180A-2	Sequence 2, Appli
35	1655.5	44.0	1157	1 US-08-315-468-2	Sequence 2, Appli
36	1655.5	44.0	1157	3 US-07-941-650A-2	Sequence 2, Appli
37	1492.5	39.7	1176	1 US-08-257-999-2	Sequence 2, Appli
38	1483	39.4	1157	2 US-08-532-547-5	Sequence 5, Appli
39	1483	39.4	1157	2 US-08-379-656B-5	Sequence 5, Appli
40	1483	39.4	1157	3 US-08-455-838-5	Sequence 5, Appli
41	1483	39.4	1157	3 US-09-019-803-5	Sequence 5, Appli
42	1483	39.4	1157	4 US-09-471-177-5	Sequence 5, Appli
43	1483	39.4	1157	4 US-09-220-806-5	Sequence 5, Appli
44	1476.5	39.2	1156	3 US-09-002-285-72	Sequence 72, Appl
45	1476.5	39.2	1156	4 US-09-589-477-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF INVENTIONS: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Thu Mar 10 14:26:04 2005

Query Match 99.4%; Score 3739; DB 3; Length 719;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
Db 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
Qy 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N O K I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N O K I S T Y A 120
Qy 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
Qy 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300
Qy 301 G T V H P H S F T S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
Db 301 G T V H P H S F T S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
Qy 361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
Db 361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
Qy 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
Qy 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540
Qy 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Qy 601 T F R T V G F T T P F S F L D V Q S T F T T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y E A Y D F E K A Q E K V 660
Db 601 T F R T V G F T T P F S F L D V Q S T F T T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y E A Y D F E K A Q E K V 660
Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupal, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 92.0%; Score 3459.5; DB 4; Length 710;
Best Local Similarity 92.1%; Pred. No. 2.4e-301;
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;
Qy 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
Db 1 M K S K N Q N M E H Q S L S N N A T V D K N F T G S L E N T N T E L Q N F N H -----EGIEPFSVSTI 51
Qy 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N O K I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N O K I S T Y A 120
Qy 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
Qy 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300
Qy 301 G T V H P H S F T S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
Db 301 G T V H P H S F T S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
Qy 361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
Db 361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420
Qy 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
Qy 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540
Qy 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Qy 601 T F R T V G F T T P F S F L D V Q S T F T T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y E A Y D F E K A Q E K V 660
Db 601 T F R T V G F T T P F S F L D V Q S T F T T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y E A Y D F E K A Q E K V 660
Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 90.1%; Score 3389; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. No. 4.4e-295;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLSWVGNRNTRARSVVKVSOYIALELMFVOKLPSFAVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLSWVGNRNTRARSVVKVSOYIALELMFVOKLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240
QY 241 TGLNLRGNTAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQTREYVTDI 300
DB 241 TGLNLRGNTAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQTREYVTDI 300
QY 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYMNW 360
DB 301 GTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYMNW 360
QY 361 GGHKLEFRITIGTLNISTQSTNTSINPVTLPTSRDVRRTESLAGNLFLOTPVNGVPR 420
DB 361 GGHKLEFRITIGTLNISTQSTNTSINPVTLPTSRDVRRTESLAGNLFLOTPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDEL.DYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDEL.DYK 600
QY 601 TFRVVGFTTFFSFLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPEVITYE 648
DB 601 TFRVVGFTTFFSFLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPEVITYE 648
RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.8%; Score 3379; DB 2; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.1e-294;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLSWVGNRNTRARSVVKVSOYIALELMFVOKLPSFAVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLSWVGNRNTRARSVVKVSOYIALELMFVOKLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240

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181 EEVPLPIYAQAANLHLLLRDASIFPKNGGLSASEISTFYNRQVERTRDYSYHCWKWN 240
241 TGLNLRGTNAESWVRYNQFRDMTLMVLVLPSPDYDTOMYPIKTTAQLTREVYTDAL 300
241 TGLNLRATNGQSWVRYNQFRDIELMVLVLPSPDYDTLVPIKTTSQLTREVYTDAL 300
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
301 GTVDNQALRSRTWYNNAPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
361 GGHKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOPVNGVPR 420
361 GGHLESRRPFGALNTSTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOPVNGVPR 420
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480
421 VDFHWKFPTLPASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480
481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
481 GSHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
541 TGTFGDIRVNIINPPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
541 STFGHIRVNIINPPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
601 TPTVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
601 TPTVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFLYDEKRELFEIVKYAKQIHIERNM 719
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFLYDEKRELFEIVKYAKQIHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; TITLE OF INVENTION: Activity
; FILE REFERENCE: Cyt11
; CURRENT APPLICATION NUMBER: US/09/218.942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2
Query Match 89.7%; Score 3374; DB 3; Length 719;
Best Local Similarity 89.7%; Pred. No. 1.2e-293;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;
1 MKLKNQKHQSSNAKVDKISTDSIKNETDIELQINNHEDCLKMSRYENVEPVSASTI 60
1 MKLKNPKHQTLSSNAKVDKIATDSIKNETDIELKNMNEIDYLRMSHESIDPVSASTI 60
61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVKQSYIALELMFVQKLPSPFAVSG 180
121 RNKALTDLKLGDALAVYHDSLESWGNRNTRARSVKQSYIALELMFVQKLPSPFAVSG 180

181 EEVPLPIYAQAANLHLLLRDASIFPKNGGLSASEISTFYNRQVERAGDYSYHCWKWYS 240
181 EEVPLPIYAQAANLHLLLRDASIFPKNGGLSASEISTFYNRQVERTRDYSYHCWKWN 240
241 TGLNLRGTNAESWVRYNQFRDMTLMVLVLPSPDYDTOMYPIKTTAQLTREVYTDAL 300
241 TGLNLRATNGQSWVRYNQFRDIELMVLVLPSPDYDTLVPIKTTSQLTREVYTDAL 300
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
301 GTVDNQALRSRTWYNNAPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYNNMW 360
361 GGHKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOPVNGVPR 420
361 GGHLESRRPFGALNTSTQGSTNTSINPVTLPFTSRDVRRTESLAGNLFLOPVNGVPR 420
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480
421 VDFHWKFPTLPASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480
481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
481 GSHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
541 TGTFGDIRVNIINPPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
541 STFGHIRVNIINPPPAQRVRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
601 TPTVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
601 TPTVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFLYDEKRELFEIVKYAKQIHIERNM 719
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFLYDEKRELFEIVKYAKQIHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.3%; Score 2795; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 6.5e-242;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKMEYENVEPFFVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKMEYENVEPFFVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESVGNRNTRARSVVKQVIALELMFVKQLPSFAVSG 180
DB 121 RNKALTDLKGDLAVYHDSLESVGNRNTRARSVVKQVIALELMFVKQLPSFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240

QY 241 TGLNLRGNTNAESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDI 300
DB 241 TGLNLRGNTNAESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDI 300

QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360

QY 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPR 420
DB 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHKALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 481 ASHKALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLKMEYENVEPFFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPVTNSFNSTQMLNSPDARIEDSLCVAEVNNDPFFVSASTVOTGINIAGRI 66

QY 71 LGTGVFPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARANKALTDLKG 130
DB 67 LGVLGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARANKALTDLKG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKQVIALELMFVKQLPSFAVSGEVPVLLPIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEVPLMLVYA 186

QY 191 QAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWSYSLGLNLRGTN 250
DB 187 QAAANLHLLLRDASIFGSEWGNWASSDVNYQYQEIIRYTEEYSHCVQWYNTGLNLRGTN 246

QY 251 AESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDIAGTVHPHPSFT 310
DB 247 AESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDIAGTVHPHPSFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMWGKHLKLEFRIT 370
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMWGKHLKLEFRIT 366

QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPRVDFHWKFTV 429
DB 367 GGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPRVDFHWKFTV 422

QY 430 HPIASDNFYPG-----YAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNTIYERGATTSYQYQVGIQDSELPPEATGQPNYESYSHRLSHIGLIS 480

QY 483 HVKALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
DB 481 TLRAVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNNPPFAQRVRYRIRYASTTDLQFTSINGKAINQGNFSAATMNRGDDLDYKTF 602
DB 541 TFGDIRVNNPPFAQRVRYRIRYASTTDLQFTSINGKAINQGNFSAATMNRGDDLDYKTF 600

QY 603 RTVGFTTTPSELDVQSTFTTIGAWNFSSGNEVYIDRIEFVPRVSVTYEAEYDFEKAQEKVTA 662
DB 601 RTAGFSTPFNFNLNAQSTFTLGAQSFNS-QEVYIDRIEFVPRVSVTYEAEYDFEKAQEKVTA 659

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QY 663 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEDFYLDKRELFELVKYANLHIERNM 719
DB 660 LFTSTNPRRLKTDVTHIDQVSNMVACLSEDFCLDEKRELFELVKYAKRLSDERNL 716

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-865-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIOTGIGIAGKI 70
DB 7 NENEIINALSIPVSNPTQMNLSPDARIEDSLCAEVNNDPVSASTVQTGINIAGRI 66

QY 71 LGTGLVPPFAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTVARNKALTDLKG 130
DB 67 LGVLGVPFAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQVTTENTRTAIRLEG 126

QY 131 LGDALAVYHDSLSWVGVRNTRNSRVVKSQYIALELMFVOKLPSFAVSGEEVLLPIYA 190
DB 127 LGRGYRSYQQALETWLDNRNDRSRIILERYVALELDITTAIPFIRNEEVLLMWYA 186

QY 191 QAAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWKYSTGLNNLRGTN 250
DB 187 QAAANLHLLLRDASLFGSEWGMASSDVNQYQEQIRYTEYSNHCQWYNTGLNNLRGTN 246

QY 251 AESWRYNQFRDRLTGLVLDLVALFPSTDTQYPIKTAQLTREYVTDAGTGVHPHPSFT 310

DB 247 AESWRYNQFRDRLTGLVLDLVALFPSTDTQYPIKTAQLTREYVTDAGTGVHPHPSFT 306
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRPTI 370
DB 307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRPTI 366

QY 371 GGTNLNISTOGST-NTSINPVTLPFTSRDVTESLAGLNLFTQPVNGVPRVDFHMKFVT 429
DB 367 GGTNLNISTOGST-NTSINPVTLPFTSRDVTESLAGLNLFTQPVNGVPRVDFHMKFVT 422

QY 430 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHLSHIGLISAS 482
DB 423 --INPQNIYERGATYSQYQGVGIQDFSETLPPEATGQPNYESYSHLSHIGLISAS 480

QY 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542
DB 481 TRAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 540

QY 543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYKTF 602
DB 541 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAFMNREGDLDYKTF 600

QY 603 RTVGFTTFFSFLDVQSTFTIGAMNFFSSGNEVYIDRIEVPVETVEAEYDFEKAQEKVTA 662
DB 601 RTAGPSTPFNPLNAQSTFTILGAQFSN-QEYIDRVEFVPAEVTFEAEYDLEAKAVNA 659

QY 663 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEDFYLDKRELFELVKYANLHIERNM 719
DB 660 LFTSTNPRRLKTDVTHIDQVSNMVACLSEDFCLDEKRELFELVKYAKRLSDERNL 716

RESULT 9
US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEVENVEPFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASFYSLFELGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQVASFYSLFELGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKVQYIALELMFVQKLPSFAVSGEVPPLPIYA 190
DB 127 LGRGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPFRIRNEEVPVLLMVA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEESNHCVMQYNTGLNNLRGTN 246

QY 251 AESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 310
DB 247 AESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMGGHKLFRFTI 370
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMGGHKLFRFTI 366

QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHVKFVT 429
DB 367 GGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHVKFVT 422

QY 430 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQGVGIQLFDSETELPPEATERPNERYESYSHRSLSHIGLIGN 480

QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGILRRNTG 542
DB 481 TLRAPIVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGILRRNTG 540

QY 543 TFGDIRLVNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKTF 602
DB 541 TFGDIRLVNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKTF 600

QY 603 RTVGFTTFFSLDQSTFTIGAMNFSNGNEVYIDRIEFVPEVYVEYAEYDFEKAQEKVTA 662
DB 601 RTAGSTPFNFLNAQSTFTILGAQSFN-QEVIYIDRVEFVPAEVTFFAEYDLERAQAVNA 659

QY 663 LFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 660 LFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 716

RESULT-10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-779-046-4

Query Match      64.8%; Score 2437.5; DB 2; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEVENVEPFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASFYSLFELGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQVASFYSLFELGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKVQYIALELMFVQKLPSFAVSGEVPPLPIYA 190
DB 127 LGRGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPFRIRNEEVPVLLMVA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEESNHCVMQYNTGLNNLRGTN 246

QY 251 AESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 310
DB 247 AESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMGGHKLFRFTI 370
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYNNMGGHKLFRFTI 366

QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHVKFVT 429
DB 367 GGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHVKFVT 422

QY 430 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQGVGIQLFDSETELPPEATERPNERYESYSHRSLSHIGLIGN 480

QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGILRRNTG 542
DB 481 TLRAPIVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGILRRNTG 540
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Thu Mar 10 14:26:04 2005

127 LGRYSYQOALETWLDRNDARSRSIILERYVALELDITTAIPLFRIERNEEVLMLVYA 186
191 QANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKWTGLNLRGCTN 250
187 QANLHLLLRDASLFGSEWGWASDVNQYQEQIRYTEYSNHCVCQWYNTGLNLRGCTN 246
251 AESWRYNQFRDRMTLMLDLVALPFSYDQOMYPIKTTAQLTREYVYDAIGTVHPHSFT 310
247 AESWRYNQFRDRMTLMLDLVALPFSYDQOMYPIKTTAQLTREYVYDAIGTVHPHSFT 306
311 STTWYNNAPSPAIAEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTOMNMWGGHKLFRFTI 370
307 STTWYNNAPSPAIAEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTOMNMWGGHKLFRFTI 366
371 GGTNLNISTQST-NTSINPVTLPFTSRDVRYSAGLNLFLTPVNGVPRVDFHWKFTV 429
367 GGTNLNISTQST-NTSINPVTLPFTSRDVRYSAGLNLFLTPVNGVPRVDFHWKFTV 422
430 HPIASDNFYYPG-----YAGIGTQDSENELPPEATGQPNYESYSHLSHIGLISAS 482
423 --INPQNIYERGATTYSQYQVGIQDFSETLPPTTERPNYESYSHLSHIGLIIGN 480
483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNG 542
481 TLAPYVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNG 540
543 TFGDIRVNPPLPFAQRYRIRYASTTDLQFTSINGKAINQGNFSAATMNRGDLDTYTF 602
541 TFGDIRVNPPLPFAQRYRIRYASTTDLQFTSINGKAINQGNFSAATMNRGDLDTYTF 600
603 RTVGFTTFFSFLDVQSTFTIGAMNFFSGNEVYIDRIEVPVETVEAEYDFEKAQKVTA 662
601 RTAGFSTPFNFNAQSTFTLGAQSPSN-QEYVYIDRVEFPVPAEVTFEAEYDLERAQKAVNA 659
663 LFTSTNPRGLKTDVVDYHIDQVSNVACLSDDEFCLDEKRELFKVKYAKRLSDERNL 719
660 LFTSTNPRGLKTDVVDYHIDQVSNVACLSDDEFCLDEKRELFKVKYAKRLSDERNL 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYVET4 AND CYVET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-881-340-4

Query Match 64.8%; Score 2437.5; DB 2; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;
13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEVENPEFVSASTTGTGIGIAGKI 70
7 NENEIINALSPTVSNPSTQNLSPDARIEDSLCVAEYVNIIDPFVSASTVGTGINIAGRI 66
71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
67 LGVLGVFPAGQLASFSFLVGLWPSGRDPWEIFLEHVEQLIRQVQVTEINTAIALEG 126
131 LGDALAVYHDSLESWGNRNNTFRASVVKSOYIALELMFVQKLPFSFAVSGEVPPLPIYA 190

RESULT 12

US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758

GENERAL INFORMATION:

APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve

TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,170

FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 424

Thu Mar 10 14:26:04 2005

QY 361 GGKLEFRTIGTGLNISTQSTNTSINPVLPTFTSRDVRVRESLAGLNLFLTPQVNGVPR 420
DB 352 GGKLEFRTIGTGLNISTQSTNTSINPVLPTFTSRDVRVRESLAGLNLFLTPQVNGVPR 411
QY 421 VDFHWKVFTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 412 VDFHWKVFTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471
QY 481 ASHKALVYSWTHRSAD 497
DB 472 ASHKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

Query Match 59.8%; Score 2250.5; DB 1; Length 1207;

Best Local Similarity 64.0%; Pred. No. 1.8e-192;
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;
QY 40 EDCLKMSYENVEPFVSASTIQTGTIGIAGKILGTIGVPPAGQVASYLFIILGELMPKGN 99
DB 10 EDSLCAEGNNIDPFVSASTVQTGINIAGILVGLVPPAGQLASFYFLVGLMPGRD 69
QY 100 QWEIFMEHVEEINOKISTYARNKALTDLKGLDALAVVHDSLSWVGNRNTRARSYVK 159
DB 70 QWEIFLEHVEQLINQITENARNTALARLOGLGDSFRAYQOQSLDWNLRDRTARSVLY 129
QY 160 SQYIALELMFVQKLPSFAVSGEEVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEIST 219
DB 130 TQYIALELDFLNAMPLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEFGLTSQEIQ 189
QY 220 FYNROVERAGDYSYHCVKMYSTGLNNLRGTNAESWRYNQFRDRMTLMLDLVALFPSYD 279
DB 190 YYERQVTRDYSYCVENYINGLNLRGTNAESWRYNQFRDRMTLMLDLVALFPSYD 249
QY 280 TQMYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFL 339
DB 250 TRTYPINTSAQLTREVTDAIGAT--GVNMAWNNWNNAPSFSAIEAAAIRSPHLLDFL 307
QY 340 EQVTIYSLRSWNTQYMMWGGHKLERTIGTGLNISTQSTNTSINPVLPTFTSRDVRV 399
DB 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVLTRFASRDVY 367
QY 400 RTESLAGLNL--LTPQVNGVPRVDFHWKVFTHP-----IASDNFYYPGYAGIGTQLODS 452
DB 368 RTESYAGVLLWGIYLEPIHGVPTVRFNF---TNPQNSDRGTANYSQP-YESPGLOLKDS 423
QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512
DB 424 ETELPPETTERPNEYSYSHRLSHIGLILQSRVNVVPSWTHRSADRTNTIEPNSITQIPL 483
QY 513 VKAFNLSSGAAVVRGPGFTGGDIILRTNTGTGDIRVNNINPPPAQRYVRIRYASTDLQ 572
DB 484 VKASELPQGTTVVRGPGFTGGDIILRTNTGTGDIRVNVGPGPIRTVNGPLTQRYRIGFRYASTVDFD 543
QY 573 FHTSINGKAINQGNFSATMNRGDELDTKTRTVGTGFTTTPPSFLDVQSTFTTIGAWNFSSGNE 632
DB 544 FFVSRGGTTVNNFRFLRTMNSGDELKYNFVRRAFTTFTTQIQTIDRTSISQGLSGNGE 603
QY 633 VYIDRIEFVPEVTEYAEYDEKAEKVTALFTSTNPRGLKTDVYHIDQVSNLVESLS 692
DB 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663
QY 693 DEFYLDKRELFVYKYNELHIERNM 719
DB 664 DEFCLDEKRELLKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 589336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-7

Query Match 59.8%; Score 2250.5; DB 2; Length 1207;
Best Local Similarity 64.0%; Pred. No. 1.8e-192;
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;
QY 40 EDCLKMSEYENVEPVASSTIQTGIGIAGKILGTLGVPPFAGQVASYSPILGELMPKGKN 99
Db 10 EDSLCAEGNNIDPFVSASTVQTGINIAGRIILGVLPFAGQVASYSPILGELMPGRD 69
QY 100 QWEIFMEHVEEIIINQISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNNTARSVK 159
Db 70 QWEIFLEHVEQLINQITENARNALRQLGLGDSFRAYQQSLEDWLENRDDARTRSVLY 129
QY 160 SQYIALELMPVOKLPSPFAVSAGEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEIST 219
Db 130 TOYIALELDFLNAFLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189
QY 220 FYNQVERAGDYSYHCKWYSTGLNLRGTNAESWRYNQFRDMLMVLDLVALFPSSYD 279
Db 190 YERQVERTRDYSYCVWEYNTGLNSLGTNAASWRYNQFRDMLMVLDLVALFPSSYD 249
QY 280 TOMYPIKTTAQLTRREVYTDAGTVHPPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDFL 339
Db 250 TRTYPINTSAQLTRREVYTDAGTAT--GYNMASNMWYNNNAPSFAIEAAAIIRSPHLLDFL 307
QY 340 EQVTIYSLLSRWSTQYNNMWGCHKLEPRTIGTGLNLTSTQGSTNTSINPVTLPTFSRDVY 399
Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRPFASRDVY 367
QY 400 RTESLAGLNLFF--LTQPVNGVPRVDFHWKFTVHP-----IASDNFYYPGYAGIGTQLQDS 452
Db 368 RTESYAGVLLWGIYLEPIHGVPVTRFNF---TNPQNISDRGTANYSQP-YESPGLQLKDS 423

QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512
Db 424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTIGENRITQIPM 483
QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNIINPPFAQRYRVRIRYASTTDLQ 572
Db 484 VKASELPQGTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGPLTQRYRIGRIRYASTVDFD 543
QY 573 FHTSINGKAINQGNFSATMNRGEDLDYKTRFTVGVFTTFFSFLDVQSTFTTICAWNFSSGNE 632
Db 544 FFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRRAFTTPTFTQIQDIIRTSIQGLSGNGE 603
QY 633 VYIDRIEFVPEVVTYEAEDYFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLS 692
Db 604 VYIDKIEIIPVTATFEAYDLEAQAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663
QY 693 DEFYLDKRELFELVKYANELHIERNM 719
Db 664 DEFCLDEKRELEKVKYAKRLSDERNL 690

Search completed: March 9, 2005, 17:27:43
Job time : 26.1512 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds
(without alignments)
4171.616 Million cell updates/sec

Title: US-10-019-823B-56
Perfect score: 3762
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELPEIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3762	100.0	719	2 I39814	insecticidal prote
2	3753	99.8	719	2 S25383	parasporal crystal
3	3743	99.5	719	2 I39815	insecticidal prote
4	3503	93.1	719	2 I40590	crv465 protein -
5	2262.5	60.1	1228	2 S00873	parasporal crystal
6	1891	50.3	380	2 B42459	hypothetical prote
7	1483	39.4	1157	1 S49247	parasporal crystal
8	1467.5	39.0	1166	2 S32645	parasporal crystal
9	1461	38.8	1174	2 S32649	parasporal crystal
10	1459	38.8	1155	2 A26513	parasporal crystal
11	1452	38.6	1155	2 JD0002	parasporal crystal
12	1452	38.6	1156	2 A29125	parasporal crystal
13	1443	38.4	1155	2 I39838	parasporal crystal
14	1439.5	38.3	934	2 A22798	parasporal crystal
15	1438.5	38.2	1176	2 JT0241	parasporal crystal
16	1435	38.1	1155	2 S02134	parasporal crystal
17	1434.5	38.1	1181	2 A41052	parasporal crystal
18	1432.5	38.1	1176	2 JC2219	parasporal crystal
19	1428.5	38.0	1176	2 A22617	parasporal crystal
20	1428.5	38.0	1176	2 S02215	parasporal crystal
21	1353	36.0	1174	2 A42459	parasporal crystal
22	1338	35.6	1138	2 A48944	parasporal crystal
23	1324.5	35.2	1156	2 A29838	parasporal crystal
24	1316.5	35.0	823	2 S04181	parasporal crystal
25	1307.5	34.8	1189	2 S00944	parasporal crystal
26	1301	34.6	1154	2 S39536	parasporal crystal
27	1257	33.4	1171	2 I40572	parasporal crystal
28	1257	33.4	1171	2 A37829	parasporal crystal
29	1254	33.3	1176	2 A48970	parasporal crystal

30 1219 32.4 1160 2 S32647 parasporal crystal
31 1210.5 32.2 1165 2 S11446 parasporal crystal
32 1200.5 31.9 655 2 JC7140 protoxin - Bacillu
33 1181 31.4 1172 2 S32689 parasporal crystal
34 1171 31.1 1160 2 I40589 parasporal crystal
35 1148.5 30.5 1178 1 USBSXH parasporal crystal
36 1148 30.5 1177 2 A49785 parasporal crystal
37 1147 30.5 652 2 A27323 parasporal crystal
38 1124 29.9 659 2 S10228 parasporal crystal
39 1091.5 29.0 652 2 I39811 parasporal crystal
40 983 26.1 649 1 JH0261 parasporal crystal
41 926 24.6 618 2 S11445 parasporal crystal
42 871 23.2 1156 2 S19306 parasporal crystal
43 820 21.8 1136 1 USBS8I parasporal crystal
44 679.5 18.1 934 2 B29838 parasporal crystal
45 656 17.4 1180 2 I39870 parasporal crystal

ALIGNMENTS

RESULT 1

I39814
insecticidal protein cryVI - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C:Accession: I39814
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61: 2402-2407, 1995
A:Title: Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I39814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: GB:L36338; NID:G540281; PIDN:AAC36999.1; PID:G540282
C:Genetics:
A:Gene: cryVI
C:Superfamily: parasporal crystal protein

Query Match 100.0%; Score 3762; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.3e-251;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFVSASTI 60
Qy 61 QTGIGTAGKITLGTGVPFAGQVASLYSFTLGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120
Db 61 QTGIGTAGKITLGTGVPFAGQVASLYSFTLGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
Qy 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240
Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240
Qy 241 TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300
Db 241 TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300
Qy 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Qy 361 GGHKLEFRITGGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTTGAWNFSNGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660
DB 601 TFRVTGFTTFFSFLDVQSTFTTGAWNFSNGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2
S25383
parasporal crystal protein cryIIa1 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin; parasporal crystal protein cryV
C;Species: Bacillus thuringiensis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25383
R;Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A;Reference number: S25383; MUID:92269582; PMID:1588820
A;Accession: S25383
A;Molecule type: DNA
A;Residues: 1-719 <FAL>
A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290
C;Genetics:
A;Gene: cryV
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 99.8%; Score 3753; DB 2; Length 719;
Best Local Similarity 99.7%; Pred. No. 5.2e-251;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVSYQYIALELMFVKLPSPFVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVSYQYIALELMFVKLPSPFVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240
DB 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240
QY 241 TGLNNLRGTNAESWVRNQFRDRTLMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300
DB 241 TGLNNLRGTNAESWVRNQFRDRTLMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300
QY 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360
DB 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTTGAWNFSNGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660
DB 601 TFRVTGFTTFFSFLDVQSTFTTGAWNFSNGNEVYIDRIEFVPEVTEYAEYDEFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3
I39815
insecticidal protein cryV - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39815
R;Gleave, A.P.; Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1993
A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for
lensis subsp. kurstaki
A;Reference number: I39815; MUID:93298009; PMID:8517758
A;Accession: I39815
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PIDN:AAA22354.1; PID:G142768
C;Genetics:
A;Gene: cryV
C;Superfamily: parasporal crystal protein

Query Match 99.5%; Score 3743; DB 2; Length 719;
Best Local Similarity 99.6%; Pred. No. 2.6e-250;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVSYQYIALELMFVKLPSPFVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVSYQYIALELMFVKLPSPFVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240
DB 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240
QY 241 TGLNNLRGTNAESWVRNQFRDRTLMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300
DB 241 TGLNNLRGTNAESWVRNQFRDRTLMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300
QY 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360
DB 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVNGVPR 420


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Qy 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGPNYESYSHRSLHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGPNYESYSHRSLHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Db 481 ASHVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Qy 541 TGTFGDIRVINPFPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLDYK 600
Db 541 TGTFGDIRVINPFPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLDYK 600
Qy 601 TFRVTGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660
Db 601 TFRVTGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 4
140590
cryV465 protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40590
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I40590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:G467234; PIDN:AAA82114.1; PID:G4672
A;Gene: cryV465
C;Superfamily: parasporal crystal protein

Query Match 93.1%; Score 3503; DB 2; Length 719;
Best Local Similarity 92.5%; Pred. No. 9.5e-234;
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MKLKNDKQHSFSSNAKVDKISTDLSKNETDIELQNIHEDCLMKSEYENVEPFPVSASTI 60
Db 1 MKLKNDKQHSFSSNAKVDKISTDLSKNETDIELQNIHEDCLMKSEYENVEPFPVSASTI 60
Qy 61 QTGIGTAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGTAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALTDLKGLDALAVYHDSLESVWGNRNTRARSVVKVSKQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALSDRLGDLALAVYHDSLESVWGNRNTRARSVVKVSKQYIALELMFVQKLPSPAVSG 180
Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSYHCVKWYS 240
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSYHCVKWYS 240
Qy 241 TGLNNLRGTNAESWRYNQFRDMLTMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLTMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
Qy 301 GTVHPHPSFTTWTWNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPNQAFSTWNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHRLSRPIGGALNTSQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
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Qy 421 VDEHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGPNYESYSHRSLHIGLIS 480
Db 421 VDFHMKFPTLPIASDNFYYLGYAGVGTQLQDSNELPPTTGTQPNYESYSHRSLHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Db 481 ASHVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGCDILRRTN 540
Qy 541 TGTFGDIRVINPFPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLDYK 600
Db 541 TGTFGDIRVINPFPFAQRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLDYK 600
Qy 601 TFRVTGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660
Db 601 TFRITGFTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 5
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:G40264; PIDN:CAA29898.1; PID:G58094;
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 60.1%; Score 2262.5; DB 2; Length 1228;
Best Local Similarity 62.4%; Pred. No. 9.6e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNIDFPVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFSYFLVGLWPRGRDQWEIFLEHVEQLINQITENARNATALARLQ 121
Qy 131 LGDALAVYHDSLESVWGNRNTRARSVVKVSKQYIALELMFVQKLPSPAVSGEVPPLPIYA 190
Db 122 LGDSFRAYQOSLEDWLENRDDARTRSVLYTQYIALELDLFLNAMPFLAIRNQEVPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSQYCVENYNTGLNLSRGTN 241
Qy 251 AESWRYNQFRDMLTMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSFT 310
Db 242 AASWRYNQFRDMLTMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAIGAT--GVNMA 299
Qy 311 STTWNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWGGHKLSPRTI 370
Db 300 SMWNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWGGHKLSPRTI 359
Qy 371 GGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPRVDFHWKFV 428
Db 360 GGGGLNSTHGTATNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPRVDFHWKFV 416
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429 THP-----IASDNFYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
 417 TNPNQISDRCTANYSQP-YESPGQLKXDSETELPPETTERPNYESYSHRLSHIGLISASH 475
 484 VKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGT 543
 476 VNPVSWTHRSADRTNTIGPNRTIQIPVKAFLNLSGAAVVRGPGTGGDILRRNTGT 535
 544 FGDIRVNINPFAQVRVIRYASTDLOFHTSINGKAINQGNFSAATMNRGBDLDYKTFR 603
 536 FGPVIRVTNGPLTQRYRIGFRYASTVDFPFVSRGGTTVNNFPLRTMNSGDELKYGNFV 595
 604 TVGFTTFFSFLDVQSTFTTIGAWNFSNGEVYIDRIEFVPEVTEAEYDFAKAEKVTAL 663
 596 RRAFTTPTFTTQIODIIRTSIQGLSGNGEVYIDKIEIIPVTAFAEYDLERAQEAVAL 655
 664 FTSTNPRGLKTDVKYDHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 6
 B42459
 hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag
 C:Species: Bacillus thuringiensis
 C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
 C:Accession: B42459
 R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
 J. Bacteriol. 173, 3966-3976, 1991
 A:Title: Isolation and characterization of a novel insecticidal crystal protein gene fro
 A:Reference number: A42459; MUID:91286178; PMID:2061280
 A:Accession: B42459
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <CHA>
 A:Cross-references: UNIPROT:Q8KY61; UNIPROT:Q45740; GB:M63897
 C:Superfamily: parasporal crystal protein

Query Match 50.3%; Score 1891; DB 2; Length 380;
 Best Local Similarity 95.3%; Pred. No. 6.7e-123;
 Matches 362; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKYDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFFVSASTI 60
 DB 1 MCLKNPDKQHFSSNAKYDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFFVSASTI 60
 QY 61 QTGTGIGAKILGTGVPFAGQVAVSLYSFILGELWPCKNQWEIFMEHVEEIIINQKISTYA 120
 DB 61 QTGTGIGAKILGTGVPFAGQVAVSLYSFILGELWPCKNQWEIFMEHVEEIIINQKISTYA 120
 QY 121 RNKALTDLKGLDALAVYHDSLESWGVRNNTFARSVVKVQYIAELMFVOKLPSFAVSG 180
 DB 121 RNKALTDLKGLDALAVYHDSLESWGVRNNTFARSVVKVQYIAELMFVOKLPSFAVSG 180
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYRQVERAGDYSYHCWKWYS 240
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYRQVERAGDYSYHCWKWYS 240
 QY 241 TGLNLRGTNAESWVRYNOPRRDMLVLDLVALFPSPYDTOMYPKTTAQLTREVTYDAI 300
 DB 241 TGLNLRGTNAESWVRYNOPRRDMLVLDLVALFPSPYDTOMYPKTTAQLTREVTYDAI 300
 QY 301 GTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
 DB 301 GTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
 QY 361 GGHKLEFRTTGGTLNISTQG 380
 DB 361 GGHKLEFRTTGGTLNISTQG 380

RESULT 7

S49247
parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIH
C;Species: Bacillus thuringiensis
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A59350; S49247
R;Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V
Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agai
A;Reference number: A59350; MUID:96141404; PMID:8572715
A;Accession: A59350
A;Molecule type: DNA
A;Residues: 1-1157 <LAM>
A;Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:g547554; PIDN:CAA85764.1; PID:g5475
A;Experimental source: serovar tolworthi
C;Comment: This parasporal crystal protein, active against corn borer and other insects,
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match	39.4%	Score 1483;	DB 1;	Length 1157;
Best Local Similarity	43.1%	Pred. No. 5.7e-94;		
Matches	321;	Conservative 113;	Mismatches 220;	Indels 90; Gaps 15;

QY	26	LKNETDIELQNIHEDCLKMEYENVEPFFVAS-----TIQTGIGIAGKILGTIGVPP	78
DB	29	LASDPNAAALQNMVYKDYQMTDEDYTSYNPISLSISGRDAVQTALTWVGRIILGALGVPP	88
QY	79	AGOVASLYFILGELWPKGKNO--WEIFMEHVEEIIINQKISTYARNKALTDKLGGLDALAV	137
DB	89	SGQIVSYFYQLLNTLWPNVDALWEAFWQVEELVNOQITFEARNQALARIQLGLGDSFNV	148
QY	138	YHDSLESWGNRNNTARSVWKSQYIALLEMEVQKLPSPFVSGEEVPLLPPIYAQANLHL	197
DB	149	YQRSLQNLWLANDRNLTRNLVWRAQFIALDLDFVNAIPLEFVNGQQVPLLSVYAQAVNLHL	208
QY	198	LLLRDASIFGKEWGLSSSISTFTFNQVERAGDYSYHCVKYSTGLNNLRGTNAESWRY	257
DB	209	LLKDAASLFGEWGQGTQGEISTYDRLQELTAKYTNCYETWYNTGLDRRLRGNTESWLRY	268
QY	258	NQFRDMTLVLDLVALFSDYDQMPYIKTTAQLTREYVTTDAIGTVHPHPSTSTTWYNN	317
DB	269	HQFRREMTLVLDVALFPYDRLVPTGSGNPQLTREYVTTDPIVFNPPANVGLCRRWGTN	328
QY	318	NAPFSAIEAAVRNPHLLDFLEQVTIYSLLSRW-S-NQYMNWVGHKLE-----	366
DB	329	PYNTFSELENAFIRPPHLPDLRLNSLTISS--NRFPVSSNFMFDYWSGHTLRRSYLNDASVQ	386
QY	367	-----FRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR	420
DB	387	EDSYGLITTTATINPGVDGTR--IESAVDFRS-----ALIG-----IYGNR	429
QY	421	VDFPHKVFVTHPIASDNFYFPGYAGT-----QLQDSENELPP--EATQPNVESYS	470
DB	430	ASF-----VPGGLFNGTTPANGGCRDLYTDNDELPPDESTG-----SST	469
QY	471	HLRSHIGLIS-----ASHVKALVSWTHRSADRTWTIENSITQIPLVKAFNLSSG	521
DB	470	HLRSHVTFVFPOTNQAGSIANAGSVPTVYVWTRRDVDLNNITNRIITQLPLVKASAPVSG	529
QY	522	AAVVRGPGFTGGDILRRNTCTFGDIRVINPNPFAQRYVRIRYASTTDLQFHTSINGKA	581
DB	530	TTVLKGPFTGGGILRRNTTNGTFLRLVTVNSPLTQQYRLRVFPAFASTGNFSIRVLRGVS	589
QY	582	INQGNFSATMRGEDLDYKTFRTVGFTT-----PFSFLDVQSTFTIGAWNFSNGVEYI	635
DB	590	IGDVRGLGSTMNRGELTYESPFTREFTTGTFNPPFTTFOAQEILTVNAEGVSTGGVEYI	649
QY	636	DRIEFVPVEVTEAEYDFEKAQEKVYALFTSTNPRGLKTDVKYHIDOVSNLYESLSDEF	695
DB	650	DRIEIVPNPAREAEDELEAAKAVASLFTTRD--GLQVNVTDYQVDQAANLVSLSDSEQ	708
QY	696	YLDEKRELFEIVKYANELHIERNM	719

Db 709 YGHDKKMLLEAVRAAKRLSRNL 732

RESULT 8

S32645

parasporal crystal protein crylGal - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S32645

R;Lambert, B.

submitted to the EMBL Data Library, April 1993

A;Reference number: S32645

A;Accession: S32645

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1166 <LAM>

A;Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:G295861; PIDN:CAA80233.1; PID:G2958

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 39.0%; Score 1467.5; DB 2; Length 1166;

Best Local Similarity 45.8%; Pred. No. 6.8e-93;

Matches 323; Conservative 100; Mismatches 207; Indels 75; Gaps 17;

Qy 41 DCLKMEYE---NVEPFVSASTIQTGIGIAGKILGTGLGVFPAGQVASLYSFI LGELWPK 96
Db 13 NCLNPESEIFNARNSNFGLVQSSSL---TRFLEAAVPEAGFALGLFDIIGAL--- 66

Qy 97 GKQWEIFMEHVEEIIINQKISTYARNKALTDKLGCDALAVYHDSLSWVGNRNTRARS 156
Db 67 GVDQWLSFLRQIEQLRQIELEARNRATAILGLSSSYLYVEALREWENDPNPNPASQE 126

Qy 157 VVKSQYIALELMFVQKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSE 216
Db 127 RVTRFRLTDDAIVTGLPTLAIRNLEVNLSVYTOAANLHLSLLRDVYFGERWGLTQAN 186

Qy 217 ISTFYNRQVRAGDYSYHCVKQWYSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFP 276
Db 187 IEDLYRLTSNIQESDHCARWYNQGLNEIGGISR---RYLDFQRDLTISVLVDI VALFP 242

Qy 277 SYDTQMYPIKTTAQLTREVTDAI--GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPH 334
Db 243 NYDIRTYPIPTQSQLTREIYTPVAVAGNI-----NFGLSIANVLRAHP 285

Qy 335 LLDLFLEQVITYLSLRWSNTQYMMNMGHKLERTIG-GLTN-----ISTQGSTNTS 385
Db 286 LMDFDIRIVITNSVR--STPY---WAGHEVISRRTGQGGNEIRFPYLGVAANAEPVPT 340

Qy 386 INPVTLPFTSRDVRTE-----LAGLNLFLTQPVNGVPRVDFHWKFWTHPIASDNFFY 439
Db 341 IRPTGFTDEORQWRARSRVVFSRSSGQDFSLVDAVG-----FLT-IFSAVSIYR 389

Qy 440 PGYAGICTOLODSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVKALVSWTHR 494
Db 390 NGF-GFNT---DTIDPIEGTDP--FTGYSHRLCHVGLASSPFFISQYARAPIFSWTHR 443

Qy 495 SADRTNTIEPNSITQPLVKAFNLSSGAAVRPGFTGGDILRRNTGTGDIRVNNPP 554
Db 444 SATLTNTIAPDVITQPLVKAFNLHSGATIVKPGFTGGDILRRNTVGSFGDMRVNITAP 503

Qy 555 PAQRVVRIRYASTTDLQFHTSINGKAINQNFSAATMRGEDLDYKTRFTVGTFTTFFSFL 614
Db 504 LSQRVVRIRYASTTDLQFYTNINGTINIGNFSSTMDSGDDLDQYGRFRVAGFTTPTFFS 563

Qy 615 DVQSTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVTALFTSTNPRGLKT 674
Db 564 DANSTFTIGAFGFPNNEVYIDRIEFVPAEVTFEAEYDLEKAQKAVNALFTSSNQIGLKT 623

Qy 675 DVKDYHIDQVNLVSLSDSEFYLDEKRELPEIVKYANELHIERNM 719
Db 624 DVTDYHIDKVNLEVECLSDSEFCLDEKRELSEKVKHAKRLSDERNL 668

RESULT 9

S32649

parasporal crystal protein crylFa3 - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S32649

R;Lambert, B.

submitted to the EMBL Data Library, April 1993

A;Reference number: S32645

A;Accession: S32649

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1174 <LAM>

A;Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G2958

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 38.8%; Score 1461; DB 2; Length 1174;

Best Local Similarity 44.6%; Pred. No. 1.9e-92;

Matches 324; Conservative 101; Mismatches 205; Indels 96; Gaps 17;

Qy 36 NINHE---DCLKMEYENVEPFVSASTIQTGIGIA-GKILGTGLGVFPAGQVASLYSFI 90
Db 4 NIQOCVPYNCLSNPEVEILSERSTGRPLDLSLSTRLLSEFVPGVGVAFLDLIW 63

Qy 91 GELWPKGKQWEIFMEHVEEIIINQKISTYARNKALTDKLGCDALAVYHDSLSWVGNRN 150
Db 64 GFITP---SEWSLFLQIEQLRQIELEARNRATILRGLADSYEVYLEALREWEENPN 120

Qy 151 NTRARSVVKSQYIALELMFVQKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW 210
Db 121 NAQLREDVIRFANTDDALITANNFTLTSFEIPLLSVYVQAANLHLSLLRDVAVSFGQGW 180

Qy 211 GLSSEISTFYNRQVRAGDYSYHCVKQWYSTGLNNLRGTNAESWVRYNQFRDMTLMVLD 270
Db 181 GLDSTATVNNHYNRLINLIHRYTEHCLDTYNQGLENLGTNTQWRSRNFQRELTTLTVD 240

Qy 271 LVALFSPYDTQMYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWNNNAPS-FAIEAAV 329
Db 241 IVALFPYDARAYPIQTSQLTREIYTSV--IEDSP-----VSANIPNGFNRAEFG- 290

Qy 330 VRNPHLLDFLEQVITYLSLRWSNTQYMMNMGHKLERTIGTGLNISTQGSTNTSINPV 389
Db 291 VRPHLMDFN-----SLFVTAETVRSQTVWGCHLV-----SSRTAGNPI 331

Qy 390 TLPF-----TSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFWTHPIAS 434
Db 332 NFPIYGFNPGGAIWADDDPRFYRT-----LSDPV-----FVRGGFGN 371

Qy 435 DNFYYPGYAGIGTQLQ-----DSENELPPEATGQPNYESYSHRLSHI---- 476
Db 372 PH-YVLGLRGVAFQQTGNHTRTRFRNSGTIDSLDEIPQDNSGAPWNDYSHVLNHTFVR 430

Qy 477 --GLISASHV-KALVYSWTHRSADRTNIEPNSITQPLVKAFNLSSGAAVRPGFTGG 533
Db 431 WPGETAGSDSWRAPMFSWTHRSADRTNIINPIITQIPAVKAHNLHSGSTVVRGGFTGG 490

Qy 534 DILRRNTGTGDIRVNNPPPAQRVVRIRYASTTDLQFHTSINGKAINQNFSAATMR 593
Db 491 DLLRRNTGTGFADIRVNITGPLSQRYVRIRYASTTDLQFTRINGTSVNQGNFQRTWNR 550

Qy 594 GEDLDYKTRFTVGTFTTTPRSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDF 653
Db 551 GGNLESNGNFRTAGFTPTFSFNAQSTFTLTGTQAFSN-QEVYIDRIEFVPAEVTFEAESDL 609

Qy 654 EKAQKVTALFTSTNPRGLKTDYKDYHIDQVNLVSLSDSEFYLDEKRELPEIVKYANEL 713
Db 610 ERAQKAVNALFTSTSQLGLKTNVTGYHIDQVNLVACLSDSEFCLDEKRELSEKVKHAKRL 669

714 HIERNM 719
670 SDRNL 675

RESULT 10
A26513
parasporal crystal protein - Bacillus thuringiensis (strain aizawai)
C:Species: Bacillus thuringiensis
C:Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004
C:Accession: A26513
R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.
Gene 53, 113-119, 1987
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis
A:Reference number: A26513; MUID:87248103; PMID:3297927
A:Accession: A26513
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1155 <OED>
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AA22551.1; PID:g143099
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 38.8%; Score 1459; DB 2; Length 1155;
Best Local Similarity 44.1%; Pred. No. 2.6e-92;
Matches 313; Conservative 112; Mismatches 230; Indels 54; Gaps 12;
QY 36 NINHEDCLKMSYENVE-PFVSASTIQTG-----IGIAGKILGTLGVFPAGQVASLYS 87
Db 4 NPNIKECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIEMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARQAIISRLGSLNLYQIYAESFREWEA 119
QY 148 NNNTRARSVKVSQYIALELMFVQKLPFAVSVEEVLPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTPALREEMRIQFNDMNSALTTAIPFAVQNYQVLLSVYVQAANLHLSVLRDVSVEG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCKWYSTGLNLRGTNAESWVRYNQFRDMTLM 267
Db 180 QRWGDAATINSRNDLITFLIGNYTHAVRWNTGLERWGPDSRDWIRYNQFRRELTLT 239
QY 268 VLDLVALPSPYDTQMPYPIKTTAQLTREYVYDTAIGTVHPHPSFTSTTWYNNAPSSAIEA 327
Db 240 VLDIVSLFFNYDSRTYPIKTVSQTREIYTNPV-----LENFDGSRALAQ 285
QY 328 AV---VRNPHLLDFLEQVITYISLLSR-----WSNTOYNNM---WGGHKLERTIGTGLNIS 377
Db 286 GIEGSIKSRPLMDIILNSITITYTDAHRGEYVWSGHQIMASPVGFGPEFTFLYGTMGNA 345
QY 378 TQGSNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFTHTPIASDNF 437
Db 346 PQORIVAQLQGQVYRTLSLTLYRRPFNIGIN---NQQLSVLDGTETAYG-----TSSNL 396
QY 438 YYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVYS 490
Db 397 PSAYVRKSGT--VDSLDEIPQNNVPVPRQGFSHRLSHVSMFRSGPSNSSVSIIRAPMFS 454
QY 491 WTHRSADRTNTIENPSITQPLVKAFNLSSGAAVVRPGFTGGDILRLRTNTGTGDIRVN 550
Db 455 WIHRSAEFNIIIPSSQITQIPLTKSTNLGSGTSVVKPGFTGGDILRLRTSPQISTLRVN 514
QY 551 INPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTT 610
Db 515 ITAPLSQRYVRIRYASTTNLQFHTSIDGRPINQGNFSATMNSGSLQSGSFRVGTFTT 574
QY 611 FSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVATLFTSTNPR 670
Db 575 FNFNSGSSVFTLSAHVFNNSNEVYIDRIEFVPAEYTPAEYDLERAQKAVNELFTSSNQI 634
QY 671 GLKTDVKDHYHDQVSNLVSLSDEFYLDKRELPEIYVKYANELHIERNM 719
Db 635 GLKTDVTDYHLDQVSNLVECLSDSEFCLEKSELSEKVKHAKRLSDERNL 683

RESULT 11

JD0002
parasporal crystal protein cryIAb3 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot
C:Species: Bacillus thuringiensis
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: A30025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from
A:Reference number: A90025
A:Accession: A90025
A:Molecule type: mRNA
A:Residues: 1-1155 <KON>
A:Cross-references: UNIPROT:P06578
R:Geiser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal prote:
A:Reference number: A91560; MUID:87163505; PMID:3557124
A:Accession: A91560
A:Molecule type: DNA
A:Residues: 1-1155 <GEI>
A:Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A:Experimental source: subsp. kurstaki
R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal;
A:Reference number: A90955; MUID:8630092; PMID:3743328
A:Accession: A90955
A:Molecule type: DNA
A:Residues: 1-1155 <WAB>
A:Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720
A:Experimental source: subsp. berliner
R:Chak, K.F.; Jen, J.C.
submitted to the EMBL Data Library, October 1990
A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry
A:Reference number: S14555
A:Accession: S14555
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1155 <CHA>
A:Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
R:Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckh
Eur. J. Biochem. 161, 273-280, 1986
A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri
A:Reference number: A26461; MUID:87054026; PMID:3023091
A:Accession: A26461
A:Molecule type: DNA
A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>
A:Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A:Experimental source: strain berliner 1715
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C:Genetics:
A:Gene: cry-1-2; bt2
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
F:82-586/Product: toxic peptide #status predicted <TXP>
F:82-300/Region: toxic #status predicted
F:300-586/Region: insecticidal #status predicted
Query Match 38.6%; Score 1452; DB 2; Length 1155;
Best Local Similarity 44.2%; Pred. No. 7.8e-92;
Matches 314; Conservative 111; Mismatches 229; Indels 56; Gaps 13;
QY 36 NINHEDCLKMSYENVE-PFVSASTIQTG-----IGIAGKILGTLGVFPAGQVASLYS 87
Db 4 NPNIKECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIEMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARQAIISRLGSLNLYQIYAESFREWEA 119
QY 148 NNNTRARSVKVSQYIALELMFVQKLPFAVSVEEVLPLPIYAQAANLHLLLRDASIFG 207

Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNVQVPLLSVYVQAANLHLSVLDRDVSFG 179
 Qy 208 KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267
 Db 180 QRWGDAATINSRYNDLTRLIGNYTDHAVRYNTGLERWGPDSRDWIRYNQFRRELTLT 239
 Qy 268 VLDLVALPPSYDTOMYPIKTTAQLTREVTDAIGTVHPPHPSFTSTTWYNNNAPS-----S 323
 Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYTNPV-----LENFQGSFRGSAQ 285
 Qy 324 AIEAAVVRNPHLLDFLEQVTIYLSLR-----WSNTQYMMN---WGHKLEPRTIGTGLNI 376
 Db 286 GIEGS-IRSPHLMIDLNSITITDAHRGEYWSGHQIMASPVGSGPEFTFPLYGTMGNA 344
 Qy 377 STQGSTNTSINPVTLPFTSRDVRTESLAGNLFQTQVNGVPRVDFHMKFVTHPIASDN 436
 Db 345 APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395
 Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489
 Db 396 LPSAVYRKSGT--VDSLDEIPQNNNVPRQGFHSHLVSMFRSGFSNSSVSIIRAPMF 453
 Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFDIRV 549
 Db 454 SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSFGQISLVR 513
 Qy 550 NINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTT 609
 Db 514 NITAPLSQRVVRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLNLSQSGSFRVTGFTT 573
 Qy 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTAFTSTNP 669
 Db 574 PFNFSNGSSVFTLSAHVFNCSGNEVYIDRIEFVPAEVTPEAEYDLERAKAVNELFTSSNQ 633
 Qy 670 RGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
 Db 634 IGLKTDVTDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 683

RESULT 12
 A29125
 parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
 C/Species: Bacillus thuringiensis subsp. kurstaki
 C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 R/Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederm
 Bio/Technology 5, 807-813, 1987
 A/Title: Insect tolerant transgenic tomato plants.
 A/Reference number: A29125
 A/Accession: A29125
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-1156 <FIS>
 A/Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21
 C/Superfamily: parasporal crystal protein
 C/Keywords: delta-endotoxin

Query Match 38.6%; Score 1452; DB 2; Length 1156;
 Best Local Similarity 44.2%; Pred. No. 7.8e-92;
 Matches 314; Conservative 111; Mismatches 229; Indels 56; Gaps 13;
 Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLVPPFAGQVSLYS 87
 Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSITQFLSEF-VPGAGFVLGLVD 62
 Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGLDALAVVHDSLSVWG 147.
 Db 63 IIWGIPI--GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLESLNLYQIYAESFREWEA 119
 Qy 148 NRNNTARSVVKVQVIALELMFVKQLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
 Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNVQVPLLSVYVQAANLHLSVLDRDVSFG 179

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267
 Db 180 QRWGDAATINSRYNDLTRLIGNYTDHAVRYNTGLERWGPDSRDWIRYNQFRRELTLT 239
 Qy 268 VLDLVALPPSYDTOMYPIKTTAQLTREVTDAIGTVHPPHPSFTSTTWYNNNAPS-----S 323
 Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYTNPV-----LENFQGSFRGSAQ 285
 Qy 324 AIEAAVVRNPHLLDFLEQVTIYLSLR-----WSNTQYMMN---WGHKLEPRTIGTGLNI 376
 Db 286 GIEGS-IRSPHLMIDLNSITITDAHRGEYWSGHQIMASPVGSGPEFTFPLYGTMGNA 344
 Qy 377 STQGSTNTSINPVTLPFTSRDVRTESLAGNLFQTQVNGVPRVDFHMKFVTHPIASDN 436
 Db 345 APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395
 Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489
 Db 396 LPSAVYRKSGT--VDSLDEIPQNNNVPRQGFHSHLVSMFRSGFSNSSVSIIRAPMF 453
 Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFDIRV 549
 Db 454 SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSFGQISLVR 513
 Qy 550 NINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTT 609
 Db 514 NITAPLSQRVVRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLNLSQSGSFRVTGFTT 573
 Qy 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTAFTSTNP 669
 Db 574 PFNFSNGSSVFTLSAHVFNCSGNEVYIDRIEFVPAEVTPEAEYDLERAKAVNELFTSSNQ 633
 Qy 670 RGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
 Db 634 IGLKTDVTDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 683

RESULT 13
 I39838
 parasporal crystal protein - Bacillus thuringiensis
 C/Species: Bacillus thuringiensis
 C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I39838
 R/Heiford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
 J. Biotechnol. 6, 307-322, 1987
 A/Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki
 A/Reference number: I39838
 A/Accession: I39838
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1155 <RES>
 A/Cross-references: UNIPROT:P06578; GB:M37263; NID:gl42885; PIDN:AAA22420.1; PID:gl42886
 C/Superfamily: parasporal crystal protein
 C/Keywords: delta-endotoxin

Query Match 38.4%; Score 1443; DB 2; Length 1155;
 Best Local Similarity 44.1%; Pred. No. 3.3e-91;
 Matches 313; Conservative 111; Mismatches 230; Indels 56; Gaps 13;
 Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLVPPFAGQVSLYS 87
 Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSITQFLSEF-VPGAGFVLGLVD 62
 Qy 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGLDALAVVHDSLSVWG 147
 Db 63 IIWGIPI--GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLESLNLYQIYAESFREWEA 119
 Qy 148 NRNNTARSVVKVQVIALELMFVKQLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
 Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNVQVPLLSVYVQAANLHLSVLDRDVSFG 179
 Qy 208 KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267

Db 180 QRMGDAATINSRYNDLTRIGNYTDHVRWYNTGLERVWGPDSRDWIRYNOFRRELTLT 239
QY 268 VLDLVALPSPDYDTQMPYIKTKTAQLTREYVYDAIGTVHPHPSFTSTTTWNNNAPSFAIEA 327
Db 240 VLDLVALPSPDYDTQMPYIKTKTAQLTREYVYDAIGTVHPHPSFTSTTTWNNNAPSFAIEA 327
QY 240 VLDLVALPSPDYDTQMPYIKTKTAQLTREYVYDAIGTVHPHPSFTSTTTWNNNAPSFAIEA 327
Db 240 VLDLVALPSPDYDTQMPYIKTKTAQLTREYVYDAIGTVHPHPSFTSTTTWNNNAPSFAIEA 327
QY 324 AIEAAVVRNPHLLDFEQVTIYSLLSRWSTQYMMNMWGGHKLKLEFRTIGT---LNISTGGS 381
Db 286 GIEGS-IRSPHLMILNSITITDAHRGEYVWGHQIMASPVGSGPFTFPLYGTMGNA 344
QY 377 STGSGTNTSINPVTLPFTSRDYRTESL---AGNLFLTPQVNGVPRVDFHMKFVTHPI 432
Db 345 APOQRIVAGLQGGVYRTLSSTLYRRPFGNIGN---NQQLSVLDGTEFAYG-----TSSN 395
QY 437 FYYPGYAGITQLODSENELPPEATGPNYESYSHRLSHIGLI-----SASHVKALVY 489
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPROGFSHRLSHVSMFRSGFSNVSIIRAPMF 453
QY 490 SWTHRSADRTNTIEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRRNTGTFGDIRV 549
Db 454 SWHRSANFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRNTGTFGDIRV 513
QY 550 NINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDELDYKTFRTVGF 609
Db 514 NITAPLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDELDYKTFRTVGF 573
QY 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVATLTSTNP 667
Db 574 PNFNSGSSVFTLSAHVFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVATLTSTNP 633
QY 670 RGLKTDVVDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719
Db 634 IGLKTDVTDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 683

RESULT 14
A22798
parasporal crystal protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: A22798
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A:Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuringiensis
A:Reference number: A22798; MUID:85232070; PMID:2989108
A:Accession: A22798
A:Molecule type: DNA
A:Residues: 1-934 <SHI>
A:Cross-references: UNIPROT:Q95SV8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713
A:Comment: The authors translated the codon ACA for residue 264 as Ser.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.3%; Score 1439.5; DB 2; Length 934;
Best Local Similarity 43.3%; Pred. No. 4.1e-91;
Matches 308; Conservative 118; Mismatches 225; Indels 61; Gaps 12;

QY 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPFAGQVSLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62

QY 88 FILGELWPKGNQWEIWFHEHVEEIIINOKISTYARNKALTDKGLGDALAVYHDSLESVWG 147
Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFARNOAISLEGSLNLYQIYAESFREWEA 119

QY 148 NRNNTARSVKVSQYIALELMFVKQLPSFVSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179

QY 208 KEWGLSSSISITFYNQVERAGDYSHCVKWTSTGLNLRGTNAESWVRYNQFRDMLTLM 267
Db 180 QRMGDAATINSRYNDLTRIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNOFRRELTLT 239

QY 268 VLDLVALPSPDYDTQMPYIKTKTAQLTREYVYDAIGTVHPHPSFTSTTTWNNNAPSFAIEA 327
Db 240 VLDLVALPSPDYDTQMPYIKTKTAQLTREYVYDAIGTVHPHPSFTSTTTWNNNAPSFAIEA 327
QY 328 AV---VRNPHLLDFEQVTIYSLLSRWSTQYMMNMWGGHKLKLEFRTIGT---LNISTGGS 381
Db 286 RIEQNIQPHLMILNSITITDAHRGEYVWGHQIMASPVGSGPFTFPLYGTMGNA 340
QY 382 TMTSINPVTLPFTSRDYRTESL---AGNLFLTPQVNGVPRVDFHMKFVTHPI 432
Db 341 AGNAAPPVLVSLTGLIPFTLSPLRRRIILGSGPN---NQQLSVLDGTEFSPASLTNTL 397
QY 433 ASDNFPYAGITQLODSENELPPEATGPNYESYSHRLSHIGLIASAS-----HVKAL 487
Db 398 PSTIYRQCTV-----DSLVIIPQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRTNTIEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRRNTGTFGDI 547
Db 451 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRNTGTFGDI 510
QY 548 RVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDELDYKTFRTVGF 607
Db 511 RVNITAPLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDELDYKTFRTVGF 570
QY 608 TTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVATLTSTNP 667
Db 571 TTPFNFSNGSSVFTLSAHVFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVATLTSTNP 630
QY 668 NPGKLTVDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719
Db 631 NQIGLKTVDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 682

RESULT 15
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N:Alternate names: 135K insecticidal protein
C:Species: Bacillus thuringiensis
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0241
R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
Agric. Biol. Chem. 52, 1565-1573, 1988
A:Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A:Reference number: JT0241
A:Accession: JT0241
A:Molecule type: DNA
A:Residues: 1-1176 <SHI>
A:Cross-references: UNIPROT:P02965
A:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein
C:Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.2%; Score 1438.5; DB 2; Length 1176;
Best Local Similarity 43.3%; Pred. No. 6.9e-91;
Matches 308; Conservative 117; Mismatches 226; Indels 61; Gaps 12;

QY 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPFAGQVSLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62

QY 88 FILGELWPKGNQWEIWFHEHVEEIIINOKISTYARNKALTDKGLGDALAVYHDSLESVWG 147
Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFARNOAISLEGSLNLYQIYAESFREWEA 119

QY 148 NRNNTARSVKVSQYIALELMFVKQLPSFVSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179

QY 208 KEWGLSSSISITFYNQVERAGDYSHCVKWTSTGLNLRGTNAESWVRYNQFRDMLTLM 267
Db 180 QRMGDAATINSRYNDLTRIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNOFRRELTLT 239

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.6029 Seconds
(without alignments)
3350.901 Million cell updates/sec

Title: US-10-019-823B-56
Perfect score: 3762
Sequence: 1 MCLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues
Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3743	99.5	719	16	US-10-782-020-10 Sequence 10, Appl
2	3743	99.5	719	16	US-10-782-141-8 Sequence 8, Appli
3	3459.5	92.0	710	15	US-10-428-961-42 Sequence 42, Appl
4	2263.5	60.2	1228	16	US-10-809-953-10 Sequence 10, Appl
5	2250.5	59.8	1207	10	US-09-988-462-7 Sequence 7, Appli
6	2171.5	57.7	1227	15	US-10-428-961-63 Sequence 63, Appl
7	2156.5	57.3	1186	9	US-09-826-660-23 Sequence 23, Appl
8	2101	55.8	1228	15	US-10-428-961-38 Sequence 38, Appl
9	2101	55.8	1228	15	US-10-614-524-2 Sequence 2, Appli
10	1923.5	51.1	643	9	US-09-826-660-25 Sequence 25, Appl
11	1707.5	45.4	1167	14	US-10-089-678-1 Sequence 1, Appli
12	1678.5	44.6	653	15	US-10-428-961-6 Sequence 6, Appli
13	1655.5	44.0	1157	16	US-10-782-141-16 Sequence 16, Appl

14	1496	39.8	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1496	39.8	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1496	39.8	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1480	39.3	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1480	39.3	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1480	39.3	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1476.5	39.2	1156	14	US-10-099-285-72	Sequence 72, Appl
21	1476.5	39.2	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1452	38.6	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1452	38.6	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1452	38.6	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1452	38.6	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1452	38.6	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1452	38.6	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1452	38.6	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1452	38.6	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1452	38.6	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1452	38.6	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1452	38.6	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1452	38.6	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1452	38.6	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1447	38.4	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1445	38.4	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1444	38.4	1177	14	US-10-102-469-24	Sequence 24, Appl
38	1428.5	38.0	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1416.5	37.7	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1416.5	37.7	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1385	36.8	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1364	36.3	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1364	36.3	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1364	36.3	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1364	36.3	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMT-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; TYPE: PRT
; LENGTH: 719
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 99.5%; Score 3743; DB 16; Length 719;
Best Local Similarity 99.6%; Pred. No. 8.2e-308;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI	60
DB	1	MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI	60
QY	61	QTGIGIAGKILGTGLVPPAGQVASLYSIFLGLWPKGNQWEIFMEHVEEIIINQKISTYA	120
DB	61	QTGIGIAGKILGTGLVPPAGQVASLYSIFLGLWPKGNQWEIFMEHVEEIIINQKISTYA	120

QY	121	RNKA	121	QY	1	MLKN
DB	121	QY	61	QY	61	QY
QY	181	QY	121	QY	181	QY
DB	181	QY	121	QY	181	QY
QY	241	QY	181	QY	241	QY
DB	241	QY	181	QY	241	QY
QY	301	QY	241	QY	301	QY
DB	301	QY	241	QY	301	QY
QY	361	QY	361	QY	361	QY
DB	361	QY	361	QY	361	QY
QY	421	QY	421	QY	421	QY
DB	421	QY	421	QY	421	QY
QY	481	QY	481	QY	481	QY
DB	481	QY	481	QY	481	QY
QY	541	QY	541	QY	541	QY
DB	541	QY	541	QY	541	QY
QY	601	QY	601	QY	601	QY
DB	601	QY	601	QY	601	QY
QY	661	QY	661	QY	661	QY
DB	661	QY	661	QY	661	QY
RESULT 3						
US-10-782-141-8						
; Sequence 8, Application US/10782141						
; Publication No. US20040197917A1						
; GENERAL INFORMATION:						
; APPLICANT: Carozzi, Nadine						
; APPLICANT: Hargiss, Tracy						
; APPLICANT: Kozel, Michael G.						
; APPLICANT: Duck, Nicholas B.						
; APPLICANT: Carz, Brian						
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and						
; TITLE OF INVENTION: Methods for Its Use						
; FILE REFERENCE: 045600/274143						
; CURRENT APPLICATION NUMBER: US/10/782,141						
; CURRENT FILING DATE: 2004-02-20						
; PRIOR APPLICATION NUMBER: 60/448,632						
; PRIOR FILING DATE: 2003-02-20						
; NUMBER OF SEQ ID NOS: 23						
; SOFTWARE: FastSeq for Windows Version 4.0						
; SEQ ID NO 8						
; LENGTH: 719						
; TYPE: PRT						
; ORGANISM: Bacillus thuringiensis						
US-10-782-141-8						
Query Match 99.5%; Score 3743; DB 16; Length 719;						
Best Local Similarity 99.6%; Pred. No. 8.2e-308;						
Matches 716; Conservative 1; Mismatches 2; Indels 0; Caps 0;						
QY	1	MLKN	1	QY	1	MLKN

; NAME/KEY: misc feature
; LOCATION: (200) (200)
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 92.0%; Score 3459.5; DB 15; Length 710;
Best Local Similarity 92.1%; Pred. No. 8.5e-284;
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPFSASTI 60
DB 1 MKSKNQNMHQSLSNATVDKNFTGSLNNTLQNFH-----EGIEPFSVSTI 51

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFYLGLWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 52 QTGIGIAGKILGTGVPFAGQVASYLSFYLGLWPKGNQWEIFMEHVEEIIINQKISTYA 111

QY 121 RNKALTDLKGDLAVHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPSPAVSG 180
DB 112 RNKALADLKGDLAVHDSLESWGNRNTRARSVVKSQVITLLELMFVQSLPSPAVSG 171

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 231

QY 241 TGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
DB 232 TGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 291

QY 301 GTVHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 360
DB 292 GTVHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 351

QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPTSDRYRTESLAGNLFILTPQVNGVPR 420
DB 352 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPTSDRYRTESLAGNLFILTPQVNGVPR 411

QY 421 VDFHWKLVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 412 VDFHWKLVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471

QY 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 472 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 531

QY 541 TGTGDIRVNIINPPFAQRVVRIRYASTDLQFTSINGKAINQGNFSAATMNRGDDLYK 600
DB 532 TGTGDIRVNIINPPFAQRVVRIRYASTDLQFTSINGKAINQGNFSAATMNRGDDLYK 591

QY 601 TFRVTGFTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 660
DB 592 TFRVTGFTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 651

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDYFYLDEKRELFEIVKYANLHIERNM 719
DB 652 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDYFYLDEKRELFEIVKYANLHIERNM 710

RESULT 4

US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US2004018125A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016

; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 60.2%; Score 2263.5; DB 16; Length 1228;
Best Local Similarity 62.4%; Pred. No. 4.3e-182;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNH-----EDCLKMSYENVEPFSASTIQTGIGIAGKI 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPFAGQVASYLSFYLGLWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 62 LGTLGVPPFAGQVASYLSFYLGLWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121

QY 131 LGDALAVHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPSPAVSGEVPVLLPIYA 190
DB 122 LGDSFRAYQQSLEDWLENRDARTSRVLTQYIALELDLFNAIPLFAIRNOEVPVLLMVYA 181

QY 191 QAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 250
DB 182 QAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 241

QY 251 AESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIQTGVPHPSFT 310
DB 242 AESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIQTGVPHPSFT 299

QY 311 STTWNNNAPSFSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGHKLEFRIT 370
DB 300 SMWYNNNAPSFSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGHKLEFRIT 359

QY 371 GGTNLNISTOGSTNTSINPVTLPTSDRYRTESLAGNLFILTPQVNGVPRVDFHKKFV 428
DB 360 GGTNLNISTOGSTNTSINPVTLPTSDRYRTESLAGNLFILTPQVNGVPRVDFHKKFV 416

QY 429 THP-----IASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
DB 417 TNPQNISDRGTANYSQP-YESPGLQKDSSETLPPEATERPNYESYSHRLSHIGLISASH 475

QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGT 543
DB 476 VNPVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGT 535

QY 544 FGDIRVNIINPPFAQRVVRIRYASTDLQFTSINGKAINQGNFSAATMNRGDDLYKTFR 603
DB 536 FGPVIRVNIINPPFAQRVVRIRYASTDLQFTSINGKAINQGNFSAATMNRGDDLYKTFR 595

QY 604 TVGFTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 663
DB 596 RRAFTTPTFTQIQTIIITSIQGLSGNEVYIDRIEFVPEVTEAEYDFEKAQEV 655

QY 664 FTSTNPRGLKTDVQYHIDQVSNLVESLSDYFYLDEKRELFEIVKYANLHIERNM 719
DB 656 FTSTNPRGLKTDVQYHIDQVSNLVESLSDYFYLDEKRELFEIVKYANLHIERNM 711

RESULT 5

US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nallini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689

SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7
Query Match 59.8%; Score 2250.5; DB 10; Length 1207;
Best Local Similarity 64.0%; Pred. No. 5.3e-181;
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;

QY 40 EDCLKMSYENVEPFVSASTIQTGIGIAGKILGTGVFPAGQVASLYSFLGELWPKGN 99
DB 10 EDSLCLAEAGNNIDPFVSASTVGTGINAGRILGVLGVPAGQVASFYSFLVGLWPKGRD 69

QY 100 QWEIFMEHVEEIIINQKISTYARKNALTDLKGLGDALAVYHDSLSWVGNRNTRARSVVK 159
DB 70 QWEIFLEHVEQLINQINQITENARNLTALRQLGLGDSFRAYQOSLEDWLENRDDARTSVLY 129

QY 160 SQYIALELMFVQKLPSFAVSGEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST 219
DB 130 TQYIALELDPLNAPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEQ 189

QY 220 FYNQVERAGDYSVHCVKWYSTGLNLRGTNAESWRYNQFRDNTLMVLDLVALFPSVD 279
DB 190 YYERQVERTRDYSYCVWEYNTGLNSLRGTNAESWRYNQFRDNTLMVLDLVALFPSVD 249

QY 280 TQMPYIKTTAQLTRVYTDATIGTVHPHSFTSTTWNNNAPSFSAIEAAVVRNPHLLDPL 339

DB 250 TRTYPINTSAQLTRVYTDATIGT--GVNMASWNNWNNAPSFSAIEAAIRSPHLLDPL 307
QY 340 EQVTIYSLRSWNTQYNNWGGHKLERTIGTGLNISTOGSTNTSINPVTLPFTSRDVS 399
DB 308 EQLTIFSSASSRWSNTRHMTYRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFSRDVS 367
QY 400 RTESLAGLNLFP--LTQPVNGVPRVDFHWKFWTHP-----IASDNFYYPGYAGIGTQLQDS 452
DB 368 RTESVAGVLLWGIIEPIHGVPTVRNF--TNPQNISDRGTANYSQP-YESPGLQKDS 423
QY 453 ENELPPEATQPNYESYSHRLSHIGLISASHVKALVTSWTHRSADRTNTIIPNSITQIPL 512
DB 424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVVSVWTHRSADRTNTIGNRIQIPM 483
QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPPFAQRYRVRIRYASTDLQ 572
DB 484 VKASELPQGTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGPLTQRYRIGFYASTVDFD 543
QY 573 FHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTTPEFSLDVQSTFTIGAWNFSSGNE 632
DB 544 PFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRRAFTTFTTQIQDIIRTSIQGLSGNE 603
QY 633 VYIDRIEFVPEVTVYEAEDPEKAQEKVTALFTSTNPRGLKTDVYHIDQVSNLVESLS 692
DB 604 VYIDKIEIIPVTATPEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663
QY 693 DEFYLDKRELFEIVKYANLHIERNM 719
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6

US-10-428-961-63
Sequence 63, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:

APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.

APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201--1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent in version 3.2
SEQ ID NO 63
LENGTH: 1227
TYPE: PRT

ORGANISM: Bacillus thuringiensis
US-10-428-961-63

Query Match 57.7%; Score 2171.5; DB 15; Length 1227;
Best Local Similarity 59.0%; Pred. No. 2.7e-174;
Matches 421; Conservative 104; Mismatches 176; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTDLSKN-----ETDIELQNIHEDCLKMSYENVEPFVSASTIQTGIG 65
DB 7 NENEINALSIPAVSNHSAQMNLSKDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTIGVFPAGQVASLYSFTLGLWPKGNQWEIFMEHVEEIIINQKISTYARKN 125
DB 62 IAGRILGVLGVPFAGQIASFYSFLVGLWPKGRDPWEIFLEHVEHLIRQVNTEDTAL 121

QY 126 TDLKGLGDALAVYHDSLSWVGNRNTRARSVVKSVQYIALELMFVQKLPSFAVSGEVEPL 185


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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PR
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match      55.8%; Score 2101; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.5e-168;
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPAVNSHSTQMDLSPDARDIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIEMFHEVVEIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQOG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKQLPSFAVSGEEVPLPIYA 190
Db 127 LGDSFRAYQOOSLEDWLENRDDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186

QY 191 QAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSHCVKWTSTGLNLRGTN 250
Db 187 QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN 246

QY 251 AESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDAGTGVHPHPSFT 310
Db 247 AASWRYNQFRDRLTLGVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDAGT--GVNMA 304

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMWGGHKLFRFI 370
Db 305 SMWYNNAPSFSAIETAVIRSPHLLDLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364

QY 371 GGTNLNSTGSGTNTSINPVTLPFTSRDVRVYTESLAGLNLFP--LTQPVNGVPRVDFHMKFV 428
Db 365 GGLNTSTHSGTNTSINPVLRSFSDRVYTESYAGVLLWGIYLEPIHGVTVRNFRNP 424

QY 429 --THPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISASHVKA 486
Db 425 QNTFERGTANYSQP--YESPGLQKQDSELTPELTPETTERPNYESYSHRSLHIGLISQSRVHV 483

QY 487 LVSQWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGD 546
Db 484 PVSQWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSSVSGPGFTGGDIIRTNVNGSVLS 543

QY 547 IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTFRTVG 606
Db 544 MGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSGTTFDQGFSTMSANESLTSQSRFAE 603

QY 607 FTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEKVTALFTS 666
Db 604 FVVGISASGSO--TAGISISNAGRQTFHFDKIEFIPITATFEAYDLEAQAQAVNALFTN 662

QY 667 TNPRGLKTDVVDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719
Db 663 TNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 9
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/139,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PR
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match      55.8%; Score 2101; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.5e-168;
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPAVNSHSTQMDLSPDARDIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIEMFHEVVEIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQOG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKQLPSFAVSGEEVPLPIYA 190
Db 127 LGDSFRAYQOOSLEDWLENRDDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186

QY 191 QAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSHCVKWTSTGLNLRGTN 250
Db 187 QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN 246

QY 251 AESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDAGTGVHPHPSFT 310
Db 247 AASWRYNQFRDRLTLGVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDAGT--GVNMA 304

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMWGGHKLFRFI 370
Db 305 SMWYNNAPSFSAIETAVIRSPHLLDLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364

QY 371 GGTNLNSTGSGTNTSINPVTLPFTSRDVRVYTESLAGLNLFP--LTQPVNGVPRVDFHMKFV 428
Db 365 GGLNTSTHSGTNTSINPVLRSFSDRVYTESYAGVLLWGIYLEPIHGVTVRNFRNP 424

QY 429 --THPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISASHVKA 486
Db 425 QNTFERGTANYSQP--YESPGLQKQDSELTPELTPETTERPNYESYSHRSLHIGLISQSRVHV 483

QY 487 LVSQWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGD 546
Db 484 PVSQWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSSVSGPGFTGGDIIRTNVNGSVLS 543

QY 547 IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTFRTVG 606
Db 544 MGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSGTTFDQGFSTMSANESLTSQSRFAE 603

QY 607 FTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEKVTALFTS 666
Db 604 FVVGISASGSO--TAGISISNAGRQTFHFDKIEFIPITATFEAYDLEAQAQAVNALFTN 662

QY 667 TNPRGLKTDVVDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719
Db 663 TNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 10
US-10-826-660-25
; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
```


FILE REFERENCE: Q68821
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: JP 2000-236140
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: PCT/JP01/06660
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1167
TYPE: PRT
ORGANISM: Bacillus thuringiensis
FEATURE:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match 51.1%; Score 1923.5; DB 9; Length 643;
Best Local Similarity 57.5%; Pred. No. 1e-153;
Matches 370; Conservative 100; Mismatches 160; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTDSLKN-----ETDIELQNIHEDCLKMEYENVEPVSASTIQTGIG 65
DB 7 NENEIINALSIPAVSNHSAQMLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTLGVPPAGQVASYFLIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
DB 62 IAGRILGVLGVPPAGQIASFYSLVGLWPRGRDPWEIFLEHVEQLIRQQVTTENTRTAL 121
QY 126 TDLKGLGDALAVYHDSLESVGNRNTRARSVVKVSYQYIALELMFVQKLPSPAVSERVPL 185
DB 122 ARLOGLNSPRAYQOSLEDWLENRDDARTSVLYTQYIALELDFLNAMPLFAIRNQEVL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKMYSTGLNN 245
DB 182 LMVYAQAANLHLLLRDASIFGSEFGLTQEIQRYYERQVETREYSDYCARWYNTGLNN 241
QY 246 LRGTHAESVRYNQPRDMTLMVLDLVALFPSPYDTQMPYIKTAQLTREVYTDAGTVHP 305
DB 242 LRGTHAESVRYNQPRDMTLMVLDLVALFPSPYDTQMPYIKTAQLTREVYTDAGTVHP 301
QY 306 HPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYISLRSWNTQYNNMGGHKL 365
DB 302 PSGFASWNNNAPSFAIAEAAVVRNPHLLDFLEQVITYISLRSWNTQYNNMGGHKL 361
QY 366 EFRTIGGLTINISQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPVNGVPRVDFHW 425
DB 362 ESRTIGSLSTHGTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPVNGVPRVDFHW 421
QY 426 KFTVTHPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHGLISASHVK 485
DB 422 RNPLNSLRGSLYTYIGTGVGTQFDSETELPETTERPNYESYSHRLSNIRLISGNTLR 481
QY 486 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFTG 545
DB 482 APVYSWTHRSADRTNTISSDITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFTG 541
QY 546 DIRVNNPPAQRVRYRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTRTV 605
DB 542 SMGLFNNTSLQRYRVRYVAASQTMVLRTVCGSTTDPQFPSTMSANESLTSQSFRA 601
QY 606 GFTTTPFSLDVQSTTTIGAWNFSSGNEVVIDRIEFVPEVTVYE 648
DB 602 EFPVGISASGSQ-TAGISISNAGROTFHFDKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
Sequence 1, Application US/10089678
Publication No. US20030017967A1
GENERAL INFORMATION:
APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

FILE REFERENCE: Q68821
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: JP 2000-236140
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: PCT/JP01/06660
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1167
TYPE: PRT
ORGANISM: Bacillus thuringiensis
FEATURE:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-10-089-678-1

Query Match 45.4%; Score 1707.5; DB 14; Length 1167;
Best Local Similarity 47.6%; Pred. No. 5.1e-135;
Matches 359; Conservative 125; Mismatches 221; Indels 49; Gaps 12;

QY 1 MKNLQNDKHQ---SFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYE-----NV 51
DB 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNKKDYLRMSEGENPELFGNP 60
QY 52 EPPVSASTIQTGIGIAGKILGTLGVPPAGQVASYFLIGELWPKGNQWEIFMEHVEE 110
DB 61 ETFISSSTVQTGIGIGVGLGALGVPPAGQIASFYSPVIGLWPSSTVSVWEMIMKQVED 120
QY 111 IINOKISTYARNKALTDLKGDLALAVYHDSLESVGNRNTRARSVVKVSYQYIALELMFV 170
DB 121 LIDQKITDSVRKTALAGLQGLDGLDVYQSKLKNWLENRNDTRARSVVVTQYIALELDFV 180
QY 171 QKLPFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGD 230
DB 181 AKIPSAISGQEVPLLSVYAQAANLHLLLRDASIFGAEWGFTTPEISTFYDQVTRTAQ 240
QY 231 YSYHCVKWTSTGLNNLRGTNAESVRYNQPRDMTLMVLDLVALFPSPYDTQMPYIKTAQ 290
DB 241 YSDYCVKWTSTGLNNLRGTNAESVRYNQPRDMTLMVLDLVALFPSPYDTQMPYIKTAQ 300
QY 291 LTREYVTDAGTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYISL 349
DB 301 LTREYVTDAGTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYISL 360
QY 350 -RWSNTQYNNMGGHKLBPRTIGTGLTINISQSTNTSINPVTLPFTSRDVRVYTESL-AGL 407
DB 361 LPLANTLEYLVWGHSHIKYKNTNASSALERNYGTITSNKIKYDLANKDIPOVRSGLADL 420
QY 408 NLFLTQPVNGVPRVDFHWKFTVTHPIASDNFYPGYAGIG-----TQLODSE 453
DB 421 ANYVQAQ-VYGVPAVSF-----TLDDKN---TSGSGVGGFTYVKPHHTMQVCTQNTYTI 469
QY 454 NELPPEATGQPNYESYSHRLSHGLIS-----ASHVKALVYSWTHRSADRTNTIEPN 505
DB 470 DEIPPE--NEPLSRGYSHRLSHITSYFSKKNASSPARYGNLVPFAWTHRSADVTNTVYSD 527
QY 506 SITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFTGDIRVNNPPAQRVRYRY 565
DB 528 KITQIPVVKHAHTLVSGTIVIKGPGFTGGNILKRTSSGLAYTSVSKSPLSORYARIRY 587
QY 566 ASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTRTVGTFTTTPFSLDVQSTFTIGAW 625
DB 588 ASTTNLRLFVTTISGTRIYSINVNKTMKGGDGLTFNTFDLATIGTAFATFNSYSDSLTVGAD 647
QY 626 NFSSGNEVVIDRIEFVPEVTVYEAEYDEKAEQKVTALFTSTNPRGKTDVKDYHIDQVS 685
DB 648 SFASGGEVVVDKFEIIPVNATFEAEEDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVQNA 706
QY 686 NLVESLSDEFYLDKRELPEIVKYANLHIERNM 719
DB 707 NLVECLSDLEYPNEKRLMDVAKEAKRLVQARNL 740

RESULT 12


```

US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MEC0201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-428-961-6

Query Match      44.6%; Score 1678.5; DB 15; Length 653;
Best Local Similarity 51.5%; Pred. No. 5.9e-133;
Matches 346; Conservative 105; Mismatches 174; Indels 47; Gaps 14;

QY 13 SSNAKVDKISTDSLXN---ETDIELQNHEDCLKMSYENVEPFVSASTIQTGIGIAGK 69
DB 2 NENEIINALSIPAVSNHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINIAG 60

QY 70 ILGTLGVFPAGQVASYSLFTLGLWPKGNQWEIFMEHVEEELINQKISTYARNKALTDLK 129
DB 61 ILGVLGVFPAGQLASFSYFLVGLWPSGRDPWEIFLEYEQILRQVVTENTARTALRE 120

QY 130 GLGDALAVYHDSLESWVGNRNTRARSVVKSYQYTALEMLFVQKLPFAVSGEVPLLPIY 189
DB 121 GLGRGYSYQQALETWLDNRNARSIIILERYVALELDITTAIPLEIRNEEVPLLMVY 180

QY 190 AQAANLHLLLRDASTFGKWLSSSEISSTFYNRQVERAGDYSYHCVKWSYTGNNLRGT 249
DB 181 AQAANLHLLLRDASTFGSEKGMASSDVQYQEQIRVTEYSNHCQWYNTGLNLRGT 240

QY 250 NAESWRYNQFRDMLVLDLVALFPSTYQYPIKTAQLTREVTDAIGTVHPHPSF 309
DB 241 NAESWLYNQFRDMLVLDLVALFPSTYQYPIKTAQLTREVTDAIGTVHPHPSF 300

QY 310 TSTTWYNNAPSFSAEAAVVRNPHLLDFLEQVITYLSLRSWNTQYNNMWGCHKLEFRT 369
DB 301 ASTNWFNNAPSFSAEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVGHRLNFRP 360

QY 370 IGTLNISTQGST-NTSINPVTLFP--TSRDVYRTESLAGNLFLLTPQVNGVPRVDFHWKF 427
DB 361 IGTLNISTQGSTNTSINPVTLHYVSSRDVYRTESNAGTNILEFTTPVNGVPRVDFHWKF 418

QY 428 VTHPIASDNFYFP-----GYAGICTQLQDSENELPPEATGQPNYSYSHLSHG-- 477
DB 419 ITRIFMKEAPLTVNRIRELGFNYLQKLNHYQK-----QONDQIMNHVIDISYR 470

QY 478 LISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR 537
DB 471 LIIGNTLRAPVYSWTHRSADRTNTIGPNRIQIPAVKGRFLFNG-SVISGPGFTGGDVVR 529

QY 538 -RTWGTGF---GDIRVNIN-PPFAQRVVRIRYASTTDLPHTSINGKAINQGNFSATMN 592
DB 530 LNRNNGNTQNRGIEVPQFTSTSTRVVRVRYASVTSIELNVNLGNSIFTNLTLPATAA 589

QY 593 RGEDLDYKTFRTVGTFTPFSLDVQSTFT-----ICAMNFSNGNEVYIDRIEVPVPEVT 646
DB 590 SLDNLQ-----SGDFGYVEINNAFTSATGNIVGARFNFSANAEVVIDRFEIPVTAT 640

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QY 647 YEAEYDFEKAQE 658
DB 641 FEVEYDLERAQK 652

RESULT 13
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-782-141-16

Query Match      44.0%; Score 1655.5; DB 16; Length 1157;
Best Local Similarity 48.8%; Pred. No. 1.3e-130;
Matches 369; Conservative 97; Mismatches 233; Indels 57; Gaps 18;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQNHEDCLKMSYE-----N 50
DB 1 MSPNNQNEYIIDATPST-SVSSDSNRYPPANEPTDALQNNYKYDKLMSGGENPELFGN 59

QY 51 VEPFVSASTIQTGIGIAGKILGTGYPFAGOVASLYSFLIGELWP-KGKNQWEIFMEHVE 109
DB 60 PETFISSSTIQTGIGIVGRILGALGVFPFASQIASFYSFIVGQLWPSKSDVINGEIMERVE 119

QY 110 EIINQKISTYARNKALTDKGLGDALAVYHDSLESWVGNRNTRARSVVKSYQYTALEMLF 169
DB 120 ELVDQKIEKYVKDKALAEKLGIALDVYQOSLEDWLENRDARTRSVVSNOFIALDLNF 179

QY 170 VQKLPSFAVSGEVPPLPIYQAANLHLLLRDASTFGKWLSSSEISSTFYNRQVERAG 229
DB 180 VSSIPSFVAVSGHEVLLLAAYAAVNHLHLLLRDASTFGGEWGTTCGEISRFYNRQVQLTA 239

QY 230 DYSYHCVKWSYTGNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYQYPIKTTA 289
DB 240 EYSDYCVKWKYKIGLDKLGKTTSKSWLNHYQFRREMTLLVLDLVALFPNYDTHMYDIETTA 299

QY 290 QLTREVTDAIGTVHPHPSFTST---TWYNNAPSFSAEAAVVRNPHLLDFLEQVITY 345
DB 300 QLTRDVTDPDIA-----FNIVTSTGFCNPSWSTHSGILFYEVENNVIRPPHLPDILSSVEIN 355

QY 346 SLLSR---WSNTQYNNMWGCHKLEFR-----TIGGTNLNISTQGSTNTSINPVTLFPTS 396
DB 356 T--SRGGITLNDAYINYWSGHTLKRYRTADSTVTVTANYGRITSEKNS-----FALEDR 408

QY 397 DVYRTESLAGNLFLLTPQVNGVPRVDFHWKFVTHPIASDNFY-----YPGAGIGTQLQD 451
DB 409 DIFEINSTVANLANYYQKAYGVGSGWFH--WVKRGTSSTTAYLSKTHALQGC-TQVYE 465

QY 452 SENELPPEATGQPNYSYSHRLSHI-----GLISASHVKALVSWTHRSADRTNTIE 503
DB 466 SSDEIPLDRT-VPVAESYSHRLSHITSHSFSKNG--SAYYGSFPFVFWTHTSADLNNTIY 522

QY 504 PNSTIQTIPLVKAFNLSSGAAVVRGPGFTGGDILRRTTGTGDIRVNINPPFAQRVVR 563
DB 504 PNSTIQTIPLVKAFNLSSGAAVVRGPGFTGGDILRRTTGTGDIRVNINPPFAQRVVR 563

```


Db 523 SDKITQIPAVKGMMLYLGSSVQPGFTGGDILKRTNPSILGTFAVTNGSLSRVRI 582
Qy 564 RYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTKTRTGVGTTTPSFLDVQSTFTIG 623
Db 583 RYASTTDFEF-TLYLGDITIEKRNFKMTMGASLTYYEFKFAFITDFQFRETQDKILLS 641
Qy 624 AWFSSGNEVYIDRIEFVPEVVEVVEAEYDFEKAQEKVLTALFTSTNPRGLKTDVKYHIDQ 683
Db 642 MGDFSSGQEVYIDRIEFVPEVVEAEYDFEKAQEKVLTALFTSTNPRGLKTDVKYHIDQ 700
Qy 684 VSNLVSLSDFEYLDEKRELFEIVKYANLHIERNM 719
Db 701 AANLVECLSDDLYPNEKRLLFDAVREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 39.8%; Score 1496; DB 13; Length 1206;
Best Local Similarity 44.1%; Pred. No. 4.4e-117;
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVNSDNSRYPFANEPTNALQNMKYDYLYKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTGLVPPAGQVAVSLYSFILGELWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSEKSKQWEIFMEQV 119
Qy 109 EEIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNRNNTNRARSVVKSOYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLNYYQLYLTALAEENPNPNSRDLRDRNRFEILDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTPYNRQVERA 228
Db 180 FTQYMPFRVTNFEVPLTVYMAANLHLLLRDASIFGKEWGLSSSEISTPYNRQVERA 239
Qy 229 GDYSYHCVKMYSTGLNNLRGTNAESWVRNQFRDRLMTLWLDLVALPSPYDTQMYPIKTT 288
Db 240 AEYSDHCVRKYETGLAKLGTSAKQWVDYQNFREMTLAVLDVVALFPNYDRTYPMETK 299
Qy 289 AQLREVTYDAIGTVHPHSFTSTTWNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLL 348
Db 300 AQLREVTYDPLGAVNVS---SIGSWY-DKAPSGVIESSVIRPPHVFYDITGLTVYQTS 355
Qy 349 SRWSNTQYNNWGGHKLFRITIGTGLNISTQGSTNTSNPV-TLPFTSRDVRVYTESLAGL 407
Db 356 RSISARYIRHWAGHQISYHRVSRGSLNQMGYGTNQNLHSTSTFDFTNYDIYKLSKDAV 415

Qy 408 NLFLTQP-----VNGVPRVDFHWKFKVTHPIASDN---FYYPGYAGIGTQLOQSDSENEUPPE 459
Db 416 LLDIVYVPGVTYIFFGMEPEVEF---FMVQNLANTRKTLKYNPVSVDIIASTRDSLELPEPE 472
Qy 460 ATQQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTEIENSITQIPLVKAF 516
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNNTIYSDKITQIPAVKCM 532
Qy 517 NLSSGAADVPGPGTGGDILR-RNTGTGFDI---RVNPPFAQRYRVRIRYASTTDLQ 572
Db 533 DNLPEVPVVKPGPGHTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKYRVRVLYATDADIV 592
Qy 573 FHTSINGKAINQGNFSATMNRGDLDTKTRTGVGTTTPSFL-----DVQST 619
Db 593 LH--VNDQI---QMPKTNWPGEDLTSKTFKVADAIITLNLATDSSALKHKNLGEDDNST 647
Qy 620 FTIGAWNFSSGNEVYIDRIEFVPEVVEVVEAEYDFEKAQEKVLTALFTSTNPRGLKTDVKDY 679
Db 648 LS-----GIVVVDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDY 697
Qy 680 HIDQVSNLVESLSDFEYLDEKRELFEIVKYANLHIERNM 719
Db 698 EVNQAANLVECLSDDLYPNEKRLLFDAVREAKRLSGARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 39.8%; Score 1496; DB 14; Length 1206;
Best Local Similarity 44.1%; Pred. No. 4.4e-117;
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVNSDNSRYPFANEPTNALQNMKYDYLYKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTGLVPPAGQVAVSLYSFILGELWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSEKSKQWEIFMEQV 119
Qy 109 EEIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNRNNTNRARSVVKSOYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLNYYQLYLTALAEENPNPNSRDLRDRNRFEILDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTPYNRQVERA 228
Db 180 FTQYMPFRVTNFEVPLTVYMAANLHLLLRDASIFGKEWGLSSSEISTPYNRQVERA 239

Thu Mar 10 14:26:05 2005

[illegible]

Search completed: March 9, 2005, 18:08:17
Job time : 73.6029 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds
(without alignments)
4539.261 Million cell updates/sec

Title: US-10-019-823B-56
Perfect score: 3762
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELPEIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3743	99.5	719	1 C1IA_BACTK	Q45752 bacillus th
2	3743	99.5	719	2 Q6X181	Q6x181 bacillus th
3	3738	99.4	719	2 Q93NJ5	Q93nj5 bacillus th
4	3737	99.3	719	2 O85796	O85796 bacillus th
5	3608	95.9	719	2 O8KV61	O8kv61 bacillus th
6	3534	93.9	719	2 Q9F0P8	Q9f0p8 bacillus th
7	3503	93.1	719	1 C1IB_BACTE	Q45709 bacillus th
8	3380	89.8	719	1 C1ID_BACTU	Q9xdl1 bacillus th
9	3379	89.8	719	1 C1IC_BACTU	O87404 bacillus th
10	2437.5	64.8	1229	1 C1BB_BACTU	Q45739 bacillus th
11	2437.5	64.8	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2263.5	60.2	1228	2 Q93T75	Q93t75 bacillus th
13	2262.5	60.1	1228	1 C1BA_BACTK	P05517 bacillus th
14	2254.5	59.9	1228	2 Q93NM5	Q93nm5 bacillus th
15	2180.5	58.0	849	2 Q6PYW8	Q6pyw8 bacillus th
16	2103.5	58.0	1227	1 C1BE_BACTU	O85805 bacillus th
17	2101.5	55.9	1231	2 O8KNY2	O8kny2 bacillus th
18	2098.5	55.8	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
19	1979.5	52.6	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1895	50.4	381	2 Q45740	Q45740 bacillus th
21	1655.5	44.0	1157	1 C8AA_BACUK	Q45704 bacillus th
22	1643	43.7	1144	2 O8KZL7	Q8kzl7 bacillus th
23	1483	39.4	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1471.5	39.1	1169	1 C8BA_BACUK	Q45705 bacillus th
25	1469	39.0	1167	1 C1JA_BACTU	Q45738 bacillus th
26	1467.5	39.0	1166	1 C1GA_BACTU	Q45746 bacillus th
27	1467	39.0	1169	1 C1FB_BACTM	O66377 bacillus th
28	1461	38.8	1174	2 Q45749	Q45749 bacillus th
29	1452	38.6	1155	1 C1AB_BACTK	P06578 bacillus th
30	1452	38.6	1155	2 Q7BE98	Q7be98 bacillus th
31	1452	38.6	1155	2 Q9F296	Q9f296 bacillus th

RESULT 1

ID	C1IA_BACTK	STANDARD;	PRT;	719 AA.
AC	Q45752; P71092; Q45750; Q45751; Q45756;			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DB	Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin)			
DE	CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein)			
GN	Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryV1;			
OS	Bacillus thuringiensis (subsp. kurstaki)			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=29339;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSIR732;			
RX	MEDLINE=93298009; PubMed=8517758;			
RA	Gleave A.P., Williams R., Hedges R.J.;			
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes and characterization of a cryV gene cloned from B. thuringiensis subsp. kurstaki";			
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=JHCC4835;			
RX	MEDLINE=92269582; PubMed=1588820;			
RA	Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RT	"Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae";			
RL	Mol. Microbiol. 6:1211-1217(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HD-1;			
RX	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus";			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AB88;			
RX	MEDLINE=96178985; PubMed=8606196;			
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,			
RT	Craig J.A., Kozel M.G., Estruch J.J.;			
RL	"Cloning of a cryV-type insecticidal protein gene from Bacillus thuringiensis: the cryV-encoded protein is expressed early in stationary phase";			
RN	J. Bacteriol. 178:2141-2144(1996).			
RP	[5]			
RC	SEQUENCE FROM N.A.			

RA Selvapandiyar A., Bhatnagar R.K.;
RT "Isolation, cloning and expression of cryV gene."
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidomic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella and Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M98544; AAA22354.1; -
CC EMBL; X62821; CAA44633.1; -
CC EMBL; L36338; AAC36999.1; -
CC EMBL; L49391; AAB00958.1; -
CC EMBL; Y08920; CAA70124.1; -
CC PIR; I39815; I39815.
CC PIR; S25383; S25383.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
KW Spore, toxin.
FT 159 159 K -> R (in strain 61).
FT 233 233 D -> Y (in strain JHCC4835 and strain HD-
FT VARIANT 1).
FT
FT VARIANT 443 443 A -> V (in strain AB88).
FT 711 712 KQ -> NE (in strain HD-1 and strain 61).
FT
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

RESULT 2

Q6X181 ID Q6X181 PRELIMINARY; PRT; 719 AA.
AC Q6X181;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Cryl.
GN Name=cryl;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.5%; Score 3743; DB 2; Length 719;
Best Local Similarity 99.6%; Pred. No. 1.9e-251;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
SQ
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIEMHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIEMHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGDLAVYHDSLEWVGNNRNRARSVVKVQYIALELMFVKLPSPFVSG 180
DB 121 RNKALTDLKGDLAVYHDSLEWVGNNRNRARSVVKVQYIALELMFVKLPSPFVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNQVERAGDYSYHCVKWS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNQVERAGDYSYHCVKWS 240

RA Selvapandiyar A., Bhatnagar R.K.;
RT "Isolation, cloning and expression of cryV gene."
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidomic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella and Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M98544; AAA22354.1; -
CC EMBL; X62821; CAA44633.1; -
CC EMBL; L36338; AAC36999.1; -
CC EMBL; L49391; AAB00958.1; -
CC EMBL; Y08920; CAA70124.1; -
CC PIR; I39815; I39815.
CC PIR; S25383; S25383.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
KW Spore, toxin.
FT 159 159 K -> R (in strain 61).
FT 233 233 D -> Y (in strain JHCC4835 and strain HD-
FT VARIANT 1).
FT
FT VARIANT 443 443 A -> V (in strain AB88).
FT 711 712 KQ -> NE (in strain HD-1 and strain 61).
FT
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.5%; Score 3743; DB 1; Length 719;
Best Local Similarity 99.6%; Pred. No. 1.9e-251;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
SQ
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIEMHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIEMHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGDLAVYHDSLEWVGNNRNRARSVVKVQYIALELMFVKLPSPFVSG 180
DB 121 RNKALTDLKGDLAVYHDSLEWVGNNRNRARSVVKVQYIALELMFVKLPSPFVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNQVERAGDYSYHCVKWS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNQVERAGDYSYHCVKWS 240
QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFSDYDTQMPYPIKTAQLTREYTDAL 300
DB 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFSDYDTQMPYPIKTAQLTREYTDAL 300
QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420

Qy	241	TGLNNLRGTTNAESWVRYNQFRDMLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
Db	241	TGLNNLRGTTNAESWVRYNQFRDMLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
Qy	301	GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTTIYLLSRWSNTQYNNMW	360
Db	301	GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTTIYLLSRWSNTQYNNMW	360
Qy	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR	420
Db	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR	420
Qy	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Qy	481	ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Qy	541	TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600
Db	541	TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600
Qy	601	TFRTVGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV	660
Db	601	TFRTVGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV	660
Qy	661	TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDFFYLDEKRELFEIVKYANLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDFFYLDEKRELFEIVKYANLHIERNM	719
RESULT 3			
Q93NJ5 PRELIMINARY; PRT; 719 AA.			
ID	Q93NJ5		
AC	Q93NJ5;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	CryIIa.		
GN	Name=cryIIa;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Song F., Zhang J., Gu A., Huang D., Li G.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF373207; AAK6742.1; -.		
DR	HSSP; P02965; 1CIY.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;		
Query Match 99.4%; Score 3738; DB 2; Length 719;			
Best Local Similarity 99.4%; Pred. No. 4.1e-251;			
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0			
Qy	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFVSASTI	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFVSASTI	60
Qy	61	QTGIGIAGKILGTGVPPAGQVASLYSFLIGELWPKGNQKQWEIFMEHVEEIIINQKISTYA	120

Db	61	QTGIGIAGKILGTGVPPAGQVASLYSFLIGELWPKGNQKQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLRLGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG	180
Db	121	RNKALTDLRLGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG	180
Qy	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS	240
Db	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS	240
Qy	241	TGLNLRGTTNAESWVRYNQFRDMLMVLDLVALFPSYDTOMYPKTTAQLTREVTDAI	300
Db	241	TGLNLRGTTNAESWVRYNQFRDMLMVLDLVALFPSYDTOMYPKTTAQLTREVTDAI	300
Qy	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWNTQYNNMW	360
Db	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWNTQYNNMW	360
Qy	361	GGHKLFRITGGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR	420
Db	361	GGHKLFRITGGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR	420
Qy	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Qy	481	ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Qy	541	TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600
Db	541	TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600
Qy	601	TFRTVGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV	660
Db	601	TFRTVGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV	660
Qy	661	TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDFFYLDEKRELFEIVKYANLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDFFYLDEKRELFEIVKYANLHIERNM	719
RESULT 4			
O85796	PRELIMINARY; PRT; 719 AA.		
ID	O85796		
AC	O85796;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Insecticidal protein.		
GN	Names=cryWI01;		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OG	Plasmid large plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=S101;		
RA	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF076953; AAC26910.1; -.		
DR	HSSP; P02965; 1CIY.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		

Tue Feb 15 10:07:53 2005

KW Plasmid. 719 AA; 81230 MW; 42746DA78359BBA7 CRC64;
SQ SEQUENCE
Query Match 99.3%; Score 3737; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 4.8e-251;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHHEDCLKMSYENVEPFFVASTI 60
1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHHEDCLKMSYENVEPFFVASTI 60
61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVQKLPFAVSG 180
121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVQKLPFAVSG 180
181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300
241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
541 TGTGDIRVNIKPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
541 TGTGDIRVNIKPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
601 TFRVTGFTTTPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDEKAQEKV 660
601 TFRVTGFTTTPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDEKAQEKV 660
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 5
Q8KY61 PRELIMINARY; PRT; 719 AA.
ID Q8KY61
AC Q8KY61
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE CRY.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278797; AAM73516.1; -
DR PIR; B42459; B42459.

HSP; P02965; 1CIV.
GO; GO:0005102; Fireceptor binding; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_N.
InterPro; IPR005639; endotoxin_C.
InterPro; IPR008979; Gal bind like.
Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;
Query Match 95.9%; Score 3608; DB 2; Length 719;
Best Local Similarity 95.8%; Pred. No. 4.5e-242;
Matches 689; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHHEDCLKMSYENVEPFFVASTI 60
1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHHEDCLKMSYENVEPFFVASTI 60
61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVQKLPFAVSG 180
121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVQKLPFAVSG 180
181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300
241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
541 TGTGDIRVNIKPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
541 TGTGDIRVNIKPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
601 TFRVTGFTTTPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDEKAQEKV 660
601 TFRVTGFTTTPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDEKAQEKV 660
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 6
Q9F0P8 PRELIMINARY; PRT; 719 AA.
ID Q9F0P8
AC Q9F0P8; (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)


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QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLGLDALAVYHDSLESWGNRNTRARSVKQSOYIALELMFVKQLPSPAVSG 180
Db 121 RNKALSDRLGLDALAVYHDSLESWGNRNTRARSVKQSOYIALELMFVKQLPSPAVSG 180
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISFYNNQVERAGDYSYHCVKWSY 240
Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISFYNNQVERAGDYSYHCVKWSY 240
QY 241 TGLNLRGTNAESWVRNQFRDMLMVLVDLVALPSPYDQMPYIKTTAQLTREYVYDAI 300
Db 241 TGLNLRGTNAESWVRNQFRDMLMVLVDLVALPSPYDQMPYIKTTAQLTREYVYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMMNW 360
QY 361 GGHKLEFRTIGTNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKVYVSWTHRSADRTNTPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540
Db 481 ASHKVYVSWTHRSADRTNTPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
QY 601 TFRVTGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Db 601 TFRVTGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSDEFFYLDEKRELFELVYKYNELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSDEFFYLDEKRELFELVYKYNELHIERNM 719

RESULT 8
CLID BACTU STANDARD; PRT; 719 AA.
ID CLID BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Names=cryIId; Synonyms=cryII(d), NRcryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RX MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
RT gene.";
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae. Active on Plutella
CC xylostella and on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

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terminus.
-!- SIMILARITY: Belongs to the delta endotoxin family.
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or send an email to license@isb-sib.ch).
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EMBL; AF047579; AAD44366.1; -.
HSSP; P02965; 1CIY.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 89.8%; Score 3380; DB 1; Length 719;
Best Local Similarity 89.4%; Pred. No. 3.2e-226;
Matches 643; Conservative 36; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLNQDKHOSFSSNAKVDKISTDSLKNETDIELQINIHEDCLMKSEYENVEPFFVSASTI 60
Db 1 MKLNQDKHOSFSSNAKVDKISTDSLKNETDIELQINIHEDCLMKSEYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLGLDALAVYHDSLESWGNRNTRARSVKQSOYIALELMFVKQLPSPAVSG 180
Db 121 RNKALTDLGLDALAVYHDSLESWGNRNTRARSVKQSOYIALELMFVKQLPSPAVSG 180
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISFYNNQVERAGDYSYHCVKWSY 240
Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISFYNNQVERAGDYSYHCVKWSY 240
QY 241 TGLNLRGTNAESWVRNQFRDMLMVLVDLVALPSPYDQMPYIKTTAQLTREYVYDAI 300
Db 241 TGLNLRGTNAESWVRNQFRDMLMVLVDLVALPSPYDQMPYIKTTAQLTREYVYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMMNW 360
QY 361 GGHKLEFRTIGTNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKVYVSWTHRSADRTNTPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540
Db 481 ASHKVYVSWTHRSADRTNTPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
QY 601 TFRVTGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Db 601 TFRVTGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSDEFFYLDEKRELFELVYKYNELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSDEFFYLDEKRELFELVYKYNELHIERNM 719

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Db 661 TAMFTSTNLRKTNVTDCHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQNIERNM 719

RESULT 9
CLIC_BACTU
ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidial crystal protein cryIIc (Insecticidal delta-endotoxin)
DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C18 / Egypt;
RA Osman Y.A., Makkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF056933; AAC62933.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR KQ Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B8905DFF CRC64;

Query Match 89.8%; Score 3379; DB 1; Length 719;
Best Local Similarity 89.7%; Pred. No. 3.8e-226;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQINIHEDCLKMSEYENVEPFVASTI 60
Db 1 MCLKNPDKHQTLSSNAKVDKIATSLKNETDIELKNMNEIDYLRMSEHSIDPFVASTI 60

QY 61 QTGIGIAGKILGTGLVPPAGQVASYSLFTLGLWPKGNQKQWEIFMEHVEEINQKISTYA 120
Db 61 QTGIGIAGKILGTGLVPPAGQVASYSLFTLGLWPKGNQKQWEIFMEHVEEINQKISTYA 120

QY 121 RNKALTDLKGLGDALAVYHDSLESWGNNRNNRARSVVVKSQYIALELMFVQKLPSFAVSG 180
Db 121 RNKALTDLKGLGDALAVYHDSLESWGNNRNNRARSVVVKSQYIALELMFVQKLPSFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSHCVKQWYS 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSHCVKQWYN 240

QY 241 TGLNNLRGTNAESWRYNQFRDQVSNLVESLSDEFYLDKRELFEIVKYAKQNIERNM 719

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Db 241 TGLNNLRGTNAESWRYNQFRDQVSNLVESLSDEFYLDKRELFEIVKYAKQNIERNM 719
QY 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
Db 301 GTVDPNQALRSTTWYNNNAPSFAIAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTINI STOGSTNTSINPVTLPSTSDVYRTESLAGNLFLTPQVNGVPR 420
Db 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLPSTSDVYRTESLAGNLFLTPQVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGFGTGGDILRRTN 540
Db 481 GSHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGFGTGGHILRRTK 540
QY 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 SGTFGHIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAYEYDFEKAQEKV 660
Db 601 TFRVTGFTTTPPSFLDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAYEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQNIERNM 719
Db 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQNIERNM 719

RESULT 10
C1BB_BACTU
ID C1BB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidial crystal protein cryIbB (insecticidal delta-endotoxin)
DE CryIb(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbB; Synonyms=cryET5, cryIb(b);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.

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Qy 543 TFGDIRVNIWPPFAQRYRVRIRYASTTDIQFHTSINGKAINQGNFSATMNRGDDLDYKTF 602
Db 541 TFGDIRVNIWPPFAQRYRVRIRYASTTDIQFHTSINGKAINQGNFSATMNRGDDLDYKTF 600
Qy 603 RTVGFTTTPFSLDVOSTFTTGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662
Db 601 RTAGFTSTPFNLNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFAEYDLEAQAQAVNA 659
Qy 663 LFTSTNPRGLKTDVVDYHIDQVSNLVESISDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 LFTSTNPRGLKTDVVDYHIDQVSNLVESISDEFYLDKRELFEIVKYANELHIERNM 716

RESULT 12
Q93T75 PRELIMINARY; PRT; 1228 AA.
ID Q93T75; STRAIN=HD-9;
AC Q93T75; Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name-cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.2%; Score 2263.5; DB 2; Length 1228;
Best Local Similarity 62.4%; Pred. No. 2.9e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVFSASTIQIGIGAKI 70
Db 2 TSNRKNENEINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPFAGQVASYLSFILGELMPKGNQWEIFMEHVVEEIIINQKISTYARNKALDLKG 130
Db 62 LGVLGVPPFAGQLASFSLFGLWPRGRQWEIFLEHVQQLNQIITENARTALARLQ 121
Qy 131 LGDALAVYHDSLESVGNRNTRARSVKVQXIALELMPVQKLPSFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQOLESLEDLWENRDARTSVLTHQYIALELDFLNAFLPFAIRNQEVPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKENGSLSEISFTYNNROVERAGDYSYCHVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIORYYERQVTRDYSDYCVWEYNTGLNSLRGTN 241
Qy 251 AESWRYNQFRDMLTLMVLDFPSPYDTQMPYPIKTAQLTREVYTDAGTVHPHPSFT 310
Db 242 AASWRYNQFRDLTLGVLDLVALFPSTYTRTYPINTSAQLTREVYTDAGT--GVNMA 299
Qy 311 STTWYNNAPSFAIEAAVVRNPHLLDLEQVTIVSYLLSRWSNTQYMNWGGHKLERTI 370
Db 300 SNWYNNAPSFAIEAAAIIRSPHLLDLEQVTIVSYLLSRWSNTQYMNWGGHKLERTI 359

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Qy 371 GGTNLISQSTNTSINPVTLPTTSRDYVYRTESLAGLNLF--LTQPVNGVPRVDFHMKFV 428
Db 360 GGGLNTSTHGATNTSINPVTLRFASRDYVYRTESYAGVLLWGIYLEPIHGVPTRVFN 416
Qy 429 THP-----IASDNFYYPGYAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPQNISDRGTANYSQP-YESPGQLKQSETELPPEPPERPNYESYSHRLSHIGLILQSR 475
Qy 484 VKALVYSWTHRSADRTNTIENPNSITQIPLVAFNLSSGAAVVRGPGFTGGDILRRNTGT 543
Db 476 VNVFYSWTHRSADRTNTIGPNRITQIPMKASELPQGTTVVRGPGFTGGDILRRNTGG 535
Qy 544 FGDIRVNIWPPFAQRYRVRIRYASTTDIQFHTSINGKAINQGNFSATMNRGDDLDYKTF 603
Db 536 FGVIRVTVNGPLTQRYRIGFRYASTVDFVFVSRGGTTVNFRLTNMSGDELKYGNFV 595
Qy 604 TVGFTTTPFSLDVOSTFTTGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 663
Db 596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFAEYDLEAQAQAVNA 655
Qy 664 FTSTNPRGLKTDVVDYHIDQVSNLVESISDEFYLDKRELFEIVKYANELHIERNM 719
Db 656 FTNTNPRGLKTDVVDYHIDQVSNLVESISDEFYLDKRELFEIVKYANELHIERNM 711

RESULT 13
C1BA BACTK
ID C1BA BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidial crystal protein cry1Ba (insecticidal delta-endotoxin
DE Cry1B(a)) (Crystalline entomocidic protoxin) (140 kDa crystal protein).
GN Name-cry1Ba; Synonyms=cryA4, cry1B(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; X06711; CAA29898.1; -.
CC EMBL; X95704; CAA65003.1; -.
CC PIR; S00873; S00873.
CC HSSP; P07130; 1DLC.

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DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; CB53A19FB5D98575 CRC64;

Query Match 60.1%; Score 2262.5; DB 1; Length 1228;
Best Local Similarity 62.4%; Pred. No. 3.5e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPAGQVVASLYSPILGELWPKGNQWEIFMEHVEELINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARQ 121

QY 131 LGDALAVYHDSLESVWGNRNTRARSVYKQVIALELMFVQKLPFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRDDARTSVLYTQVIALELDFNAMPLFAIRNQEVPLLMVA 181

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQETQRYRYERQVTRDYSDYCVWYNTGLNLRGTN 241

QY 251 AESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDALGTVHPHPSFT 310
Db 242 AASWRYNQFRDILTGLVLDLVALFPSYDTRYPINTSAQLTREVYTDALGAT--GVNMA 299

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKLFRFTI 370
Db 300 SMWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSAASRWSNTHMTYWRGHTIQSRPI 359

QY 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLF--LTQPVNGVPRVDFHWKFV 428
Db 360 GGGLNTSTHGATNTSINPVTLPFASRDVYRTESYAGVLLWGIYLEPIHGVTVRNF--- 416

QY 429 THP-----IASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPQNISDRGTANYSQP--YESPGLQKDSSETLPETTERPNYESYSHRLSHIGLILQSR 475

QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 543
Db 476 VNVVYVSWTHRSADRTNTIGPNRIQIIPWKASELPQGTTVVRGPGFTGGDILRRTNTGG 535

QY 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTFR 603
Db 536 FGPIRVTVNGPLTQRYRIGFRYASTVDFFVSRGGTTVANNFRFLRTMNSGDELKYGNEV 595

QY 604 TVGFTTTPSFLDVQSTFTIGAMNFFSSGNEVYIDRIEFVPVEVTEAEYDEKAQEKVTAL 663
Db 596 RRAFTTPTFTQIDIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 14
Q93NM5 ID Q93NM5 PRELIMINARY; PRT; 1228 AA.
AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry1Ba.
GN Name=cry1Ba;

OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBAJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0008952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341PB439 CRC64;

Query Match 59.9%; Score 2254.5; DB 2; Length 1228;
Best Local Similarity 62.3%; Pred. No. 1.2e-147;
Matches 446; Conservative 79; Mismatches 166; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPAGQVVASLYSPILGELWPKGNQWEIFMEHVEELINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARQ 121

QY 131 LGDALAVYHDSLESVWGNRNTRARSVYKQVIALELMFVQKLPFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRDDARTSVLYTQVIALELDFNAMPLFAIRNQEVPLLMVA 181

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQETQRYRYERQVTRDYSDYCVWYNTGLNLRGTN 241

QY 251 AESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDALGTVHPHPSFT 310
Db 242 AASWRYNQFRDILTGLVLDLVALFPSYDTRYPINTSAQLTREVYTDALGAT--GVNMA 299

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKLFRFTI 370
Db 300 SMWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSAASRWSNTHMTYWRGHTIQSRPI 359

QY 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLF--LTQPVNGVPRVDFHWKFV 428
Db 360 GGGLNTSTHGATNTSINPVTLPFASRDVYRTESYAGVLLWGIYLEPIHGVTVRNF--- 416

QY 429 THP-----IASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPQNISDRGTANYSQP--YESPGLQKDSSETLPETTERPNYESYSHRLSHIGLILQSR 475

QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT 543
Db 476 VNVVYVSWTHRSADRTNTIGPNRIQIIPWKASELPQGTTVVRGPGFTGGDILRRTNTGG 535

QY 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKTFR 603
Db 536 FGPIRVTVNGPLTQRYRIGFRYASTVDFFVSRGGTTVANNFRFLRTMNSGDELKYGNEV 595

QY 604 TVGFTTTPSFLDVQSTFTIGAMNFFSSGNEVYIDRIEFVPVEVTEAEYDEKAQEKVTAL 663
Db 596 RRAFTTPTFTQIDIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 15

Q6PYW8 PRELIMINARY; PRT; 849 AA.
AC Q6PYW8; 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Crib type crystal protein (fragment).
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI;
RA Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570734; AAS93797.1; -
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON_TER 849
SQ SEQUENCE 849 AA; 95886 MW; FCB98495787CF763 CRC64;

Query Match 58.0%; Score 2180.5; DB 2; Length 849;
Best Local Similarity 59.1%; Pred. No. 1e-142;
Matches 422; Conservative 105; Mismatches 174; Indels 13; Gaps 3;
QY 13 SSNAKVDKISTDSLKN-----ETDIEIQINIHEDCKMSEYENVEFVSASTIQTGIG 65
DB 7 NENEIINALSPAVNSHSAQWNLSTDARI-----EDSLCIAEGNNIDFVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVASYLFGELWPKGNQWEIPMEHVBEIINQKISTYARNKAL 125
DB 62 IAGRIILGVLPFAGQIASPYSLVFLGELWPRGRDPWEIFLEHVEQLIRQQVTENTRTAL 121
QY 126 TDLKGLDALAVYHDSLESWSVGNRNNTARSVKSOYIALELMPVQKLPSPFAVSGEEVPL 185
DB 122 ARLOGLNSFRAYQOSLEDWLENRDDARTSRVLTQYIALELDFLNAMPFLAIRNQEVPL 181
QY 186 LPIYQAANLHLLLRDASIFGKEWGLSSEISTFYNRQVERAGDYSYHCVKWTSTGLNN 245
DB 182 LMVYQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRYSYCARWYNTGLNN 241
QY 246 LRGTNAESWRYNQPRRDMTLMVLDLVALFPSPYDTQMYPIKTTAQLTREVVYTDAGTVHP 305
DB 242 LRGTNAESWRYNQPRRDLTGLVLDLVALFPSPYDTRVPMNTSAQLTREIYTDPIGRNTA 301
QY 306 HPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKL 365
DB 302 PSGFASTWYNNAPSAEAAVVRNPHLLDFPEQLTFISVLSRWSNTQYMNWVGHR 361
QY 366 EPRITGTLNISTQGSTNTSINPVTLPFTSRDVRTTESLAGLNLFLTOPVNGVPRVDFHW 425
DB 362 ESRTIRGSLSTSTHGNTNTSINPVTLOFTSRDVRTTESFAGINILLTTPVNGVPRVDFHW 421
QY 426 KFTVHTPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLISASHVK 485
DB 422 RNPLNSLRGSLLYTIGYTGVTQQLFDSELPETTERPERNYESYSHRLSNIRLISGNTLR 481
QY 486 ALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAADVVRGPGFTGGDILRRNTGTFG 545
DB 482 APVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAADVVRGPGFTGGDILRRNTGTFG 541
QY 546 DIRVNIINPPFAQRYRVRIRYASTTDIQFHTSINGKAINQGNFSATMNRGDLDTKTRTV 605

Db 542 SMGLNFNNTSLQYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSPRFA 601
QY 606 GFTTTPPSFLDVQSTFTIGAWNFSSGNEYIYIDRIEFVPEVETVEAEYDFEKAQEKVTALFT 665
Db 602 EFPVGISASGSQ-TAGISISNNAGROTFHFHFKIEFIPITATFEAEYDLERAEAVNALFT 660
QY 666 STNPRGLKTDVYHIDOVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 NTNPRRLKTGVTDYHIDEVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 714

Search completed: February 14, 2005, 20:40:27
Job time : 84.1112 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds
(without alignments)
3909.384 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELPEIVKYANLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3743	99.5	719	16	US-10-782-020-10
2	3743	99.5	719	16	US-10-782-141-8
3	3459.5	92.0	710	15	US-10-428-961-42
4	2263.5	60.2	1228	16	US-10-809-953-10
5	2250.5	59.8	1207	10	US-09-988-462-7
6	2171.5	57.7	1227	15	US-10-428-961-63
7	2156.5	57.3	1186	9	US-09-826-660-23
8	2101	55.8	1228	15	US-10-428-961-38
9	2101	55.8	1228	15	US-10-614-524-2
10	1923.5	51.1	643	9	US-09-826-660-25
11	1707.5	45.4	1167	14	US-10-089-678-1
12	1678.5	44.6	653	15	US-10-428-961-6
13	1655.5	44.0	1157	16	US-10-782-141-16

14	1496	39.8	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1496	39.8	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1496	39.8	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1480	39.3	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1480	39.3	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1480	39.3	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1476.5	39.2	1156	14	US-10-099-285-72	Sequence 72, Appl
21	1476.5	39.2	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1452	38.6	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1452	38.6	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1452	38.6	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1452	38.6	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1452	38.6	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1452	38.6	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1452	38.6	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1452	38.6	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1452	38.6	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1452	38.6	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1452	38.6	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1452	38.6	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1452	38.6	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1447	38.5	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1445	38.4	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1444	38.4	1177	14	US-10-102-469-24	Sequence 24, Appl
38	1428.5	38.0	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1416.5	37.7	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1416.5	37.7	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1385	36.8	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1364	36.3	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1364	36.3	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1364	36.3	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1364	36.3	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782, 020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448, 810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match	99.5%	Score 3743	DB 16	Length 719
Best Local Similarity	99.6%	Pred. No. 1e-307		
Matches 716	Conservative 1	Mismatches 2	Indels 0	Gaps 0
Qy	1	MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQININHEDCLKMSYENVEFPVFASTI	60	
Db	1	MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQININHEDCLKMSYENVEFPVFASTI	60	
Qy	61	QTGIGTAGKILGTGLGVFPAGQVASYLSYFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA	120	
Db	61	QTGIGTAGKILGTGLGVFPAGQVASYLSYFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA	120	

QY	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKQLPSFAVSG	180
DB	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKQLPSFAVSG	180
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNROVERAGDYSYHCVKWS	240
DB	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNROVERAGDYSYHCVKWS	240
QY	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI	300
DB	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI	300
QY	301	GTVPHPSTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW	360
DB	301	GTVPHPSTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW	360
QY	361	GGHKLFRITGGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFQTQVNGVPR	420
DB	361	GGHKLFRITGGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFQTQVNGVPR	420
QY	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS	480
DB	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN	540
DB	481	ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN	540
QY	541	TGTFGDIRVNIINPPPAQRYRIRYASTDLOPHTSINGKAINQGNFSAATMNRGDLGYK	600
DB	541	TGTFGDIRVNIINPPPAQRYRIRYASTDLOPHTSINGKAINQGNFSAATMNRGDLGYK	600
QY	601	TPRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV	660
DB	601	TPRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	719
DB	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.5%; Score 3743; DB 16; Length 719;			
Best Local Similarity 99.6%; Pred. No. 1e-307;			
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI	60

NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match
Best Local Similarity 92.1%; Score 3459.5; DB 15; Length 710; Indels 9; Gaps 1;
Matches 662; Conservative 16; Mismatches 32

Qy 1 MGLKQNDKQSPSSNAKVDKISTDLSLQNETDIELQNHEDCLKMSYENVEPVFASSTI 60
Db 1 MKSKQNMHQSLSNNAVDKNTGSLNNTNTELQNFH-----EGIEPVFVSSTI 51
Qy 61 QTGIGTAGKILGTLGVPFAGQVASYLSPILGELMPKGNQWEIFMEHVEEINQKISTYA 120
Db 52 QTGIGTAGKILGTLGVPFAGQVASYLSPILGELMPKGNQWEIFMEHVEEINQKISTYA 111
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRRSVVKSYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGGLDALAVYHDSLESWGNRNTRRSVVKSYIALELMFVQKLPSPFAVSG 171
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISFTYNRQVERAGDYSYHCVKMWYS 240
Db 172 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISFTYNRQVERAGDYSYHCVKMWYS 231
Qy 241 TGLNLRGCTNAESWRYNQFRDMLVLDLVALPSPDYTMQYPIKTTAQLTREVYTDAL 300
Db 232 TGLNLRGCTNAESWRYNQFRDMLVLDLVALPSPDYTMQYPIKTTAQLTREVYTDAL 291
Qy 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 351
Qy 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPR 420
Db 352 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPR 411
Qy 421 VDFHWKFTVTHIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKFTVTHIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471
Qy 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 472 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRKN 531
Qy 541 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Db 532 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 591
Qy 601 TPTVGTTPPSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
Db 592 TPTVGTTPPSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 651
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Db 652 TALFTSTNPRGLKTDVKDYHIDQVNLVSLDSDEFYLDKRELFEIVKYANLHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Botterman, Johan
APPLICANT: Van Mellaert, Herman
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match
Best Local Similarity 60.2%; Score 2263.5; DB 16; Length 1228;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNH-----EDCLKMSEYENVEPVFASSTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPEAGQVASYLSPILGELMPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPEAGQVASYLSPILGELMPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 121
Qy 131 LGDALAVYHDSLESWGNRNTRRSVVKSYIALELMFVQKLPSPFAVSGEVPVLLPIYA 190
Db 122 LGDSFRAYQOSLEDWLENRDARTRSVLHTQYIALELDFLNAFLFAIRNQEVPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKWLSSSEISFTYNRQVERAGDYSYHCVKMWYSTGLNNLRGTN 250
Db 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYERQVERTRDYSYCVHEWYNTGLNSLRGTN 241
Qy 251 AESWRYNQFRDMLVLDLVALPSPDYTMQYPIKTTAQLTREVYTDALGTVHPHPSFT 310
Db 242 AASWRYNQFRDMLVLDLVALPSPDYTMQYPIKTTAQLTREVYTDALGTAT--GVNMA 299
Qy 311 STTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMWGCHKLEFRTI 370
Db 300 SMWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMWGCHKLEFRTI 359
Qy 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPRVDFHWKFTV 428
Db 360 GGLNLTSTHATNTSINPVTLPFTSRDVRYESLAGLNLFTQPVNGVPRVDFHWKFTV 416
Qy 429 THP-----IASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPQNISDRGTANTYQSP--YESPGQLQKQSETELPETTERPNYESYSHRLSHIGLISASH 475
Qy 484 VKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 543
Db 476 VNPVYVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 535
Qy 544 PGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 603
Db 536 PGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 595
Qy 604 TVGFTTPPSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 663
Db 596 RRAFTTTPPSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 655
Qy 664 FTSTNPRGLKTDVKDYHIDQVNLVSLDSDEFYLDKRELFEIVKYANLHIERNM 719
Db 656 FTSTNPRGLKTDVKDYHIDQVNLVSLDSDEFYLDKRELFEIVKYANLHIERNM 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

Tue Feb 15 10:07:52 2005

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689

SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7
Query Match 59.8%; Score 2250.5; DB 10; Length 1207;
Best Local Similarity 64.0%; Pred. No. 5.9e-181;
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;

QY 40 EDCLKMSYENVEPFVSASTIQTGIGIAGKILGTGVFPAGQVASYLFIPLGELWPKGKN 99
DB 10 EDSLCLAEAGNNIDPFVSASTVGTGINAGRLGLVGLVPFAGQLASFYSLVGLWPRGRD 69
QY 100 QWEIFMEHVEEIIQKISTYARNKALTDLKGGLDALAVYHDSLSWVGNRNTRARSVVK 159
DB 70 QWEIFLEHVEQLINQITENARNALARQLGLGDSFRAYQOQSLDWLENRDARTSRVLY 129
QY 160 SQYALELMEFVKLPSFAVSGEEVPLLPYQAQANLHLLLRDASIFGKEWGLSSSEIST 219
DB 130 TQYIALELDFLNAPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189
QY 220 FYNQVERAGDYSYHCVKWTGCLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSSYD 279
DB 190 YERQVERTRDYSYCVIEWNTGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSSYD 249
QY 280 TQMPYIKTTAQLTREVTYDAIGTVHPHSFTSTTWTNNNAPSFAIEAAVVRNPHLLDPL 339

DB 250 TRTYPINTSAQLTREVTYDAIGAT--GVNMAWMWNNNAPSFAIEAAIRSPHLLDPL 307
QY 340 EQVTIYLLSRWSNTQYNNMGHKLBFRTIGTILNISTQGSTNTSINPVTLPSTSDVY 399
DB 308 EQLTIFSSASSRWSNTRHWTYRGHTIQSRPIGGGLTSTHGATNTSINPVTLPASRDVY 367
QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHWFVTHP-----IASDNFYPYGYAGTQLQDS 452
DB 368 RTESYAGVLLMGYILEPIHGVTVRNF--TNPNISDRGTANYSQP-YESPGQLKXDS 423
QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQPL 512
DB 424 ETELPPETTERPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQPL 483
QY 513 VKAFNLSSGAAYVRGPGTGGDILRRNTGPDIRVNINPPFAQRYVRIRYASTTDLQ 572
DB 484 VKASELPQGTTVVRGPGTGGDILRRNTGPGPIRVTVNGPLTORIGRFRYASTVDFD 543
QY 573 PHTSINGKAINQGNFSAWNRGDDLDYKTRFTVGTTPFSLDVQSTFTIGAMNFSGNE 632
DB 544 FVSRGGTTVNPFRLTWNMGDELKYGNFVRAFTTPTFTQIQDIIRTSIOGLSGNGE 603
QY 633 VYIDRIEFVEVETVYAEYDFEKAQKVTALTSTNPRGLKTDVXDYHIDQVSNLVESLS 692
DB 604 VYIDKLEIIPVTAIFAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663
QY 693 DEFYLDKRELFEIVKYANLHIERNM 719
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6

US-10-428-961-63
Sequence 63, Application US/10428961
Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Ruper, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201--1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent in version 3.2
SEQ ID NO 63
LENGTH: 1227
TYPE: PRT
ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 57.7%; Score 2171.5; DB 15; Length 1227;
Best Local Similarity 59.0%; Pred. No. 3e-174;
Matches 421; Conservative 104; Mismatches 176; Indels 13; Gaps 3;
QY 13 SSNAKVDDKISTDSLKN-----ETDIELQNIHEDCLNKESEYENVEPFVSASTIQTGIG 65
DB 7 NENEIINALSIPAVSNHSAQMLNSTDARI-----EDSLCLAEAGNNIDPFVSASTVQTGIN 61
QY 66 IAGTILGTGVFPAGQVASYLFIPLGELWPKGKNOWEIFMEHVEEIIQKISTYARNKAL 125
DB 62 IAGRLGLVGLVPFAGQIASFYSLVGLWPRGRDPWEIFLEHVEHLIRQVTTNTRDTAL 121
QY 126 TDLKGLDALAVHDSLSWVGNRNTRARSVVKSQVIALELMEFVKLPSFAVSGEEVPL 185

; NUMBER OF SEQ ID NOS: 13		
; SOFTWARE: PatentIn Ver. 2.0		
; SEQ ID NO 2		
; LENGTH: 1228		
; TYPE: PRT		
; ORGANISM: Bacillus thuringiensis		
US-10-614-524-2		
Query Match 55.8%; Score 2101; DB 15; Length 1228;		
Best Local Similarity 59.2%; Pred. No. 2.8e-168;		
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;		
QY	13	SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSYENVEPFSASTIQTGIGIAGKI 70
DB	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY	71	LGTGLVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB	67	LGVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQ 126
QY	131	LGDAVAVHDSLESVWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSAGEEVLPIYA 190
DB	127	LGDSFRAYQQSLEDWLENRDDARTSRVLYTYQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186
QY	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTSTGLNNLRGTN 250
DB	187	QAANLHLLLRDASLFGSEFGLTSQEIORYYERQVEQTRDYSYCVWYNTGLNSLRGTN 246
QY	251	AESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYTDAGT--GVNMA 310
DB	247	AASWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYTDAGT--GVNMA 304
QY	311	STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRIT 370
DB	305	SMWYNNAPSFSAIETAVIRSPHLLDFLEQVITYSLSRWSATRHTMYRGHTIQSRPI 364
QY	371	GGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNL--LTOPVNGVPRVDFHWKFV 428
DB	365	GGGLNTSTHGTNTSINPVLRSFFSRDVRVYTESYAGVLLWGIYLEPIHGVPTRFNRNP 424
QY	429	--THPIASDNFYPGYAGIGTQLODSNELPPEATQPNYESYSHRLSHIGLISASHVKA 486
DB	425	QNTFERGTANTSQP--YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISQSRVHV 483
QY	487	LVYSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTNTGTGPD 546
DB	484	PVYSWTHRSADRNTNIEPNSITQIPLVKSFLNLSGTSVSGPGFTGGDIIRTNVNGSVLS 543
QY	547	IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEBDLYKTFRTVG 606
DB	544	MGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGPSTMSANESLTSQSRFAE 603
QY	607	FTTPFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVITYEAEYDFEKAQEKVTAFTS 666
DB	604	FPVGISASGSQ--TAGISISNNAAGRTQTFHDKIEFIPITATFEAEYDLERAQEAVALFTN 662
QY	667	TNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB	663	TNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 715
RESULT 10		
US-09-826-660-25		
; Sequence 25, Application US/09826660		
; Patent No. US20010026940A1		
; GENERAL INFORMATION:		
; APPLICANT: Cardineau, Guy A.		
; APPLICANT: Stelman, Steven J.		
; APPLICANT: Narva, Kenneth E.		
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins		
; FILE REFERENCE: MA-714XC2D1		
; CURRENT APPLICATION NUMBER: US/09/826,660		
; CURRENT FILING DATE: 2001-04-05		

Query Match		55.8%; Score 2101; DB 15; Length 1228;
Best Local Similarity		59.2%; Pred. No. 2.8e-168;
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;		
Qy	13	SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPFSASTIQTGIGIAGKI 70
Db	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
Qy	71	LGTGLVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db	67	LGVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLOG 126
Qy	131	LGDAVAVHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSAGEEVPLLPIYA 190
Db	127	LGDSFRAYQQSLEDWLENRDDARTSRVLYTYQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186
Qy	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTSTGLNNLRGTN 250
Db	187	QAANLHLLLRDASLFGSEFGLTSQEIORYYERQVEQTRDYSYCVWYNTGLNSLRGTN 246
Qy	251	AESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYTDAGT--GVNMA 310
Db	247	AASWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYTDAGT--GVNMA 304
Qy	311	STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLERTI 370
Db	305	SMWYNNAPSFSAIETAVIRSPHLLDFLEQVITYSLSRWSATRHTMYRGHTIQSRPI 364
Qy	371	GGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNL--LTOPVNGVPRVDFHWKFV 428
Db	365	GGGLNTSTHGTNTSINPVLRSFFSRDVRVYTESYAGVLLWGIYLEPIHGVPTRFNRNP 424
Qy	429	--THPIASDNFYPGYAGIGTQLODSNELPPEATQPNYESYSHRLSHIGLISASHVKA 486
Db	425	QNTFERGTANYQSP--YESPGQLKDSLETLPETTERPNYESYSHRLSHIGLISQSRVHV 483
Qy	487	LVYSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTNTGTGFD 546
Db	484	PVYSWTHRSADRNTNIEPNSITQIPLVKSFLNLSGTSVSGPGFTGGDIIRTNVNGSVLS 543
Qy	547	IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEBDLYKTFRTVG 606
Db	544	MGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGPSTMSANESLTSQSRFAE 603
Qy	607	FTTPFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVITYEAEYDFEKAQEKVTAFTS 666
Db	604	FPVGISASGSQ--TAGISISNNAAGRTQTFHDKIEFIPITATFEAEYDLERAQEAVALFTN 662
Qy	667	TNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db	663	TNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 715
RESULT 9		
US-10-614-524-2		
Sequence 2, Application US/10614524		
Publication No. US20040016020A1		
GENERAL INFORMATION:		
APPLICANT: Arnaut, Greta		
APPLICANT: Boets, Anemie		
APPLICANT: Damme, Nicole		
APPLICANT: Mathieu, Eva		
APPLICANT: Vanneste, Stijn		
APPLICANT: Van Rie, Jeroen		
TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.		
FILE REFERENCE: NEWBTSUS2		
CURRENT APPLICATION NUMBER: US/10/614,524		
CURRENT FILING DATE: 2003-07-08		
PRIOR APPLICATION NUMBER: US/09/739,243		
PRIOR FILING DATE: 2000-12-19		
PRIOR APPLICATION NUMBER: 60/173387		
PRIOR FILING DATE: 1999-12-28		

FILE REFERENCE: Q68821
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: JP 2000-236140
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: PCT/JP01/06660
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1167
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-089-678-1

Query Match 45.4%; Score 1707.5; DB 14; Length 1167;
Best Local Similarity 47.6%; Pred. No. 5.5e-135;
Matches 359; Conservative 125; Mismatches 221; Indels 49; Gaps 12;
Qy 1 MSLKNDKHO---SFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYE-----NV 51
Db 1 MSPNNQNEVEILDASSSTSVSDNSVRYPLANDQTTLQNMNKKYDLRMSEGENPELFCNP 60
Qy 52 EPFVSASTIGTIGIAGKILGTGVFPAGQVASYSLFELGELMPKKG-NQWEIFMEHVEE 110
Db 61 ETFISSSTVGTIGIVGVQVLCALGVFPAGQIASFYFIVGQLWPSSTVSVMWIMKQVED 120
Qy 111 IINQKISTYARNKALTDLKGLGDALAVVHDSLESWVGNRNNTARSVVKSQYIALELMFV 170
Db 121 LIDQKITDSVRKLTALAGLQGLDGLDVYQKSLKNWLENRNDTRARSVVVYQYIALELDFV 180
Qy 171 QKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGD 230
Db 181 AKIPSPFAISQGEVPLSVYAQAANLHLLLRDASIFGAEWGFTPEGEISTFYDRQVTRTAQ 240
Qy 231 YSYHCVKWYSTGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPYSYDTQMYPIKTTAQ 290
Db 241 YSDYCVKWTNTGLDKLKGTAASWLYKHQFRREMTLLVLDLVALFPNYDTRTYPIETTAQ 300
Qy 291 LTREVVYTDALGTVHPHPSPTSTTWNNNAPSFAIAEAAVVRNPHLLDLEQVITYSLLS- 349
Db 301 LTREVVYTDPIVFNRETSGFCRRWSLNSDISFSEVESAVIRSPHLFDLSEIEFYTTTAAQ 360
Qy 350 -RWSNTQYMNWGGHKLERTIGTGLNTSTQSGTNTSINPVTLPFTSDVYTESL-AGL 407
Db 361 LPLNTEYLEYVWVGHSIKYKNTNASSALERNYGTITSNKIKYDLANKDIFQVRSLGADL 420
Qy 408 NLFLTQPVNGVRVDFHWKVFTHPIASDNFYYPGYAGTG-----TQLODSE 453
Db 421 ANYYAAQ-VYGVPIYASF-----TLDDKN---TGSGSVGGFTYSKPHMTMQVCTQNYNTI 469
Qy 454 NELPPEATGQPNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRSADRTNTIEPN 505
Db 470 DEIPPE--NEPLSRGYSHRLSHITSYFSKNASSPARYGNLPFAWTHRSADVTNTVYSD 527
Qy 506 SITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNIINPPFAQRYRIRY 565
Db 528 KITQIPVKAHTLVSGTTVIKPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRIRY 587
Qy 566 ASTTDLQFHTSINGKAINQNFSAATMNRGDDLYKTFRTVFTTFFSLDVGSTFTTGAW 625
Db 588 ASTTNLRLFTVITSGTRIYSINVNKTMKGDDLTFTNTFDLATIGTATFTSYNSDSLTVGAD 647
Qy 626 NFSSNGEVYIDRIEFPVPEVTEYAEYDFEKAQEKVATLTSTNPRGLKTDVKDYHIDQVS 685
Db 648 SFASGGEVYVDKFEIIPVNATFEAEEDLDVAKKAVNGLUFTSKD-ALQTSVTDYQVNOQA 706
Qy 686 NLVESLSDEFYLDKEKRELFVVKYANLHIERNM 719
Db 707 NLVECLSDLEYPNEKRMMLWDVAKKRLVQARNL 740

RESULT 12

PRIOR APPLICATION NUMBER: 09/178,252
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 643
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25
Query Match 51.1%; Score 1923.5; DB 9; Length 643;
Best Local Similarity 57.5%; Pred. No. 1.1e-153;
Matches 370; Conservative 100; Mismatches 160; Indels 13; Gaps 3;
Qy 13 SSNAKVDKISTDSLKN-----ETDIELQNHEDCLKXSEYENVEPVFVASTIQTGIG 65
Db 7 NENEIINALSIPAVSHSAQNLSTDAI-----EDSLCIAEGNNIDFVSASTVQTGIN 61
Qy 66 IAGKILGTGVFPAGQVASYSLFELGELWPKKNOWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGRIILGVLPFPAGQIASFYSLFELGELWPRGPDPWEIPLHEVQELRIQQVNTERTDAL 121
Qy 126 TDLKGLGDALAVVHDSLESWVGNRNNTARSVVKSQYIALELMFVQKLPSFAVSGEEVPL 185
Db 122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSVLTQYIALELDFNAMPLFAIRNQEVPL 181
Qy 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSYHCWKYSTGLNN 245
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEKREYSYCARWYNTGLNN 241
Qy 246 LRGTNAESWVRYNQFRDRTLMLVDLVALFPYSYDTQMYPIKTTAQLTREVVYTDALGTVHP 305
Db 242 LRGTNAESWLRYNQFRDRTLGLVDLVALFPYSYDTRVYPMNTSAQLTREIYTDPIGRNTA 301
Qy 306 HPSFTSTTWNNNAPSFAIAEAAVVRNPHLLDLEQVITYSLLSRWSNTQYMNWGGHKL 365
Db 302 PSGFASTWNNNAPSFAIAEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNWVGHRL 361
Qy 366 EFTTIGTGLNTSTQSGTNTSINPVTLPFTSRDVYTESLAGNLFLTOPVNGVRVDFHW 425
Db 362 ERTIRGSLTSTHGTNTSINPVTLOFTSRDVYTESFAGINILLTTPVNGVFWPARNW 421
Qy 426 KFWTHPIASDNFYYPGYAGITQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 485
Db 422 RNPLSLRGSLLYTYGTGVTQQLDFDSETELPPTTERPENYESYSHRLSNIRLISGNTLR 481
Qy 486 ALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFG 545
Db 482 APVYSWTHRSADRTNIESSDITQIPLVKSFLNSGTSVVGPGFTGGDIIRTNVNGSVL 541
Qy 546 DIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMNRGDDLYKTFRTV 605
Db 542 SMGLNFNTSLQRYRVRVYAAQTWVLRVTVGSTTFDQGFPSMTSANSLSQSFRPA 601
Qy 606 GTTTPPSFLDQSTFTIGAWNFSSNGEVYIDRIEFPVPEVTEY 648
Db 602 EFPVGISASGQ-TAGISISNAGRQTFHFDKIEFIPITATLE 643
RESULT 11
US-10-089-678-1
Sequence 1, Application US/10089678
Publication No. US20030017967A1
GENERAL INFORMATION:
APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR FILING DATE: 2000-09-13
; PRIOR FILING DATE: 2000-09-13
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 44.6%; Score 1678.5; DB 15; Length 653;
Best Local Similarity 51.5%; Pred. No. 6.4e-133;
Matches 346; Conservative 105; Mismatches 174; Indels 47; Gaps 14;

QY 13 SSNAKVDKISTDSIKN---ETDIELQINHEDCMKSEYENVEPFVSASTIQTGIGIAGK 69
Db 2 NENEIINALSIPAVNSHAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINIAGR 60

QY 70 ILGTLGVPPAGQVASYLGFILGELWPKQKQWEIFMEHVEEIIINQKISTYARNKALTDLK 129
Db 61 ILGVLGVPPAGQVASYLGFILGELWPKQKQWEIFMEHVEEIIINQKISTYARNKALTDLK 120

QY 130 GLGDALAVTHDSLESVWGNRNTRARSVVKSQYIALELMFVQKLSFAVSGEEVPLLPY 189
Db 121 GLGRGYRSYQQALETWLDNRDARSRIILERYVALELDITTAIPLFIRNEEVLLMVY 180

QY 190 AQANLHLLLRDASIFGKWLSSSEISTFYNNQVERAGDYSHCVKMYSTGLNNLRGT 249
Db 181 AQANLHLLLRDASLFSSEWMASSDVNQYQEQRYTEYSNHCVQWNTGLNNLRGT 240

QY 250 NAESWVRYNQFRDMLTMVLDLVALFPSTYDQMPYPIKTTAQLTREYVTDAGTVHPHPSF 309
Db 241 NAESWVRYNQFRDMLTMVLDLVALFPSTYDQMPYPIKTTAQLTREYVTDAGTVHPHPSF 300

QY 310 TSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLRSWNTQYMNWGGHKLFRPT 369
Db 301 ASTWNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLRSWNTQYMNWGGHKLFRPT 360

QY 370 IGGTLNISTQGST-NTSINPVTLPF-TSRDVRVYTESLAGNLFLLTPQVNGVPRVDFHWKF 427
Db 361 IGGTLNISTQGST-NTSINPVTLPF-TSRDVRVYTESLAGNLFLLTPQVNGVPRVDFHWKF 418

QY 428 VTHPIASDNFYYP-----GYAGIGTQLODSLENELPPEATGQPNYESYSHRSLSHIG-- 477
Db 419 ITLRFMKAPLPTVNRITRELGNLYLQKLNHYQK-----QQNDQIMNHIVDISVR 470

QY 478 LISASHVXKALVYSWTHRSADRTNTIEPNSITQIPVKAFNLSGGAAVVRGPGFTGGDILR 537
Db 471 LIIGNTLRAPVYSWTHRSADRTNTIEPNSITQIPVKAFNLSGGAAVVRGPGFTGGDILR 529

QY 538 -RTWGTGF---GDIRVNTN-PPFAQRVVRIRYASTTDLOPHTSINGKAINQGNFSAWN 592
Db 530 LNRNNGNIQNRGYIEVPTQFTSTSTRVVRVRYASVTSIELNVNLGNSSIFTNTIPATAA 589

QY 593 RGEDLDYKTFRTVGFTTTPFSLDVQSTFT-----IGAWNFSNGNEVYIDRIEFVPEVT 646
Db 590 SLDLNQ-----SGDFGYVEINNAFTSATGNI VGARNFSAEVIIDRFEPVPTAT 640

QY 647 YEAEYDFEKAQE 658
Db 641 FEVEYDLERAQK 652

RESULT 13
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match 44.0%; Score 1655.5; DB 16; Length 1157;
Best Local Similarity 48.8%; Pred. No. 1.4e-130;
Matches 369; Conservative 97; Mismatches 233; Indels 57; Gaps 18;

QY 1 MKLKNQKHQSFSNAKVDKISTDS---LKNETDIELQINHEDCMKSEYE-----N 50
Db 1 MSFNNQNEYEIIDATPST-SVSSDSNRYPFANEPTDALQNNYKDYLYKMSGGENPELFGN 59

QY 51 VEPFVSASTIQTGIGIAGKILGTGVFPAGQVASYLGFILGELWP-KGKNQWEIFMEHVE 109
Db 60 PETFISSTIQTGIGIAGKILGTGVFPAGQVASYLGFILGELWP-KGKNQWEIFMEHVE 119

QY 110 EIINQKISTYARNKALTDKGLGDALAVTHDSLESVWGNRNTRARSVVKSQYIALELMF 169
Db 120 ELVDQKIEKYVKDKALAEKGLGNALDVYQQSLEDWLENRDARTSRVSVNQFTALDLNF 179

QY 170 VQKLPSFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEISTFYNNQVERAG 229
Db 180 VSSIPSAVSGEEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEISTFYNNQVERAG 239

QY 230 DYSYHCVKMYSTGLNNLRGTNAESVVRYNQFRDMLTMVLDLVALFPSTYDQMPYPIKTTA 289
Db 240 EYSDYCVKMYKIGLDKLGKTTSKSWLNHYQFRREMTELLVLDLVALFPNYDTHMYPIETTA 299

QY 290 QLTREVTDAIGTVHPHPSFTST---TWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIY 345
Db 300 QLTREVTDAIGTVHPHPSFTST---TWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIY 355

QY 346 SLLSR-----WSNTQYMNWGGHKLFR-----TIGTLNISTQGSTNTSINPVTLPFTSR 396
Db 356 T--SRGGITLNDAYINYSWGHITLKYRTADSTVITYTANYGRITSEKNS-----PALEDR 408

QY 397 DVYRTESLAGNLFLLTPQVNGVPRVDFHWKFVTHPIASDNFY-----YPGYAGTQLOQD 451
Db 409 DIFEINSTVANLANYQKAYGVPGSMFH--NVKRGTSSTTAYLYSKTHTALQGC-TQVYE 465

QY 452 SENELPPEATGQPNYESYSHRSLSHI-----GLISASHVXKALVYSWTHRSADRTNTIE 503
Db 466 SSDEIPDLRT-VFVAESYSHRSLSHITSHSFSKNG--SAYGSPFPVFWTHTSADLNTIY 522

QY 504 PNSTIQIPVKAFNLSGGAAVVRGPGFTGGDILRNTNTGTFGDIRVNTNPPFAQRVVR 563
Db 504 PNSTIQIPVKAFNLSGGAAVVRGPGFTGGDILRNTNTGTFGDIRVNTNPPFAQRVVR 563


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Db 523 SDKITOIPAVKGMVLYGSSVVGQPGFTGGDILKRTNPISILGTFAVTWNGSLSQRYRVI 582
Qy 564 RYASTTDLOFHTSINGKAINQGNFSATMNRGEDIYKTFRTVGTTPFSLDVQSTFTIG 623
Db 583 RYASTTDFEF-TLYLGDITIKNRFNKTMONGASLTYYEFKFPASFITDFQFRETQDKILLS 641
Qy 624 AWFSSGNEVYIDRIEFVPEVVEAEYDFEKAQEKVTALFTSTNPRGLKTDVQYHIDQ 683
Db 642 MGFSSGQEVYIDRIEFIPVDETYEAEQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700
Qy 684 VSNLVESLSEFYLDEKRELFEIVKYANLHIERNM 719
Db 701 AANLVESLSDLLYPNEKRLIFDAVREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 39.8%; Score 1496; DB 13; Length 1206;
Best Local Similarity 44.1%; Pred. No. 4.8e-117;
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFANEPTNALQNMVDYKYLKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVAVSLYSFILGELWPKG-KNWEIFMEHV 108
Db 60 PEVLVSGQDAAKAIDIVGKLLSGLGVFPVPIVSLYTLQIDILWPSGKESQWEIFMEQV 119
Qy 109 EEIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNPGRALDRVRNRFELDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERA 228
Db 180 FTQYMPFSFRVTNFEVPLFTVYAMAANLHLLLRDASIFGEEWGSTTTNNYDRQMKLT 239
Qy 229 GDYSYHCVKWTSTGLNNLRGNAESWVRNQFRDMTLMVLDLVALFSPSYDTQYPIKTT 288
Db 240 AEYSDHCVKYETGLAKLKGTSAKQWVDYVQFRREMTLAVLDVVALFPNYDTRTPMETK 299
Qy 289 AQLTREYVTDAGTVPHPSTSTTWYNNNAPSFAIEAAVRNPHLLDFLEQVITYSLL 348
Db 300 AQLTREYVTDPLGAVNV---SIGSWY-DKAPSGFVIESVIRPHVFDYITGLTVTQTS 355
Qy 349 SRWSNTQYMMWGGHKLFRITGGTTLNISTQGSTNTSINPV-TLPFTGRDVRVYTESLAGL 407
Db 356 RSISSARYIRHWAGHQISYHRVSRGSLNQMYGTQNQLHSTSTFDTNYDIYKTLKSDAV 415
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Qy 408 NLFLTOP-----VNGVPRVDFHMKFVTHPIASDN---FYYPGVAGIGTQLODSENELPPE 459
Db 416 LLDIVYPGVGYIIFGMEPEF---FMVNQLNTRKTLKYNPVSKDIIASTRDSLELPE 472
Qy 460 ATGPQNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKAF 516
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVPSWTHRSADLNNITYSDKITQIPAVKCW 532
Qy 517 NLSSGAAVRGPFGTGGDILR-RTNTGTFGDI---RVNINPPFAQRYVRIRYASTTDLQ 572
Db 533 DNLPRVPVVGPGHGTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIV 592
Qy 573 FHTSINGKAINQGNFSATMNRGEDIYKTFR-----TVGFTTTPFSFL-----DVQST 619
Db 593 LH--VNDQI---QMPKTMNPGEDLTSKTFKVADAITLNLATDSSLALKHNLGEPNST 647
Qy 620 FTIGAWNFSNGNEVYIDRIEFVPEVVEAEYDFEKAQEKVTALFTSTNPRGLKTDVQDY 679
Db 648 LS-----GIVYVDRIEFIPVDETYEAEQDLAAKAVNALFTNTKD-GLRPGVTDY 697
Qy 680 HIDQVSNLVESLSEFYLDEKRELFEIVKYANLHIERNM 719
Db 698 EVNQAAANLVESLSDLLYPNEKRLIFDAVREAKRLSEARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 39.8%; Score 1496; DB 14; Length 1206;
Best Local Similarity 44.1%; Pred. No. 4.8e-117;
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFANEPTNALQNMVDYKYLKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVAVSLYSFILGELWPKG-KNWEIFMEHV 108
Db 60 PEVLVSGQDAAKAIDIVGKLLSGLGVFPVPIVSLYTLQIDILWPSGKESQWEIFMEQV 119
Qy 109 EEIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNPGRALDRVRNRFELDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERA 228
Db 180 FTQYMPFSFRVTNFEVPLFTVYAMAANLHLLLRDASIFGEEWGSTTTNNYDRQMKLT 239
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds
(without alignments)
2403.590 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELPEIVKYANLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3739	99.4	719	3	US-08-286-870A-8
2	3459.5	92.0	710	4	US-09-661-322A-42
3	3389	90.1	648	3	US-08-286-870A-4
4	3379	89.8	719	2	US-09-003-217-2
5	3374	89.7	719	3	US-09-218-942-2
6	2795	74.3	535	3	US-08-286-870A-6
7	2437.5	64.8	1229	1	US-08-100-709-4
8	2437.5	64.8	1229	1	US-08-176-865-4
9	2437.5	64.8	1229	1	US-08-474-038-4
10	2437.5	64.8	1229	2	US-08-779-046-4
11	2437.5	64.8	1229	2	US-08-881-340-4
12	2335.5	62.1	488	1	US-08-448-170-10
13	2335.5	62.1	488	3	US-08-961-803-10
14	2250.5	59.8	1207	1	US-07-951-715A-7
15	2250.5	59.8	1207	2	US-08-459-448A-7
16	2250.5	59.8	1207	3	US-08-459-505A-7
17	2250.5	59.8	1207	3	US-08-459-504B-7
18	2250.5	59.8	1207	3	US-08-459-444-7
19	2250.5	59.8	1207	3	US-09-053-549-8
20	2250.5	59.8	1207	3	US-09-547-422-7
21	2250.5	59.8	1207	4	US-09-988-462-7
22	2249.5	59.8	1227	3	US-09-053-549-2
23	2180.5	58.0	1227	1	US-08-448-170-8
24	2180.5	58.0	1227	3	US-08-961-803-9
25	2171.5	57.7	1227	4	US-09-661-322A-63
26	2156.5	57.3	1186	3	US-09-178-252-23
27	2156.5	57.3	1186	4	US-09-826-660-23

28	2101	55.8	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1923.5	51.1	643	3	US-09-178-252-25	Sequence 25, Appl
30	1923.5	51.1	643	4	US-09-826-660-25	Sequence 25, Appl
31	1891	50.3	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1678.5	44.6	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1655.5	44.0	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1655.5	44.0	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1655.5	44.0	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1655.5	44.0	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1492.5	39.7	1176	1	US-08-257-999-2	Sequence 5, Appl
38	1483	39.4	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1483	39.4	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1483	39.4	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1483	39.4	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1483	39.4	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1483	39.4	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1476.5	39.2	1156	3	US-09-002-285-72	Sequence 72, Appl
45	1476.5	39.2	1156	4	US-09-589-477-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Query Match 99.4%; Score 3739; DB 3; Length 719;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVKLPSFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVKLPSFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 300

QY 301 GTVHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360
DB 301 GTVHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360

QY 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480

QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600

QY 601 TFRVGTFTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TFRVGTFTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661.322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)-(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match 92.0%; Score 3459.5; DB 4; Length 710;
Best Local Similarity 92.1%; Pred. No. 2.4e-301;
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;

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DB 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLIFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVKLPSFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVKLPSFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 300

QY 301 GTVHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360
DB 301 GTVHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360

QY 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480

QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600

QY 601 TFRVGTFTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
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DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 90.1%; Score 3389; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. No. 4.4e-295;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKNSEYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKNSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNKQWEIFMEHVVEIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNKQWEIFMEHVVEIINOKISTYA 120
QY 121 RNKALTDKLGIDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180
Db 121 RNKALTDKLGIDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300
Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
QY 361 GGKLEFRTIGTGLNISTQGSTNTSINPVLFTSDVYRTESLAGNLFLLTPQVNGVPR 420
Db 361 GGKLEFRTIGTGLNISTQGSTNTSINPVLFTSDVYRTESLAGNLFLLTPQVNGVPR 420
QY 421 VDFHWKFVTHPTIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPTIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGDLDYK 600
QY 601 TERTVGTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVETYE 648
Db 601 TERTVGTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVETYE 648

RESULT 4

US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.8%; Score 3379; DB 2; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.1e-294;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKNSEYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKNSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNKQWEIFMEHVVEIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNKQWEIFMEHVVEIINOKISTYA 120
QY 121 RNKALTDKLGIDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180
Db 121 RNKALTDKLGIDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

Db 181 BEVPLLPYAAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERTRDYSYHCVKWN 240
Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD 300
Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD 300
Qy 301 GTVHPHPSFTSTWYNNAPSPFSAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
Db 301 GTVDPNQALRSTTWYNNAPSPFSAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
Qy 361 GGHKLEFRTTGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRRTK 540
Db 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRRTK 540
Qy 541 TCTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 SGTFGHIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGTPPSFSDVQSTFTTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDPEKAQEKV 660
Db 601 TFRVTGTPPSFSDVQSTFTTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDPEKAQEKV 660
Qy 661 TALFTSNPRGLKTDVKDYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSNPRGLKTDVKDYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: CryII
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2
Query Match 89.7%; Score 3374; DB 3; Length 719;
Best Local Similarity 89.7%; Pred. No. 1.2e-293;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MKLKNQDKHQSFSNAKVDKISTDLSKNETDIELQNHEDCLKMEYENVEPVSASTI 60
Db 1 MKLKNPDKHQTLSSNAKVDKIATDLSKNETDIELKNNEDYLRMSHEHSDPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVASLYSIFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASLYSIFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSVIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSVIALELMFVQKLPFAVSG 180

Qy 181 BEVPLLPYAAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERTRDYSYHCVKWN 240
Db 181 BEVPLLPYAAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERTRDYSYHCVKWN 240
Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD 300
Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD 300
Qy 301 GTVHPHPSFTSTWYNNAPSPFSAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
Db 301 GTVDPNQALRSTTWYNNAPSPFSAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
Qy 361 GGHKLEFRTTGGTLNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRRTK 540
Db 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRRTK 540
Qy 541 TCTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 SGTFGHIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGTPPSFSDVQSTFTTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDPEKAQEKV 660
Db 601 TFRVTGTPPSFSDVQSTFTTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDPEKAQEKV 660
Qy 661 TALFTSNPRGLKTDVKDYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSNPRGLKTDVKDYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKOLIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.3%; Score 2795; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 6.5e-242;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEPFSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEPFSASTI 60

Qy 61 QTGIGIAGKILGTLGVFPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

Qy 121 RNKALTDLKGIGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMFVQKLPSPAVSG 180

Qy 181 BEVPLPIYAQAANLHLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 181 BEVPLPIYAQAANLHLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

Qy 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300
Db 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300

Qy 301 GTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

Qy 361 GGHKLEPRTIGTLNISTQSTNTSINPVTLPFTSRDVRATESLAGNLFLTPQVNGVPR 420
Db 361 GGHKLEPRTIGTLNISTQSTNTSINPVTLPFTSRDVRATESLAGNLFLTPQVNGVPR 420

Qy 421 VDFHWKPVTHPIASDNFYFGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHWKPVTHPIASDNFYFGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
City: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSDPDRIEDSLCVAEYNNIDPFSVASTVQTGINIAGRI 66

Qy 71 LGTLGVFPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126

Qy 131 LGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMFVQKLPSPAVSGEVEPPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIERNEEYVPLLMVYA 186

Qy 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWSYSTGLNLRGTN 250
Db 187 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWSYSTGLNLRGTN 246

Qy 251 AESWRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDIAGTVHPHPSFT 310
Db 247 AESWRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDIAGTVHPHPSFT 306

Qy 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMWGHHKLEPRTI 370
Db 307 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMWGHHKLEPRTI 366

Qy 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRATESLAGNLFLTPQVNGVPRVDFHWKPV 429
Db 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRATESLAGNLFLTPQVNGVPRVDFHWKPV 422

Qy 430 HPIASDNFYFGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTSYQPYQGVIGLFDSETELPETTERPNYESYSHRLSHIGLIS 480

Qy 483 HVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAPIVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540

Qy 543 TFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLQYKTF 602
Db 541 TFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLQYKTF 600

Qy 603 RTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVDRIEFVPEVTEYAEYDFEKAQEKVTA 662
Db 601 RTAGSTPFPFLNAQSTFTILGAQFSN-QEYVIDRVEFPVPEVTEYAEYDFEKAQEKVTA 659

Tue Feb 15 10:07:52 2005

QY 663 LFTSTNPRGLKTDVYHIDQVSNLVESLDEFYLDKRELFELVYKYNELHIERNM 719
DB 660 LFTSTNPRRLKTDVYHIDQVSNMVACLSEDFCLDEKRELFELVYKYNELHIERNL 716
RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-865-4
Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;
QY 13 SSNAKVDKISTDSKN-ETDIELQ-NINHEDECLMSEYENVEPVFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNSTQNLSPDARIEDSLCVAENVNIDPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEHVEIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGQVASYLSFILGELMPKGNQWEIFMEHVEHVEIINQKISTYARNKALTDLKG 126
QY 131 LGDALAVVHDSLSWGNRNTRARSVVKSQVIALELMFVQKLPFSFAVSGEEVPLLPYIA 190
DB 127 LGRGYSYQQALETWLDNRNDARSILERYVALEDDITPAIFRIRNEEVPLLMVYA 186
QY 191 QAAANLHLLLRDASIFGKRWGLSSSEISTFFYNQVERAGDYSYHCVKWYSTGLNLRGTN 250
DB 187 QAAANLHLLLRDASIFGKRWGLSSSEISTFFYNQVERAGDYSYHCVKWYSTGLNLRGTN 246
QY 251 AESWRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRNAPSFGA 306

DB 247 AESWRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRNAPSFGA 306
QY 311 STTWYNNAPSFAIEAAVVRNPHLLDFLEQVTTIYLLSRWSNTQYMMNMGHGLEPRTI 370
DB 307 STTWYNNAPSFAIEAAVVRNPHLLDFLEQVTTIYLLSRWSNTQYMMNMGHGLEPRTI 366
QY 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNLFLOTPVNGVPRVDFHWKFTV 429
DB 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNLFLOTPVNGVPRVDFHWKFTV 422
QY 430 HPIASDNFYYPG-----YAGIGTQLODSNELPPEATQPNYESYSHRSLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQFYQGVGIQDFDSETELPETTERPNYESYSHRSLSHIGLIGN 480
QY 483 HVKALVYSWTHRSADRTNTIENSIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
DB 481 TLRAPIVSWTHRSADRTNTIENSIQIPLVKALNLHSGVTVVGGPGFTGGDILRRNTG 540
QY 543 TFGDIRVNINPPFAORYVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDIYKTF 602
DB 541 TFGDIRVNINPPFAORYVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDIYKTF 600
QY 603 RTVGFTTFFSLDVQSTFTIGAMNFSNGNEVIDRIEFVPEVYEAEDFEKAEKQVTA 662
DB 601 RTAGSTFPFNLAQSTFTLGAQSFN-QEVYIDRVFVPAEVTFEAEYDLERAQAVNA 659
QY 663 LFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFELVYKYNELHIERNM 719
DB 660 LFTSTNPRRLKTDVYHIDQVSNMVACLSEDFCLDEKRELFELVYKYNELHIERNL 716

RESULT 9

US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVASITQIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVASTVQTGINIAGRI 66

Qy 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVPPFAGQLASFSYFLGELWPSGRDPWEIFLEHVQQLIRQQVTENTRTAIARLEG 126

Qy 131 LGDALAVYHDSLESVWGNRNTRARSVKVSKQYIALELMFVQKLPSPFVSGEVEPLPIYA 190
Db 127 LGRGVRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPLLMVA 186

Qy 191 QAAHLHLLLRDASIFGKESLSSEISITFYNRQVERAGDYSYHCVKYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEWGMASSDVNQYQEQIRYTEEYSNHCVQWYNTGLNNLRGTN 246

Qy 251 AESWRYNQFRDRLMTLMDLVALPSPDYDTQMYPIKTTAQLTREYVTDATGTVHPHPSFT 310
Db 247 AESWLYNQFRDRLTGLVDLVALPSPDYTRTYPIINTSAQLTREIYTDPIGRNAPSFGA 306

Qy 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLERTI 370
Db 307 STNWFNNAPSFSAIEAAIFRPPHLLDFPEQLTIYASRWSSTQHMNYVWGHRLNFRPI 366

Qy 371 GGTNLNSTQGST-NTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNGVPRVDFHWFVT 429
Db 367 GGTNLNSTQGLTNNTSINPVTLOFTSRDVYRTESNAGTNILFTTPVNGVPAWFENF 422

Qy 430 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRSLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQPVQGVGLPDSSETLPETTERPNYESYSHRSLSHIGLIIGN 480

Qy 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGPGFTGGDILRRNTG 540

Qy 543 TFGDIRVNPFPFAQYRVRIYASTDQLQFHTSINGKAINQGNFSAWNRGBDLDYKTF 602
Db 541 TFGDIRLNPVLSQRYRVRIYASTDQLQFTRINGTIVNIGNFSRTWNRGDNLEYSF 600

Qy 603 RTVGFTTFFSLDVQSTFTIGAMNFSNGEYVIDRIEFVPEVETYEAEYDFEKAQEKVTA 662
Db 601 RTAGFSTPFNFNAQSTFTLGAQSPSN-QEYVIDRVEFPAEVTFEAEYDLERAQKAVNA 659

Qy 663 LFTSTNPRGLTKDVKYHIDQVSNLVESLSEDFYLDKEKELFEIVKYANELHIERNM 719
Db 660 LFTSTNPRRLTKDVTYHIDQVSNMVACLSEDFCLDEKELFEIVKYAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYBET4 AND CYBET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      64.8%; Score 2437.5; DB 2; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVASITQIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVASTVQTGINIAGRI 66

Qy 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVPPFAGQLASFSYFLGELWPSGRDPWEIFLEHVQQLIRQQVTENTRTAIARLEG 126

Qy 131 LGDALAVYHDSLESVWGNRNTRARSVKVSKQYIALELMFVQKLPSPFVSGEVEPLPIYA 190
Db 127 LGRGVRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPLLMVA 186

Qy 191 QAAHLHLLLRDASIFGKESLSSEISITFYNRQVERAGDYSYHCVKYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEWGMASSDVNQYQEQIRYTEEYSNHCVQWYNTGLNNLRGTN 246

Qy 251 AESWRYNQFRDRLMTLMDLVALPSPDYDTQMYPIKTTAQLTREYVTDATGTVHPHPSFT 310
Db 247 AESWLYNQFRDRLTGLVDLVALPSPDYTRTYPIINTSAQLTREIYTDPIGRNAPSFGA 306

Qy 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLERTI 370
Db 307 STNWFNNAPSFSAIEAAIFRPPHLLDFPEQLTIYASRWSSTQHMNYVWGHRLNFRPI 366

Qy 371 GGTNLNSTQGST-NTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNGVPRVDFHWFVT 429
Db 367 GGTNLNSTQGLTNNTSINPVTLOFTSRDVYRTESNAGTNILFTTPVNGVPAWFENF 422

Qy 430 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRSLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQPVQGVGLPDSSETLPETTERPNYESYSHRSLSHIGLIIGN 480

Qy 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGPGFTGGDILRRNTG 540

```


[illegible]

127	LGRGYSYQOALETWLDNRNDARSRIILERYVALELDITTAIPLFIRINEEVPLLMYVA	186
191	QAANLHLLLRDASIFGEKWEGLSSSEISFTFNRQVERACGYSHCVKMYSTGLNNLRGTN	250
187	QAANLHLLLRDASLFGSEWGMASSDVNQYIQEIRYTEYESNHCVMQVYNTGLNNLRGTN	246
251	AESWRYNQFRDMLMVLVALPSPDYDTQMPYIKTTAQLTREYVYTDALGTVHPHPSPFT	310
247	AESWLYNQFRDRLTLGVLDLVALPSPDYDTYPIINTSAQLTREIYITDPIGRTNAPSFGA	306
311	STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMWGGHKLFRITL	370
307	STWFWNNAPSFAIEAAIFRPHLLDFPEQLTIYSSASSRWSSTQHMNYVWGHRLNFRPI	366
371	GGTLNISTQGST-NTSINPVTLPPTSRDVTYTESLAGLNLFLTPQVNGVPRVDHFKPVT	429
367	GGTLNTSTQGLTNTSINPVTLQFTSRDVTYTESNAGTNILFTTPVNGVPEWARENF----	422
430	HPIASDNFYYPG-----YAGICTQLQDSENELPPATGQPNYSESYSHRLSHIGLISAS	482
423	--INPQNIYERGATTYSQPYQGVGIQLFDSETELPPTTERPNYESYSHRLSHIGLIIGN	480
483	HYKALVYSWTHRSADRTNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNTG	542
481	TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTTVGGPGFTGGDILARTNTG	540
543	TFGDIRVNINPPFAQRYVRIRYASTDLDQHTSINGKAINQGNFSATMNRGEDLDYKTF	602
541	TFGDIRLNVLPFSQRYVRIRYASTDLDQFTTRINGTTVNIQGNFSATMNRGDNLEYSRF	600
603	RTVGFTTTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVPEVYEAEDYPEKAQEKVTA	662
601	RTAGFSTPFPFNLAQSTFTTIGAQSFSN-QEVYIDRVEFPVPAEVTTFEAYIDLERAQKAVNA	659
663	LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEBIVKANELHIERNM	719
660	LFTSTNPRLKTVDYHIDQVSNVACISDEFCLDKRELFEBKVKYAKRISDERNL	716

RESULT 12
 US-08-448-170-10
 ; Sequence 10, Application US/08448170
 ; Patent No. 5723758
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Payne, Jewel
 ; APPLICANT: Cummings, David A.
 ; APPLICANT: Cannon, Raymond J.C.
 ; APPLICANT: Narva, Kenneth E.
 ; APPLICANT: Stelman, Steve
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
 ; NUMBER OF SEQUENCES: 10
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/448,170
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/069,902
 ; FILING DATE: 01-JUNE-1993
 ; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA: US 07/759,247
;; APPLICATION NUMBER: 10
;; FILING DATE: 13-SEPT-1991
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, David R.
;; REGISTRATION NUMBER: 31,794
;; REFERENCE/DOCKET NUMBER: M/S 102D.C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (904) 375-8100
;; TELEFAX: (904) 372-5800
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 488 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-448-170-10

Query Match 62.1%; Score 2335.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 9.6e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFSASTI 60
Db 1 M KSKQNMHQSLSNATVDKNTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFIILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFIILGELWPKGQWEIFMEHVEELINOKISTYA 111

Qy 121 RNKALTDLKGDLALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWIENRNTRRSVVKSQYITLELMFVQSLPSPFAVSG 171

Qy 181 BEVPLLPYQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWSY 240
Db 172 BEVPLLPYQAANLHLLLRDASIFGKWLSDSEISTFYNRQSGKSEYSDHCVRWYN 231

Qy 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALFPSPYDTQMYPIKTTAQLTREYVTDI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMLMVLDLVALFPSPYDTQMYPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 351

Qy 361 GGHKLEFRITGTLNSTQSGTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPQVNGVPR 420
Db 352 GGHKLEFRITGTLNSTQSGTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPQVNGVPR 411

Qy 421 VDFHWKPVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS 480
Db 412 VDFHWKPVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS 471

Qy 481 ASHVKALVYSWTHRSAD 497
Db 472 ASHVKALVYSWTHRSAD 488

RESULT 13

US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

;; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jay M. Sanders
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: Florida
;; COUNTRY: USA
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/961,803
;; FILING DATE: 31-OCT-1997
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/069,902
;; FILING DATE: 01-JUNE-1993
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/759,247
;; FILING DATE: 13-SEPT-1991
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/448,170
;; FILING DATE: 23-MAY-1995
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sanders, Jay M.
;; REGISTRATION NUMBER: 39,355
;; REFERENCE/DOCKET NUMBER: M/S 102DCD1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (352) 375-8100
;; TELEFAX: (352) 372-5800
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 488 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-961-803-10

Query Match 62.1%; Score 2335.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 9.6e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFSASTI 60
Db 1 M KSKQNMHQSLSNATVDKNTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFIILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFIILGELWPKGQWEIFMEHVEELINOKISTYA 111

Qy 121 RNKALTDLKGDLALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWIENRNTRRSVVKSQYITLELMFVQSLPSPFAVSG 171

Qy 181 BEVPLLPYQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWSY 240
Db 172 BEVPLLPYQAANLHLLLRDASIFGKWLSDSEISTFYNRQSGKSEYSDHCVRWYN 231

Qy 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALFPSPYDTQMYPIKTTAQLTREYVTDI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMLMVLDLVALFPSPYDTQMYPIKTTAQLTREYVTDI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 351

QY 361 GGHKLEPTIGTNTSTQSTNTSINPVTLPFTSRDVTYRTESLAGLNLFLTQPVNGVPR 420
DB 352 GGHKLEPTIGTNTSTQSTNTSINPVTLPFTSRDVTYRTESLAGLNLFLTQPVNGVPR 411
QY 421 VDFHWKFTHTPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 412 VDFHWKFTHTPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471
QY 481 ASHVKALVYSWTHRSAD 497
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

Query Match 59.8%; Score 2250.5; DB 1; Length 1207;

Best Local Similarity 64.0%; Pred. No. 1.8e-192;
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;
QY 40 EDCLKMBEYENVEPFVSASITQTGIGIAGKILGTLPVPAGQVAVSLYFILGELWPKGN 99
DB 10 EDSLCIABGNIDPPFVSASITQTGIGIAGKILGTLPVPAGQVAVSLYFILGELWPKGN 69
QY 100 QWEIFMEHVEEINQKISTYARNKALTDLKGDLAVYHDSLESWGNRNTRARSVVK 159
DB 70 QWEIFLEHVEQLINQITENARNTALRQGLGDSFRAYQQSLDLEWNRDARTSRVLY 129
QY 160 SQYIALELMFVQKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST 219
DB 130 TQYIALELDLFNAMPFLFAIRNQEVPFLMVYAQAANLHLLLRDASLFGSEFGLTSEIQR 189
QY 220 FYNQVERAGDYSYHCVKMYSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSPYD 279
DB 190 YYERQVTRDYSYCVWEYNTGLNSURGTNAESWVRYNQFRDMLTGLVLDLVALFPSPYD 249
QY 280 TQYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFL 339
DB 250 TRTPINTSAQLTREVTDAIGAT--GVNMAAMNWNNAAPSFSAIEAAIRSHLLDFL 307
QY 340 EQVTIYSLRSWNTQYNNMGCHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTY 399
DB 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDVTY 367
QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFTVTHP-----IASDNFYYPGYAGIGTQLODS 452
DB 368 RTESYAGVLLWGIYLEPIHGVTVRNF--TNPQNISDRGTANYSQP-YESPGIQLKDS 423
QY 453 ENELPPEATQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPL 512
DB 424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTEPNSITQIPM 483
QY 513 VKAFNLSSGAAVVRGPGFTGGDIILRRNTGTGDIRVNNINPFPFAQRYRVRIRYASTDLQ 572
DB 484 VKASELPQGTTVRGPFGFTGGDIILRRNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFD 543
QY 573 PHTSINGKAINQGNFSATWNRGDELDTKFTFTVGTFTTFFSFLDVQSTFTTIGAWNFSGNE 632
DB 544 FVVSRGGTVNNFRFLRTWNSGDELKYGNVRRRAFTTFTTQIIDIIRTSIQLSGNGE 603
QY 633 VYIDRIEFPVEVTEAEYDPEKAEKVTALFTSTNPRGLKTDVYKHIDQVSNLVESLS 692
DB 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663
QY 693 DEFYLDKRELPEIVKYANELHIERNM 719
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds
(without alignments)
2827.419 Million cell updates/sec

Title: US-10-019-823B-56
Perfect score: 3762
Sequence: 1 MLKKNQDKHQSFSSNAKVDK.....KRELFVIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3762	100.0	719	4	AAB66909 Insectici
2	3762	100.0	719	6	AAB66909 B. thurin
3	3753	99.8	719	4	AU02095 Bacillus
4	3749	99.7	719	4	AAB66911 Insectici
5	3749	99.7	719	6	AAB66911 B. thurin
6	3743	99.5	719	4	AAB66908 Insectici
7	3743	99.5	719	6	AAB66908 B. thurin
8	3743	99.5	719	8	ADR89421 cryIIa. 1
9	3741	99.4	719	2	ADR89421 81 KD end
10	3739	99.4	719	4	AAB66910 Insectici
11	3739	99.4	719	6	AAB66910 B. thurin
12	3730.5	99.2	718	6	AAB66907 Insectici
13	3724.5	99.0	718	4	AAB66907 B. thurin
14	3534	93.9	719	7	ADM74717 B. thurin
15	3503	93.1	719	4	AAB66912 Insectici
16	3503	93.1	719	6	AAB66912 B. thurin
17	3459.5	92.0	710	4	AU02041 B. thurin
18	3380	89.8	719	3	ABB07073 Bacillus
19	3379	89.8	719	2	AAM49089 Bacillus
20	3295	87.6	1217	4	AU02092 Bacillus
21	2719	72.3	1208	4	AU02093 Bacillus
22	2439	64.8	1230	8	ADK98484 B thuring
23	2439	64.8	1230	8	ADK98489 B thuring
24	2439	64.8	1230	8	ADK98481 B thuring
25	2439	64.8	1230	8	ADK98491 B thuring

26	2439	64.8	1230	8	ADK98487
27	2437.5	64.8	1229	2	AAR54074
28	2437.5	64.8	1229	2	AAW35259 Bacillus
29	2437.5	64.8	1229	2	AAW17699
30	2437.5	64.8	1229	2	AAW87633
31	2437.5	64.8	1229	2	AAW30923 B. thurin
32	2437.5	64.8	1229	8	ADK98479
33	2335.5	62.1	488	2	AAW44322
34	2335.5	62.1	488	4	AAW19947
35	2263.5	60.2	1228	2	AAR50955
36	2258.5	60.0	1209	4	AAU02094
37	2249.5	59.8	1227	4	AAW31990
38	2180.5	58.0	1227	2	AAW44321
39	2180.5	58.0	1227	4	AAB19950
40	2171.5	57.7	1227	4	AAU02046
41	2156.5	57.3	1186	2	AAW16796
42	2141.5	56.9	1221	4	AAU00421
43	2127.5	56.6	1221	4	AAU00420
44	2101	55.8	1228	4	AAB84628
45	2101	55.8	1228	4	AAU02039

ALIGNMENTS

RESULT 1
AAB66909
ID AAB66909 standard; protein; 719 AA.
AC AAB66909;
XX
DT 12-APR-2001 (first entry)
DE Insecticidal protein cryIIa3.
XX
XX Insecticide; transgenic plant; insect-resistance.
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
(ZENE) ZENECA LTD.
PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
DR Novel insecticidal protein obtained from species of Paecilomyces for
XX controlling insects, and for insect-resistant transgenic plant
production.
PT Claim 14; Page 57-59; 72pp; English.
XX
XX The present invention relates to novel insecticidal proteins obtained
from Paecilomyces sp. (see AAB66909 to AAB66901 and AAB66913). The
insecticidal proteins can be used to produce transgenic plants, which are
insect-resistant. Also, the insecticidal proteins are useful for
controlling insects by providing them at a locus where insects feed
SQ Sequence 719 AA;

Query Match 100.0%; Score 3762; DB 4; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.5e-294;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLSKNETDIELQINHEDECLKMSYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSNAKVDKISTDSLSKNETDIELQINHEDECLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPSYDTOMYPIKTTAQLTREVTYDAI 300
DB 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPSYDTOMYPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGGLTNI STQSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRITGGLTNI STQSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420
QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTFTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTTPFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
DB 601 TFRVTGFTTTPFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2
AAE36273
ID AAE36273 standard; protein; 719 AA.

AC AAE36273;
XX 26-JUN-2003 (first entry)
DT B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.
DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX Bacillus thuringiensis.
XX WO200298911-A2.
XX 12-DEC-2002.
XX 30-MAY-2002; 2002WO-GB002666.
XX 07-JUN-2001; 2001GB-00013900.
XX (SYGN) SYNGENTA LTD.

PI Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT Claim 12; Page 47-50; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX Sequence 719 AA;

Query Match 100.0%; Score 3762; DB 6; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.5e-294;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLNQDKHQSFSNAKVDKISTDSLSKNETDIELQINHEDECLKMSYENVEPVSASTI 60
DB 1 MKLNQDKHQSFSNAKVDKISTDSLSKNETDIELQINHEDECLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPSYDTOMYPIKTTAQLTREVTYDAI 300
DB 241 TGLNLRGNTNAESWVRNQFRDMLVLDLVALFSPSYDTOMYPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGGLTNI STQSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRITGGLTNI STQSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420
QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTFTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTTPFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
DB 601 TFRVTGFTTTPFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX
AC AAU02095;
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.
KW Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;
KW mutant; mutein.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Signal_peptide
FT Protein 20..719 /label= Mature_CryIIa
XX
EP1099760-A1.
XX
PD 16-MAY-2001.
XX
PF 09-NOV-1999; 99EP-00203723.
XX
PR 09-NOV-1999; 99EP-00203723.
XX
PA (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.
XX
PI De Maagd RA, Bosch HJ;
XX
DR WPI; 2001-337141/36.
DR N-PSDB; AAS04855.
XX
PT New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT domains derived from at least 2 different crystal proteins, such as
PT CryIIa and CryIIa, and having insecticidal activity, useful for combating
PT insects.
XX
PS Example; Page 30-32; 43pp; English.
XX
CC The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
CC encoding which was mutated to allow cloning of domain III or domains I
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins
CC of the invention, having structural domains I, II and III in this order
CC starting from the N-terminal derived from at least 2 different crystal
CC proteins, are useful for protecting plants against pest insects, e.g.
CC moths, butterflies and Colorado potato beetle or for combating insects
XX
SQ Sequence 719 AA;
Query Match 99.8%; Score 3753; DB 4; Length 719;
Best Local Similarity 99.7%; Pred. No. 1.9e-293;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFPSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFPSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIAELMFVQKLPSPFVSG 180
DB 121 RNKALTDKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIAELMFVQKLPSPFVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKWLSSSEISTFYNNROVERAGDYSYHCVKWS 240
DB 181 EEVPLLPYQAANLHLLLRDASIFGKWLSSSEISTFYNNROVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI 300
DB 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMW 360
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
QY 541 TGTFGDIRVNIINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEKAEQSKV 660
DB 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEKAEQSKV 660
QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQLHIERNM 719
RESULT 4
AAB66911
ID AAB66911 standard; protein; 719 AA.
XX
AC AAB66911;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa5.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
XX
PS Claim 14; Page 62-64; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are

CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
XX
SQ Sequence 719 AA;

Query Match 99.7%; Score 3749; DB 4; Length 719;
Best Local Similarity 99.7%; Pred. No. 4e-293;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMLKNDKQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFVSASTI 60
DB |||||
QY 1 MMLKNDKQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFVSASTI 60
DB |||||
QY 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB |||||
QY 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB |||||
QY 121 RNKALTDLKGDLAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKLPSPFAVSG 180
DB |||||
QY 121 RNKALTDLKGDLAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKLPSPFAVSG 180
DB |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
DB |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
DB |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREYTTDAI 300
DB |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREYTTDAI 300
DB |||||
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMNW 360
DB |||||
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMNW 360
DB |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVP 420
DB |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVP 420
DB |||||
QY 421 VDFHWKFVTHPIASDNFYPYAGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB |||||
QY 421 VDFHWKFVTHPIASDNFYPYAGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
DB |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
DB |||||
QY 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB |||||
QY 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB |||||
QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
DB |||||
QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
DB |||||
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFELVKYANELHIERNM 719
DB |||||
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFELVKYANELHIERNM 719
DB |||||

RESULT 5
AAE36275 standard; protein; 719 AA.
XX
XX
AC
XX
XX
DT 26-JUN-2003 (first entry)
XX
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.
XX
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
XX
OS Bacillus thuringiensis.
XX
XX
PN WO200298911-A2.

XX
PD
XX
XX
PF
XX
XX
XX
PR
XX
PA
XX
XX
PI
XX
XX
DR
XX
PT
XX
PS
XX
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

12-DEC-2002.
30-MAY-2002; 2002WO-GB002666.
07-JUN-2001; 2001GB-00013900.
(SYGN) SYNGENTA LTD.
Vincent JL, Viner R;
WPI; 2003-175137/17.

New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

Claim 12; Page 53-56; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Sequence 719 AA;

Query Match 99.7%; Score 3749; DB 6; Length 719;
Best Local Similarity 99.7%; Pred. No. 4e-293;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMLKNDKQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFVSASTI 60
DB |||||
QY 1 MMLKNDKQKQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKMSYENVEPFVSASTI 60
DB |||||
QY 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB |||||
QY 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB |||||
QY 121 RNKALTDLKGDLAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKLPSPFAVSG 180
DB |||||
QY 121 RNKALTDLKGDLAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKLPSPFAVSG 180
DB |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
DB |||||
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240
DB |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREYTTDAI 300
DB |||||
QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREYTTDAI 300
DB |||||
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMNW 360
DB |||||
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMNW 360
DB |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVP 420
DB |||||
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVP 420
DB |||||
QY 421 VDFHWKFVTHPIASDNFYPYAGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB |||||
QY 421 VDFHWKFVTHPIASDNFYPYAGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
DB |||||
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
DB |||||
QY 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB |||||
QY 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB |||||

Qy 601 TTRTVGTTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQSKV 660
Db 601 TTRTVGTTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQSKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
RESULT 6
AAB66908
ID AAB66908 standard; protein; 719 AA.
XX AAB66908;
AC AAB66908;
DT 12-APR-2001 (first entry)
XX Insecticidal protein cryIIa2.
DE Insecticide; transgenic plant; insect-resistance.
KW Paecilomyces sp.
OS Paecilomyces sp.
XX WO200100841-A1.
PN 04-JAN-2001.
PD 23-JUN-2000; 2000WO-GB002457.
PF 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
DR Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
PS Claim 14; Page 55-57; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;
SQ Query Match 99.5%; Score 3743; DB 4; Length 719;
Best Local Similarity 99.6%; Pred. No. 1.2e-292;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEVENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEVENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTLPVFPAGQVASYLSPILGELWPKQKQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLPVFPAGQVASYLSPILGELWPKQKQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDKGLDALAVYHDSLESWGNRNTRRSVVKSQYIALELMFVQKLPSPFVSG 180
Db 121 RNKALTDKGLDALAVYHDSLESWGNRNTRRSVVKSQYIALELMFVQKLPSPFVSG 180
Qy 181 BEVPLLPYQAANLHLLLRDASIFGKWLGLSSSEISTPYNRQVERAGDYSYHCVKWYS 240
Db 181 BEVPLLPYQAANLHLLLRDASIFGKWLGLSSSEISTPYNRQVERAGDYSYHCVKWYS 240

Qy 241 TGLNNLRGTNAESWRYNQFRDRTLMLVDLVALFPSPDYDTOMYPIKTTAQLTREYVTDAL 300
Db 241 TGLNNLRGTNAESWRYNQFRDRTLMLVDLVALFPSPDYDTOMYPIKTTAQLTREYVTDAL 300
Qy 301 GTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360
Qy 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRTVGTTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQSKV 660
Db 601 TFRTVGTTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQSKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
RESULT 7
AAE36272
ID AAE36272 standard; protein; 719 AA.
XX AAE36272;
AC AAE36272;
XX 26-JUN-2003 (first entry)
DT B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX Bacillus thuringiensis.
OS WO200298911-A2.
PN 12-DEC-2002.
PD 30-MAY-2002; 2002WO-GB002666.
PF 07-JUN-2001; 2001GB-00013900.
PR (SYGN) SYNGENTA LTD.
XX Vincent JL, Viner R;
PI WPI; 2003-175137/17.
DR New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Claim 12; Page 44-47; 67pp; English.
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify

QY 241 TGLNNLRGTNAESWVRYNQFRDMDTLMLVLDLVALFPSPYDQMYPIKTTAQLTREVTDAI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMDTLMLVLDLVALFPSPYDQMYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTPFSLDQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TFRVGTFTPFSLDQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 9

AAR08041
ID AAR08041 standard; protein; 719 AA.

XX AC AAR08041;
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 27-FEB-1991 (first entry)
XX DE 81 kD endotoxin deduced from DNA carried on pJH12.
XX KW Crystal; insecticide; toxin; delta endotoxin.
XX OS Bacillus thuringiensis; JHCC 4353 and 4835.
XX PN WO9013651-A.
XX PD 15-NOV-1990.
XX PF 09-MAY-1989; 89GB-00010624.
XX PR 09-MAY-1989; 89GB-00010624.
XX PA (ICIL) IMPERIAL CHEM IND PLC.
XX PI Blenk RG, Ely S, Tailor RH, Tippet JM;
XX DR WPI; 1990-361486/48.
XX DR N-PSDB; AAQ06636.
XX PT Bacillus thuringiensis strains - used for producing an endotoxin for
XX PT protecting plants against insects, partic. Lepidoptera and Coleoptera.
XX PS Claim 5; Fig 5-10; 66pp; English.
XX CC The sequence carried on pJH12 which was isolated from B. thurin- giensis
CC strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can
CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,
CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11

CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be
CC used in formulations for combatting Lepidoptera and Coleoptera pests.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX SQ Sequence 719 AA;

Query Match 99.4%; Score 3741; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.7e-292;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGELMPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGELMPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRARSVVKSOYIALELMFVQKLPSPFAVSG 180
DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRARSVVKSOYIALELMFVQKLPSPFAVSG 180
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSVHCWKYS 240
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSVHCWKYS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMDTLMLVLDLVALFPSPYDQMYPIKTTAQLTREVTDAI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMDTLMLVLDLVALFPSPYDQMYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTPFSLDQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TFRVGTFTPFSLDQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSISDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 10

AAB66910
ID AAB66910 standard; protein; 719 AA.

XX AC AAB66910;
XX DT 12-APR-2001 (first entry)
XX DE Insecticidal protein cryIIa4.
XX KW Insecticide; transgenic plant; insect-resistance.
XX OS Paecilomyces sp.

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541 TGTGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600
601 TERTVGTTPFSFLDVOSTFTIGAWNFSSGNEVYIDRIFVPVEVYTAEYDFEKAQEKV 660
601 TERTVGTTPFSFLDVOSTFTIGAWNFSSGNEVYIDRIFVPVEVYTAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719
661 TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 11

AAE36274 AAE36274 standard; protein; 719 AA.

XX AAE36274;

AC AAE36274;

XX 26-JUN-2003 (first entry)

XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.
DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX Bacillus thuringiensis.
OS WO200298911-A2.
XX 12-DEC-2002.
XX 30-MAY-2002; 2002WO-GB002666.
XX 07-JUN-2001; 2001GB-00013900.
XX (SYGN) SYNGENTA LTD.
XX Vincent JL, Viner R;
PI WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT Claim 12; Page 50-53; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 6; Length 719;
Best Local Similarity 99.4%; Pred. No. 2.5e-292;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60
1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60
61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKQLPSPFVSG 180
121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKQLPSPFVSG 180
181 BEVPLLPYQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSCHVKWYS 240

XX SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 4; Length 719;
Best Local Similarity 99.4%; Pred. No. 2.5e-292;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60
1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60
61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKQLPSPFVSG 180
121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKQLPSPFVSG 180
181 BEVPLLPYQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSCHVKWYS 240
181 BEVPLLPYQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSCHVKWYS 240
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPFPSTQMPYIKTTAQLTREVYTDI 300
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPFPSTQMPYIKTTAQLTREVYTDI 300
301 GTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
301 GTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFLOPVGNGVPR 420
361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFLOPVGNGVPR 420
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDLRRTN 540
481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDLRRTN 540
541 TGTGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600

XX WO200100841-A1.
XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
XX 29-JUN-1999; 99GB-00015215.
XX 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
XX Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.
XX Claim 14; Page 60-62; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKESSEISFYNRQVERAGDYSCHVKWYS 240
Qy 241 TGLNLRGTNAESWRYNQFRDMLMVLVALPSPDYDTQMYPIKTTAQLTREVTDAI 300
Db 241 TGLNLRGTNAESWRYNQFRDMLMVLVALPSPDYDTQMYPIKTTAQLTREVTDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQSKV 660
Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQSKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12
AAE36271
ID AAE36271 standard; protein; 718 AA.
XX
AC AAE36271;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIal.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-CB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 42-44; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as

CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 718 AA;
Query Match 99.2%; Score 3730.5; DB 6; Length 718;
Best Local Similarity 99.4%; Pred. No. 1.2e-291;
Matches 715; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNEDYIELQNIHEDCLKMKSEYENVEPVSASTI 60
Db 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNEDYIELQNIHEDCLKMKSEYENVEPVSASTI 60
Qy 61 QTGIGTAGKILGTGLVPFAGQVASLYSFTLGEWPKGNQWEIFMEHVEEIIINQISTYA 120
Db 61 QTGIGTAGKILGTGLVPFAGQVASLYSFTLGEWPKGNQWEIFMEHVEEIIINQISTYA 120
Qy 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPFVSG 180
Db 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPFVSG 180
Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKESSEISFYNRQVERAGDYSYCHVKWYS 240
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKESSEISFYNRQVERAGDYSYCHVKWYS 240
Qy 241 TGLNLRGTNAESWRYNQFRDMLMVLVALPSPDYDTQMYPIKTTAQLTREVTDAI 300
Db 241 TGLNLRGTNAESWRYNQFRDMLMVLVALPSPDYDTQMYPIKTTAQLTREVTDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQSKV 660
Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQSKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719
RESULT 13
AAE66907
ID AAE66907 standard; protein; 718 AA.
XX
AC AAE66907;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIal.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX

OS Paecilomyces sp.
XX WO200100841-A1.
PN 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
XX 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.
PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
XX Vincent JL, Lee MD;
PI WPI; 2001-123015/13.
XX Novel insecticidal protein obtained from species of Paecilomyces for
XX controlling insects, and for insect-resistant transgenic plant
XX production.
XX Claim 14; Page 53-55; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained
XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
XX insecticidal proteins can be used to produce transgenic plants, which are
XX insect-resistant. Also, the insecticidal proteins are useful for
XX controlling insects by providing them at a locus where insects feed
XX
XX Sequence 718 AA;
SQ Query Match 99.0%; Score 3724.5; DB 4; Length 718;
Best Local Similarity 99.3%; Pred. No. 3.7e-291;
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNHEDCLKMSYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNHEDCLKMSYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKLGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPFAVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKWLSSSEISTFYNNQVERAGDYSYHCVKWS 240
DB 181 EEVPLLPYQAANLHLLLRDASIFGKWLSSSEISTFYNNQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTNAESWVRVQFRDMTLMVLDLVALPSPYDTQMPYIKTTAQLTREVYTDI 300
DB 241 TGLNLRGTNAESWVRVQFRDMTLMVLDLVALPSPYDTQMPYIKTTAQLTREVYTDI 300
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAARNPHLLDFEQVTIYSLLSRWSTQYNNMW 360
DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAARNPHLLDFEQVTIYSLLSRWSTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTQPVN-VPR 419
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
QY 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 480 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
QY 541 TGTFGDIRVNPFPFAQRYRIRYASTDQLQFHTSINGKAINQGNFSATMNRGEDLDYK 600

DB 540 TGTFGDIRVNPFPFAQRYRIRYASTDQLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
QY 601 TFRVVGFTTTPFSLDVQSTFTTIGAMNFGSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 600 TFXTVGFTTTPFSLDVQSTFTTIGAMNFGSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659
QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFELVVKYAKQLHIERNM 719
DB 660 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFELVVKYAKQLHIERNM 718
RESULT 14
ADM74717
ID ADM74717 standard; protein; 719 AA.
XX ADM74717;
AC 03-JUN-2004 (first entry)
XX 03-JUN-2004 (first entry)
DT B. thuringiensis cryIIel SEQ ID NO:2.
XX B. thuringiensis cryIIel
DE cryI; toxicity; lepidoptera; cryIa; cryIIa; coleoptera; diptera;
XX cryIIel.
KW Bacillus thuringiensis.
XX CN1401772-A.
XX 12-MAR-2003.
PD 20-AUG-2001; 2001CN-00124163.
XX 20-AUG-2001; 2001CN-00124163.
XX 20-AUG-2001; 2001CN-00124163.
PR (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.
PA Song F, Zhang J, Huang D;
PI WPI; 2003-442339/42.
XX N-PSDB; ADM74716.
DR Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence
XX with high-toxicity to lepidoptera pests, encoded protein, primer
XX sequences and the shuttle vector pSXY422b, useful as a pesticide.
PT Example 3; SEQ ID NO 2; 29pp; Chinese.
PS The invention relates to a novel Bacillus thuringiensis cryI gene, gene
XX combination, expression vector, nucleotide sequence of the B
XX thuringiensis cryI gene with high-toxicity to lepidoptera pests and the
XX amino acid sequence of the protein encoded by it, cooperative use of the
XX cryI gene with the expression product of cryIa or cryIIa, primer
XX sequences for expressing the genes, and the constructed shuttle vector
XX pSXY422b. The gene in combination with the cryIa or cryIIa genes
XX displays high toxicity to the lepidoptera, coleoptera and diptera pests.
XX The present sequence represents the cryIIel protein.
SQ Sequence 719 AA;

Query Match 93.9%; Score 3534; DB 7; Length 719;
Best Local Similarity 93.2%; Pred. No. 8.7e-276;
Matches 670; Conservative 27; Mismatches 22; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNHEDCLKMSYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNHEDCLKMSYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPFAVSG 180

Db 121 RNTALADLKGGLDALAVYHESLESMTKRNARATSVKSOYIALELLEFVKLPSPFAVSG 180
Qy 181 BEVPLLPYQAANLHLLLRDASIFGKESSEISFYNNQVERAGDYSYHCVKWS 240
Db 181 BEVPLLPYQAANLHLLLRDASVFGKESLSQISFYNNQVERTSDYSYHCVKWS 240
Qy 241 TGLNLRGTNAESWVRYNQPRDMLTMDLVALPSPYDTQMYPIKTTAQLTRVYTDAT 300
Db 241 TGLNLRGTNAESWVRYNQPRDMLTMDLVALPSPYDTQMYPIKTTAQLTRVYTDAT 300
Qy 301 GTVHPSPFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYLLSRWSNTQYNNMW 360
Db 301 GTVHPNASFSTWYNNAPSFSAIESAVVRNPHLLDFLEQVTTIYLLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPVNGVPR 420
Db 361 GGHKLEFRTIGVLTNTSQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFATLPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TERTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 660
Db 601 TERTVGFTTPPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 15

AAB66912 ID AAB66912 standard; protein; 719 AA.

XX AC AAB66912;

XX DT 12-APR-2001 (first entry)

XX DE Insecticidal protein cryIb1.

XX KW Insecticide; transgenic plant; insect-resistance.

XX OS Paecilomyces sp.

XX PN WO200100841-A1.

XX PD 04-JAN-2001.

XX PF 23-JUN-2000; 2000WO-GB002457.

XX PR 29-JUN-1999; 99GB-00015215.

XX PR 23-DEC-1999; 99GB-00030536.

XX PA (ZENE) ZENECA LTD.

XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX PI Vincent JL, Lee MD;

XX DR WPI; 2001-123015/13.

XX PT Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

PT production.

XX Claim 14; Page 64-66; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66912 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;
SQ
Query Match 93.1%; Score 3503; DB 4; Length 719;
Best Local Similarity 92.5%; Pred. No. 2.8e-273;
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;
Qy 1 MKLKQDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLMKSEYENVEPVASSTI 60
Db 1 MKLKQDKHOSLSSNAKVDKIATDSLKNETDIELKMNEDYLRMSEHESIDPFVASTI 60
Qy 61 QTGIGTAGKILGTGVPFAGQIASLYSFILGELWPKGKQWEIFMEHVEEIIQKISTYA 120
Db 61 QTGIGTAGKILGTGVPFAGQIASLYSFILGELWPKGKQWEIFMEHVEEIIQKILTYA 120
Qy 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNTRARSVVKSOYIALELMPVKLPSPFAVSG 180
Db 121 RNKALSDLRGLGDALAVYHDSLESWVGNRNTRARSVVKQNYIALELMPVKLPSPFAVSG 180
Qy 181 BEVPLLPYQAANLHLLLRDASIFGKESSEISFYNNQVERAGDYSYHCVKWS 240
Db 181 BEVPLLPYQAANLHLLLRDASIFGKESSEISFYNNQVERTRDYSYHCVKWN 240
Qy 241 TGLNLRGTNAESWVRYNQPRDMLTMDLVALPSPYDTQMYPIKTTAQLTRVYTDAT 300
Db 241 TGLNLRGTNAESWVRYNQPRDMLTMDLVALPSPYDTQMYPIKTTAQLTRVYTDAT 300
Qy 301 GTVHPSPFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYLLSRWSNTQYNNMW 360
Db 301 GTVHPNQAFSTWYNNAPSFSAIEAAVVRSPHLLDFLEQVTTIYLLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPVNGVPR 420
Db 361 GGHKLESRPIGGALNTSQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPTLPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TERTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 660
Db 601 TERTVGFTTPPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQSKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: February 14, 2005, 20:50:30
Job time : 101.351 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds
(without alignments)
4539.261 Million cell updates/sec

Title: US-10-019-823B-57
Perfect score: 3760
Sequence: 1 MKLKNQKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	719	1 C11A_BACTK	Q45752 bacillus th
2	3756	99.9	719	2 Q6X181	Q6x181 bacillus th
3	3751	99.8	719	2 Q93NJ5	Q93nj5 bacillus th
4	3750	99.7	719	2 Q85796	Q85796 bacillus th
5	3621	96.3	719	2 Q8KY61	Q8ky61 bacillus th
6	3547	94.3	719	2 Q9F0P8	Q9f0p8 bacillus th
7	3516	93.5	719	1 C11B_BACTE	Q45709 bacillus th
8	3393	90.2	719	1 C11D_BACTU	Q9xd11 bacillus th
9	3373	89.7	719	1 C11C_BACTU	Q87404 bacillus th
10	2445.5	65.0	1229	1 C1BB_BACTU	Q45739 bacillus th
11	2445.5	65.0	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2277.5	60.6	1228	2 Q93T75	Q93t75 bacillus th
13	2276.5	60.5	1228	1 C1BA_BACTK	P05517 bacillus th
14	2268.5	60.3	1228	2 Q93NM5	Q93nm5 bacillus th
15	2195.5	58.4	849	2 Q6PYW8	Q6pyw8 bacillus th
16	2195.5	58.4	1227	1 C1BE_BACTU	Q85805 bacillus th
17	2111.5	56.2	1231	2 Q8KNY2	Q8kny2 bacillus th
18	2106.5	56.0	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
19	1984.5	52.8	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1904	50.6	381	2 Q45740	Q45740 bacillus th
21	1669.5	44.4	1157	1 C8AA_BACUK	Q45704 bacillus th
22	1660	44.1	1144	2 Q8KZL7	Q8kz17 bacillus th
23	1494	39.7	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1485.5	39.5	1169	1 C8BA_BACUK	Q45705 bacillus th
25	1482.5	39.4	1166	1 C1GA_BACTU	Q45746 bacillus th
26	1482	39.4	1167	1 C1JA_BACTU	Q45738 bacillus th
27	1475	39.2	1169	1 C1FB_BACTM	Q66377 bacillus th
28	1469	39.1	1174	2 Q45749	Q45749 bacillus th
29	1465	39.0	1155	1 C1AB_BACTK	P06578 bacillus th
30	1465	39.0	1155	2 Q7BE98	Q7be98 bacillus th
31	1465	39.0	1155	2 Q9F296	Q9f296 bacillus th

RESULT 1

C11A_BACTK

ID	C11A_BACTK	STANDARD	PRT	719 AA
AC	Q45752; P71092; Q45750; Q45751; Q45756;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin)			
DE	CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
GN	Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryVI;			
OS	Bacillus thuringiensis (subsp. kurstaki).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=29339;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSIR732;			
RX	MEDLINE=93298009; PubMed=8517758;			
RA	Gleave A.P., Williams R., Hedges R.J.;			
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes and characterization of a cryV gene cloned from B. thuringiensis subsp. kurstaki.";			
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=JHCC4835;			
RX	MEDLINE=92269582; PubMed=1588820;			
RA	Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RT	"Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";			
RL	Mol. Microbiol. 6:1211-1217(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HD-1;			
RX	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus.";			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AB88;			
RX	MEDLINE=96178985; PubMed=8606196;			
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V., Craig J.A., Koziel M.G., Estruch J.J.;			
RT	"Cloning of a cryV-type insecticidal protein gene from Bacillus thuringiensis: the cryV-encoded protein is expressed early in stationary phase.";			
RL	J. Bacteriol. 178:2141-2144 (1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=61;			

32	1463	38.9	1118	2	Q9AM83	Q9am83 bacillus th
33	1460	38.8	1156	2	Q6GUA7	Q6gua7 bacillus th
34	1458.5	38.8	1180	2	Q9S5V8	Q9s5v8 bacillus th
35	1457.5	38.8	1176	2	Q7WZT9	Q7wzt9 bacillus th
36	1455	38.7	1177	2	Q6EIX3	Q6eix3 bacillus th
37	1453	38.6	1155	2	Q93T21	Q93t21 bacillus th
38	1452.5	38.6	793	2	Q6PYW7	Q6pyw7 bacillus th
39	1451.5	38.6	1176	2	Q45736	Q45736 bacillus th
40	1447.5	38.5	1176	1	C1AA_BACTK	P02965 bacillus th
41	1447.5	38.5	1176	2	Q9RC30	Q9rc30 bacillus th
42	1447.5	38.5	1181	1	C1AE_BACTL	Q03748 bacillus th
43	1437.5	38.2	1169	2	Q8GHE8	Q8ghe8 bacillus th
44	1430.5	38.0	1169	1	C1GB_BACTZ	Q9zaz6 bacillus th
45	1424.5	37.9	1179	1	C1AD_BACTA	Q03744 bacillus th

ALIGNMENTS

661	GGHKLPEFTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR	420
421	VDFHWKVFVTHPIASDNFYYPGCVGIGTQLQDSENELPPEATGQPNYSYSHRLSHIGLIS	480
421	VDFHWKVFVTHPIASDNFYYPGCVGIGTQLQDSENELPPEATGQPNYSYSHRLSHIGLIS	480
481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540
481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540
541	TGTFGDIRWINPPFAQRYRVRIRVASTTDLQFHTSINGKAINCGNFATMNRGEDLDYK	600
541	TGTFGDIRWINPPFAQRYRVRIRVASTTDLQFHTSINGKAINCGNFATMNRGEDLDYK	600
601	TFRTVGFTTTPFSFLDVQSTFTIGAMNFGSSGNEVYIDRIEFVPVEVTYEAYDEFEKAQEKV	660
601	TFRTVGFTTTPFSFLDVQSTFTIGAMNFGSSGNEVYIDRIEFVPVEVTYEAYDEFEKAQEKV	660
661	TALTSTNPRGLKTDVVDXHYHDQVSNLVESLSDEFYLDKREKLEPEIVKYAKQLHIERNM	719
661	TALTSTNPRGLKTDVVDXHYHDQVSNLVESLSDEFYLDKREKLEPEIVKYAKQLHIERNM	719

RESULT 2

[illegible]

	Query Match	99.9%; Best Local Similarity Matches 718;	Score 3756; Pred. No. 6.1e-251; Conservative 0;	DB 2; Indels 1; Mismatches 0;	Length 719; Gaps 0;
QY	1	MKLKNQDKHQSFSSNAKVDKI	STDLSLKNETDIELQNINHEDCLKMSEYNVPPFVSASTI	60	
DB	1	MKLKNQDKHQSFSSNAKVDKI	STDLSLKNETDIELQNINHEDCLKMSEYNVPPFVSASTI	60	
QY	61	QTGGIAGKILGTILGVPPAGQVASLYSFI	LGEMLPWPKGNQWEIFMEHVVEEII	NQKISTYA	120
DB	61	QTGGIAGKILGTILGVPPAGQVASLYSFI	LGEMLPWPKGNQWEIFMEHVVEEII	NQKISTYA	120
QY	121	RNKALTDLKGGLDALAVYHDSLSWVGNRNNTARS	VVKSQYITALELMFVKLPSPFAVSG	180	
DB	121	RNKALTDLKGGLDALAVYHDSLSWVGNRNNTARS	VVKSQYITALELMFVKLPSPFAVSG	180	
QY	181	EEVPLLPIYAQAANHLHLLLRDASIFGKEWGLSSSEIS	TFTYNRQVERAGDYSDHCVKWYS	240	
DB	181	EEVPLLPIYAQAANHLHLLLRDASIFGKEWGLSSSEIS	TFTYNRQVERAGDYSDHCVKWYS	240	

Selvapandiyar A., Bhatnagar R.K.;
"Isolation, cloning and expression of cryV gene."
Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RRL
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella and Bombyx mori.
CC
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC
CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

	-	-----					K -> R (in strain 61).
CC						D -> Y (in strain JHCC4835 and strain HD-	
DR	EMBL;	M98544;	AAA22354.1;	--		1).	
DR	EMBL;	X62821;	CAA44633.1;	--		A -> V (in strain AB88).	
DR	EMBL;	L36338;	AAC36999.1;	--		KQ -> NE (in strain HD-1 and strain 61).	
DR	EMBL;	L49391;	AAB00958.1;	--			
DR	EMBL;	Y08920;	CAA70124.1;	--			
DR	PIR;	I39815;	I39815.				
DR	PIR;	S25383;	S25383.				
DR	HSSP;	P02965;	LCIY.				
DR	InterPro;	IPR001178;	Endotoxin.				
DR	InterPro;	IPR005638;	endotoxin_C.				
DR	InterPro;	IPR005639;	endotoxin_N.				
DR	InterPro;	IPR008979;	Gal_bind_like.				
DR	Pfam;	PF03944;	Endotoxin_C_1.				
DR	Pfam;	PF00555;	Endotoxin_M_1.				
DR	Pfam;	PF03945;	Endotoxin_N_1.				
DR	Sporulation;	Toxin.					
KW	VARIANT	159					
FT	VARIANT	233					
FT	VARIANT	233					
FT	VARIANT	443					
FT	VARIANT	711					
SO	SEQUENCE	719 AA;	81216 MW;				
			3627ESA6C2SDAFF5 CRC64;				

[illegible]


```
QY 241 TGLNLRGTNAESWVRNQFRDRLMVLVLDLVALPSPYDTQMPYPIKTTAQLTREVTYDAI 300
Db 241 TGLNLRGTNAESWVRNQFRDRLMVLVLDLVALPSPYDTQMPYPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEPRTIGTGLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEPRTIGTGLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTTSPFSLDVQSTFTIGAMNFSNGEVYIDRIEVPVVEVTEAEYDPEKAQEKV 660
Db 601 TFRVGTFTTSPFSLDVQSTFTIGAMNFSNGEVYIDRIEVPVVEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFLDEKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFLDEKRELFEIVKYAKQLHIERNM 719

RESULT 3
Q93NJ5 PRELIMINARY; PRT; 719 AA.
ID Q93NJ5
AC Q93NJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Crylia.
GN Name=crylia;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; ICY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.8%; Score 3751; DB 2; Length 719;
Best Local Similarity 99.7%; Pred. No. 1.3e-250;
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLFI LGELWPKGKNQWEI FMEHVVEEII NQKISTYA 120
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Db 61 QTGIGIAGKILGTGVFPAGQVASYLFI LGELWPKGKNQWEI FMEHVVEEII NQKISTYA 120
QY 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRASVVKSYQYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRASVVKSYQYIALELMFVQKLPFAVSG 180
QY 181 BEVPLLPYIAAANLHLLLRDASIFGKEWGLSSSEISIFYNROVERAGDYSDDHCVKWYS 240
Db 181 BEVPLLPYIAAANLHLLLRDASIFGKEWGLSSSEISIFYNROVERAGDYSDDHCVKWYS 240
QY 241 TGLNLRGTNAESWVRNQFRDRLMVLVLDLVALPSPYDTQMPYPIKTTAQLTREVTYDAI 300
Db 241 TGLNLRGTNAESWVRNQFRDRLMVLVLDLVALPSPYDTQMPYPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEPRTIGTGLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEPRTIGTGLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTFTTSPFSLDVQSTFTIGAMNFSNGEVYIDRIEVPVVEVTEAEYDPEKAQEKV 660
Db 601 TFRVGTFTTSPFSLDVQSTFTIGAMNFSNGEVYIDRIEVPVVEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFLDEKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFLDEKRELFEIVKYAKQLHIERNM 719

RESULT 4
O85796 PRELIMINARY; PRT; 719 AA.
ID O85796
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryVI01;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S101;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; ICY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin_C.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
```


KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;
SQ SEQUENCE 99.7%; Score 3750; DB 2; Length 719;
Query Match 99.7%; Pred. No. 1.6e-250;
Best Local Similarity 99.7%; Mismatches 2; Indels 0; Gaps 0;
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLIFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLIFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180
DB 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREYVYTDI 300
DB 241 TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREYVYTDI 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTPQVNGVPR 420
QY 421 VDFHWKFTVHTPIASDNFYPGYAGIGTQLQDSENELEPPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVHTPIASDNFYPGYAGIGTQLQDSENELEPPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
QY 601 TFRVGVFTTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TFRVGVFTTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
Q8KY61 PRELIMINARY; PRT; 719 AA.
AC Q8KY61
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 26, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278797; AAM73516.1; -
DR PIR; B42459; B42459.

HSSP; P02965; 1CIY.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind like.
Pfam; PF03944; Endotoxin C; 1.
Pfam; PF00555; Endotoxin M; 1.
Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;
Query Match 96.3%; Score 3621; DB 2; Length 719;
Best Local Similarity 96.1%; Pred. No. 1.3e-241;
Matches 691; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLIFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLIFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180
DB 121 RNKALTDLKGIGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREYVYTDI 300
DB 241 TGLNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREYVYTDI 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTPQVNGVPR 420
QY 421 VDFHWKFTVHTPIASDNFYPGYAGIGTQLQDSENELEPPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVHTPIASDNFYPGYAGIGTQLQDSENELEPPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLKY 600
QY 601 TFRVGVFTTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TFRVGVFTTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719
RESULT 6
Q9FOP8 PRELIMINARY; PRT; 719 AA.
AC Q9FOP8
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)


```
DE GN CryII.
OS Bacillus thuringiensis.
OC Plasmid pB7C19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BT0007;
RX MEDLINE=22837682; PubMed=12957903;
PX DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
RA Hu Y., Li G., Huang D.;
RT "Identification of cryII-type genes from Bacillus thuringiensis
RL Appl. Environ. Microbiol. 69:5207-5211(2003).";
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 94.3%; Score 3547; DB 2; Length 719;
Best Local Similarity 93.5%; Pred. No. 1.7e-236;
Matches 672; Conservative 26; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60
Db 1 MKLKNPDKHQSLSNAKVDKISTDSLNKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTLPVFPAGVAVSLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLPVFPAGVAVSLYSFILGELWPKGKSQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGIGDALAVHDSLESVGNRNTRARSVVKVSKQYIALELMFVQKLPSPFAVSG 180
Db 121 RNIALADLKGIGDALAVHDSLESVGNRNTRARSVVKVSKQYIALELMFVQKLPSPFAVSG 180
Qy 181 BEVPLPIYAQAANLHLLRDASIFGKEWGLSSSEISFTFYNQVERAGDSDHCVKWS 240
Db 181 BEVPLPIYAQAANLHLLRDASIFGKEWGLSSQISFTFYNQVERSDSDHCVKWS 240
Qy 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPSPSYDTQMPYIKTKAQLTREVYTDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPSPSYDTQMPYIKTKAQLTREVYTDAI 300
Qy 301 GTVHPHPSTTTWNNNAPSFAEAADVVRNPHLLDFLEQVITYLSLLSRWSNTQYNNMW 360
Db 301 GTVHPNAPASTTTWNNNAPSFAESAVVRNPHLLDFLEQVITYLSLLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTTLNISTQSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHLEFRTIGTTLNISTQSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYYPGVIGTQLQDSENLPPATGPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGVIGTQLQDSENLPPATGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAADVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAADVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Db 541 TGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600

541 TGTFGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
601 TFRVTGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660
601 TFRVTGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660
661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 7
CLIB_BACTE STANDARD; PRT; 719 AA.
AC Q45709;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticial crystal protein cryIb (Insecticidal delta-endotoxin
DE CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIb; Synonyms=cryII(b), cryV, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U07642; AAA82114.1; -.
DR PIR; I40590; 140590.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

Query Match 93.5%; Score 3516; DB 1; Length 719;
Best Local Similarity 92.8%; Pred. No. 2.4e-234;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60
Db 1 MKLKNPDKHQSLSNAKVDKISTDSLNKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60
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QY	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120
Db	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120
QY	121	RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPAVSG	180
Db	121	RNKALSDRLGDLALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPAVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKGLSSSEISFTFYNROVERAGDYSDHCWKYS	240
Db	181	EEVPLLPPIYAQAANLHLLLRDASIFGKGLSSSEISFTFYNROVERAGDYSDHCWKYS	240
QY	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDAL	300
Db	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDAL	300
QY	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW	360
Db	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW	360
QY	361	GGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTQPVNGVPR	420
Db	361	GGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTQPVNGVPR	420
QY	421	VDFHMKFVTHPIASDNFYYPGVGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHMKFVTHPIASDNFYYPGVGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK	600
Db	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK	600
QY	601	TFRTVGTTPPSFLVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
Db	601	TFRTVGTTPPSFLVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKEKRELFEIVKYAKQLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKEKRELFEIVKYAKQLHIERNM	719
RESULT 8			
CLID	BACTU	STANDARD;	PRT; 719 AA.
ID	CLID BACTU		
AC	Q9XDL1;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Pesticidal crystal protein cryII (Insecticidal delta-endotoxin		
DE	CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).		
GN	Name=cryIId; Synonyms=cryII(d), NRcryV;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BR30;		
RX	MEDLINE=20374042; PubMed=10919402;		
RA	Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;		
RT	"Cloning of a new Bacillus thuringiensis cryII-type crystal protein		
RT	gene.";		
RL	Curr. Microbiol. 41:65-69(2000).		
CC	-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut		
CC	epithelial cells of many lepidopteran larvae. Active on Plutella		
CC	xylostella and on Bombyx mori.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		

CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; AF047579; AAD44366.1; -.		
DR	HSP; P02965; 1CIY.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal_bind_Like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
KW	Sporulation; Toxin.		
SQ	SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;		
Query Match			
Best Local Similarity 89.7%; Pred. No. 7.6e-226;			
Matches 645; Conservative 35; Mismatches 39; Indels 0; Gaps 0;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNMETHLQINHEHEDCLKMEYENVEPFFVSASTI	60
Db	1	MKSQKQWYRFSFSSNATVDKFTDPLEHNTNMLQNSHEDCLKMEYSEVPEFFVSSTI	60
QY	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120
Db	61	QTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120
QY	121	RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPAVSG	180
Db	121	RNKALADLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPAVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKGLSSSEISFTFYNROVERAGDYSDHCWKYS	240
Db	181	EEVPLLPPIYAQAANLHLLLRDASIFGKGLSSSEISFTFYNROVERAGDYSDHCWKYS	240
QY	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDAL	300
Db	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDAL	300
QY	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW	360
Db	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW	360
QY	361	GGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTQPVNGVPR	420
Db	361	GGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTQPVNGVPR	420
QY	421	VDFHMKFVTHPIASDNFYYPGVGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHMKFVTHPIASDNFYYPGVGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK	600
Db	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK	600
QY	601	TFRTVGTTPPSFLVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
Db	601	TFRTVGTTPPSFLVQSTTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKEKRELFEIVKYAKQLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDFYLDKEKRELFEIVKYAKQLHIERNM	719

Db	661	TAMFTSTNLRRLKTNVTDCHIDQVSNLAVESLSDEFYLDKRELFELVYKAKQLNIERNM	719
RESULT 9			
CLIC_BACTU			
ID	CLIC_BACTU	STANDARD;	PRT; 719 AA.
AC	O87404;		
DT	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Pesticidial crystal protein cryIIc (Insecticidal delta-endotoxin		
DE	CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).		
GN	Name=cryIIc; Synonyms=cryII(c);		
OS	Bacillus thuringiensis.		
OG	Plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C18 / Egypt;		
RA	Osman Y.A., Madkour M.A., Bulla L.A. Jr.;		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut		
CC	epithelial cells of insects.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF056933; AAC62933.1; -.		
DR	HSSP; P02965; 1CIY.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin C; 1.		
DR	Pfam; PF00555; Endotoxin M; 1.		
DR	Pfam; PF03945; Endotoxin N; 1.		
DR	Plasmid; Sporulation; Toxin.		
QW	SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64; -		
Query Match 89.7%; Score 3373; DB 1; Length 719;			
Best Local Similarity 89.7%; Pred. No. 1.8e-224;			
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;			
Qy	1	MKLKNDKQHSFSSNAKVDTKSTDSIKNETDIELQNIHEDCLKMSVEYNEVPFVSASTI	60
Db	1	MKLKNDKQHSFSSNAKVDTKSTDSIKNETDIELKMNEDYLRMSHESIDPFVSASTI	60
Qy	61	QTGIGTAGKILGTGVFAGQVASYLSFILGELWPKGNQWEIPMEHVEEINQKISTYA	120
Db	61	QTGIGTAGKILGTGVFAGQVASYLSFILGELWPKGNQWEIPMEHVEEINQKISTYA	120
Qy	121	RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVKQYIALELMFVQKLPFVAVSG	180
Db	121	RNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVKQYIALELMFVQKLPFVAVSG	180
Qy	181	EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISFTYNROVERAGDYSBHCVKWYS	240
Db	181	EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISFTYNROVERAGDYSBHCVKWYN	240
Qy	241	TGLNLRGTNAESWRYNQFRDWTMLVLDLVALFPSPDYTMQYPIKTTAQLTREVTDAI	300
Db	241	TGLNLRGTNAESWRYNQFRDWTMLVLDLVALFPSPDYTMQYPIKTTAQLTREVTDAI	300

Db	241	TGLNLRGTNAESWRYNQFRDWTMLVLDLVALFPSPDYTMQYPIKTTAQLTREVTDAI	300
Qy	301	GTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW	360
Db	301	GTVDNQALRSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSNTQYMNW	360
Qy	361	GSHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTOPVNGVPR	420
Db	361	GSHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTOPVNGVPR	420
Qy	421	VDHFKFVTHPIASDNFYPGYVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDHFKFVTHPIASDNFYPGYVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
Qy	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTK	540
Qy	541	TGTFGDIRVINPPEAQRVVRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK	600
Db	541	TGTFGDIRVINPPEAQRVVRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK	600
Qy	601	TPRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEKAEKV	660
Db	601	TPRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDEKAEKV	660
Qy	661	TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLNIERNM	719
Db	661	TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLNIERNM	719
RESULT 10			
CLIBB_BACTU			
ID	C1BB_BACTU	STANDARD;	PRT; 1229 AA.
AC	Q45739;		
DT	30-MAY-2000	(Rel. 39, Created)	
DT	30-MAY-2000	(Rel. 39, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Pesticidial crystal protein cryIIB (Insecticidal delta-endotoxin		
DE	CryIIB(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).		
GN	Name=cryIIB; Synonyms=cryET5, cryIIB(b);		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NRRL B-21110 / EG5847;		
RA	Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;		
RT	"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins		
RT	toxic to lepidopteran insects.";		
RL	Patent number US5322687, 21-JUN-1994.		
CC	-!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut		
CC	epithelial cells of many lepidopteran larvae.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; L32020; AAA22344.1; -.		
DR	HSSP; P02965; 1CIY.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin C; 1.		
DR	Pfam; PF00555; Endotoxin M; 1.		
DR	Pfam; PF03945; Endotoxin N; 1.		
DR	Plasmid; Sporulation; Toxin.		
QW	SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64; -		

[illegible]


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QY 543 TFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMNRGDLDTYTF 602
DB 541 TFGDIRLNIWVPLSQRYRIRYASTTDLQFHTSINGKAINQNFSAATMNRGDLDTYTF 600
QY 603 RTVGFTTTPFSLDVOSTFTTGAWNPFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTA 662
DB 601 RTAGFTTTPFSLDVOSTFTTGAWNPFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTA 659
QY 663 LFTSTNPRGLKTDVYDHYDQVSNLVESLDEYDFEKAQEKVTA 719
DB 660 LFTSTNPRGLKTDVYDHYDQVSNLVESLDEYDFEKAQEKVTA 716

RESULT 12
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match
Best Local Similarity 60.6%; Score 2277.5; DB 2; Length 1228;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELOINNH-----EDCLAMSEVENPEPVSASTIQGIGIAGKI 70
DB 2 TSNRKNENEINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINAGRI 61
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINQKISTYARKALTDLKG 130
DB 62 LGVLGVPPAGQLASFYSLVGLWPRGRDQWEIIEHVEQLINQITENARTALRLQ 121
QY 131 LGDALAVYHDSLESWGNRNNTARSKVSKQYIALELMFVKLPSPFVSGEYVPLPIYA 190
DB 122 LGDSFRAYQOQSLDLENRDARTSVLTQYIALELDFLNPALFAIRNQVEPFLMVA 181
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYSTGLNLRGTN 250
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYERQVTRTDYSDYCVENYNTGLNLRGTN 241
QY 251 AESWRYNQFRDMLVLDLVALPSPDYTMQYPIKTTAQLTRVYTTAIGTVHPHSFT 310
DB 242 AASWRYNQFRDMLVLDLVALPSPDYTMQYPIKTTAQLTRVYTTAIGTVHPHSFT 299
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLRSWNTQYNNMGGHKLFRPTI 370
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLRSWNTQYNNMGGHKLFRPTI 359
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QY 371 GGTNLNISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLF--LTQPVNGVPRVDFHMKV 428
DB 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRVYRTESLAGLNLF--LTQPVNGVPRVDFHMKV 416
QY 429 THP-----TASDNFYVPGYVIGTQLODSENELPPEATGQPNVYESYHRLSHIGLISASH 483
DB 417 TNPQNISDRGTANYSQP-YESPGQLKDSSETLPPETTERPNVYESYHRLSHIGLISASH 475
QY 484 VKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGT 543
DB 476 VNPVYVSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGT 535
QY 544 FGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMNRGDLDTYTF 603
DB 536 FGIPIRVTVNGPLTORIRIGFRYASTVDFFVSRGGTIVNNFRFLRTMNSGDELKYGNFV 595
QY 604 TVGFTTTPFSLDVOSTFTTGAWNPFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTA 663
DB 596 RRAFTTTPFTQIQDIIRTSIQGLSGNGEYIDKIEIIPVTATFEAYDLEAQAQVNAL 655
QY 664 FTSTNPRGLKTDVYDHYDQVSNLVESLDEYDFEKAQEKVTA 719
DB 656 FTNTNPRRLKTDVYDHYDQVSNLVESLDEYDFEKAQEKVTA 711

RESULT 13
C1BA BACTK
ID C1BA BACTK STANDARD; PRT; 1228 AA.
AC P05571; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIa (Insecticidal delta-endotoxin
DE CryIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIa; Synonyms=cryA4, cryIb(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis."
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -.
DR EMBL; X95704; CAA65003.1; -.
DR PIR; S00873; S00873.
DR HSSP; P07130; 1DLC.
```


DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 60.5%; Score 2276.5; DB 1; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2.6e-148;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFVSASTIQTGIGIAGKI 70
DB 2 TSNRKNEEIIINAVSNHSAQMDDLDPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPFAGQVASYSLFELGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKG 130
DB 62 LGVLGVPPFAGQLASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQ 121

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPFAVSGEEVPLPIYA 190
DB 122 LGDSFRAYQQSLEDWLENRDDARTSVLYTQYIALELDFNAMPLFAIRNQEVPLLMVYA 181

QY 191 QAAHLHLLLRDASIFGKWLGSSEISTFYNRQVRAGDYSCHVKWYSTGLNLRGTN 250
DB 182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYYERQVTRDYSDYCVWEYNTGLNLRGTN 241

QY 251 AESWRYNQFRDRLTGLVLDLVALFPSTQYPIKTTAQLTREVTDAIGTVHPHPSFT 310
DB 242 AASWRYNQFRDRLTGLVLDLVALFPSTQYPIKTTAQLTREVTDAIGAT--GVNMA 299

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMGGHKLERTI 370
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTRHMTYWRGHTIQSRPI 359

QY 371 GGTNLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 428
DB 360 GGGLNSTHGATNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 416

QY 429 THP-----IASDNFYYPGVIGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISASH 483
DB 417 TNPQNI SDRGTANYSP-YESPGLQKDSETELPETTERPNYESYSHRLSHIGLISASH 475

QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 543
DB 476 VNPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 535

QY 544 FGDIRVNINPPAQRVRYRYASTTDLPHTSINGKAINQGNFSAIATMNRGDLDTKTR 603
DB 536 FGPVIRVTVNGPLTQRYRIGRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYNFV 595

QY 604 TVGFTTTPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFAEKAEKVTA 663
DB 596 RRAFTTPTFTTQIQDIIRTSIQGLSGNGEYIDKIEIIPVTATFEAEYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 14
Q93NM5 PRELIMINARY; PRT; 1228 AA.
ID Q93NM5
AC Q93NM5
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Cry1Ba.
GN Name=cry1Ba;

OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match 60.3%; Score 2268.5; DB 2; Length 1228;
Best Local Similarity 62.6%; Pred. No. 9.4e-148;
Matches 448; Conservative 80; Mismatches 163; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFVSASTIQTGIGIAGKI 70
DB 2 TSNRKNEEIIINAVSNHSAQMDDLDPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPFAGQVASYSLFELGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKG 130
DB 62 LGVLGVPPFAGQLASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQ 121

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPFAVSGEEVPLPIYA 190
DB 122 LGDSFRAYQQSLEDWLENRDDARTSVLYTQYIALELDFNAMPLFAIRNQEVPLLMVYA 181

QY 191 QAAHLHLLLRDASIFGKWLGSSEISTFYNRQVRAGDYSCHVKWYSTGLNLRGTN 250
DB 182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYYERQVTRDYSDYCVWEYNTGLNLRGTN 241

QY 251 AESWRYNQFRDRLTGLVLDLVALFPSTQYPIKTTAQLTREVTDAIGTVHPHPSFT 310
DB 242 AASWRYNQFRDRLTGLVLDLVALFPSTQYPIKTTAQLTREVTDAIGAT--GVNMA 299

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMGGHKLERTI 370
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTRHMTYWRGHTIQSRPI 359

QY 371 GGTNLNSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 428
DB 360 GGGLNSTHGATNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 416

QY 429 THP-----IASDNFYYPGVIGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISASH 483
DB 417 TNPQNI SDRGTANYSP-YESPGLQKDSETELPETTERPNYESYSHRLSHIGLISASH 475

QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 543
DB 476 VNPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 535

QY 544 FGDIRVNINPPAQRVRYRYASTTDLPHTSINGKAINQGNFSAIATMNRGDLDTKTR 603
DB 536 FGPVIRVTVNGPLTQRYRIGRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYNFV 595

QY 604 TVGFTTTPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFAEKAEKVTA 663
DB 596 RRAFTTPTFTTQIQDIIRTSIQGLSGNGEYIDKIEIIPVTATFEAEYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 711

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds
(without alignments)
4171.616 Million cell updates/sec

Title: US-10-019-823B-57
Perfect score: 3760
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	2 I39815	insecticidal prote
2	3747	99.7	719	2 S25383	parasporal crystal
3	3739	99.4	719	2 I39814	insecticidal prote
4	3516	93.5	719	2 I40590	cryv465 protein -
5	2276.5	60.5	1228	2 S00873	parasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1494	39.7	1157	1 S49247	parasporal crystal
8	1482.5	39.4	1166	2 S32645	parasporal crystal
9	1472	39.1	1155	2 A26513	parasporal crystal
10	1469	39.1	1174	2 S32649	parasporal crystal
11	1465	39.0	1155	2 JD0002	parasporal crystal
12	1465	39.0	1156	2 A29125	parasporal crystal
13	1458.5	38.8	934	2 A22798	parasporal crystal
14	1457.5	38.8	1176	2 JT0241	parasporal crystal
15	1451.5	38.6	1176	2 JC2219	parasporal crystal
16	1448	38.5	1155	2 S02134	parasporal crystal
17	1447.5	38.5	1176	2 A32617	parasporal crystal
18	1447.5	38.5	1176	2 S02215	parasporal crystal
19	1447.5	38.5	1181	2 A41052	parasporal crystal
20	1444	38.4	1155	2 I39838	parasporal crystal
21	1358	36.1	1174	2 A42459	parasporal crystal
22	1353	36.0	1138	2 A48944	parasporal crystal
23	1339.5	35.6	1156	2 A29838	parasporal crystal
24	1329.5	35.4	823	2 S04181	parasporal crystal
25	1320.5	35.1	1189	2 S00944	parasporal crystal
26	1310	34.8	1154	2 S39536	parasporal crystal
27	1270	33.8	1171	2 I40572	parasporal crystal
28	1270	33.8	1171	2 A37829	parasporal crystal
29	1261	33.5	1176	2 A48970	parasporal crystal

30	1238	32.9	1160	2 S32647	parasporal crystal
31	1223.5	32.5	1165	2 S11446	parasporal crystal
32	1207.5	32.1	655	2 JC7140	protoxin - Bacilli
33	1195	31.8	1172	2 S32689	parasporal crystal
34	1186	31.5	1160	2 I40589	parasporal crystal
35	1161.5	30.9	1178	1 USBSXH	parasporal crystal
36	1161	30.9	1177	2 A49785	parasporal crystal
37	1154	30.7	652	2 A27323	parasporal crystal
38	1135	30.2	659	2 S10228	parasporal crystal
39	1104.5	29.4	652	2 I39811	parasporal crystal
40	984	26.2	649	1 JH0261	parasporal crystal
41	933	24.8	618	2 S11445	parasporal crystal
42	889	23.6	1156	2 S19306	parasporal crystal
43	827	22.0	1136	1 USBS8I	parasporal crystal
44	691.5	18.4	934	2 B29838	parasporal crystal
45	666	17.7	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I39815
insecticidal protein cryV - Bacillus thuringiensis
C:Species: Bacillus thuringiensis

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: I39815

R:Gleave, A.P.; Williams, R.; Hedges, R.J.

Appl. Environ. Microbiol. 59, 1683-1687, 1993

A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for t

ensis subsp. kurstaki.

A:Reference number: I39815; MUID:93298009; PMID:8517758

A:Accession: I39815

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PID:AAA22354.1; PID:g142768

C:Genetics:

A:Gene: cryV

C:Superfamily: parasporal crystal protein

Query Match 99.9%; Score 3756; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 9.8e-256;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVFASTI	60
Db	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVFASTI	60
Qy	61	QTGIGIAGKILGTLGVPPAGQVASYLSFTLGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTLGVPPAGQVASYLSFTLGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLKGIGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSPAVSG	180
Db	121	RNKALTDLKGIGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSPAVSG	180
Qy	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS	240
Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS	240
Qy	241	TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSPYDTOMYPITKTAQLTREYVTDAI	300
Db	241	TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSPYDTOMYPITKTAQLTREYVTDAI	300
Qy	301	GTVHPSPFTSTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
Db	301	GTVHPSPFTSTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
Qy	361	GGHKLFEFTIGTGLNISTQSGTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR	420
Db	361	GGHKLFEFTIGTGLNISTQSGTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR	420

QY 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
QY 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
DB 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
QY 601 TFRVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TFRVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2
S25383
parasporal crystal protein cryIla1 - Bacillus thuringiensis
N/Alternate names: delta-endotoxin; parasporal crystal protein cryV
C/Species: Bacillus thuringiensis
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C/Accession: S25383
R/Tailor, R.; Rippert, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A/Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A/Reference number: S25383; MUID:92269582; PMID:1588820
A/Molecule type: DNA
A/Residues: 1-719 <TAI>
A/Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:940290
C/Genetics:
A/Gene: cryV
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 99.7%; Score 3747; DB 2; Length 719;
Best Local Similarity 99.7%; Pred. No. 4.2e-255;
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMPVQKLPSPAVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMPVQKLPSPAVSG 180
QY 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYIKTTAQLTREYITDAI 300
DB 241 TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYIKTTAQLTREYITDAI 300
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540
QY 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
DB 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
QY 601 TFRVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TFRVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
I39814
insecticidal protein cryVI - Bacillus thuringiensis
C/Species: Bacillus thuringiensis
C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C/Accession: I39814
R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A/Reference number: I39814; MUID:95314293; PMID:7793960
A/Accession: I39814
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-719 <RES>
A/Cross-references: GB:L36338; NID:9540281; PIDN:AAC36999.1; PID:9540282
C/Genetics:
A/Gene: cryVI
C/Superfamily: parasporal crystal protein

Query Match 99.4%; Score 3739; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.5e-254;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMPVQKLPSPAVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMPVQKLPSPAVSG 180
QY 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYIKTTAQLTREYITDAI 300
DB 241 TGLNLRGTNAESWVRNQFRDMDTLMVLDLVALPFSYDTQMPYIKTTAQLTREYITDAI 300
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTPQVNGVPR 420


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Qy 421 VDFHKKFVTHPIASDNFYYPGVGIGTQLQDSSENLPPREATGPNYESYSHRLSHIGLIS 480
Db 421 VDFHKKFVTHPIASDNFYYPGVGIGTQLQDSSENLPPREATGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVINPNPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVINPNPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDYDPEKAQEKV 660
Db 601 TFRVTGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDYDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
I40590
cryV465 protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40590
R;Shin, B.S.; Choi, S.H.; Park, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I40590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672
C;Genetics:
A;Gene: cryV465
C;Superfamily: parasporal crystal protein

Query Match 93.5%; Score 3516; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 7.1e-239;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MKLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNMNEIDYLRMSEHESIDPVSASTI 60
Qy 61 QTGIGTAGKILGTGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGTAGKILGTGVPPFAGQIASLYSFILGELWPKGQWEIFMEHVEEIIINOKILTYA 120
Qy 121 RNKALTDLKGDLAVYHDSLESWVGNRNNTARSVVKSQYIALELMFVQKLPSPFVSG 180
Db 121 RNKALSDRLGDLAVYHDSLESWVGNRNNTARSVVKSQYIALELMFVQKLPSPFVSG 180
Qy 181 EKVPLPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNQVERAGDYSCHVCWKWYS 240
Db 181 EKVPLPIYAQAANLHLLLRDASIFGKMWGLSSSEISTFYNQVERAGDYSCHVCWKWYN 240
Qy 241 TGLNLRGTNAESWVRYNQRRDMLMVLVLPSPSYDTQMYPIKTTAQLTREVTYDAI 300
Db 241 TGLNLRGTNAESWVRYNQRRDMLMVLVLPSPSYDTQMYPIKTTAQLTREVTYDAI 300
Qy 301 GTVHPHPSPTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNW 360
Db 301 GTVHPNQAFATWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNW 360
Qy 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
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Qy 421 VDEHKKFVTHPIASDNFYYPGVGIGTQLQDSSENLPPREATGPNYESYSHRLSHIGLIS 480
Db 421 VDFHKKFVTHPIASDNFYYPGVGIGTQLQDSSENLPPREATGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVINPNPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVINPNPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDYDPEKAQEKV 660
Db 601 TFRVTGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDYDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 60.5%; Score 2276.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2e-151;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;
Qy 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 62 LGVLGVPPFAGQLASFSYFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNATALARLQ 121
Qy 131 LGDALAVYHDSLESWVGNRNNTARSVVKSQYIALELMFVQKLPSPFVSGEYVPLLPYIA 190
Db 122 LGDSFRAYQOSLEDWLENRDARTRSVLYTQYIALELDFLNAFLFAIRNOEQVPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKMWGLSSSEISTFYNQVERAGDYSCHVCWKWYSTGLNNLRGTN 250
Db 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYERQVTRTDYSYCVWEYNTGLNSLRGTN 241
Qy 251 AESWVRYNQRRDMLMVLVLPSPSYDTQMYPIKTTAQLTREVTYDAIGTVHPHPSFT 310
Db 242 AASWVRYNQRRDMLTGLVLDLVALFPSTYDTRTYPTINTSAQLTREVTYDAIGAT--GVNMA 299
Qy 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNWGGHKLFEPTI 370
Db 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTRHTMYWRGHTIQSRPI 359
Qy 371 GGTLANISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 428
Db 360 GGGLANTSTHGATNTSINPVTLPFTSRDVRVYTESYAGVLLWGIYLEPIHGVTPTVRFNF--- 416
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JD0002		parasporal crystal protein cry1Ab3 - Bacillus thuringiensis		parasporal crystal protein cry1Ab3 - Bacillus thuringiensis	
N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot		C;Species: Bacillus thuringiensis		C;Species: Bacillus thuringiensis	
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004		C;Accession: S32649		C;Accession: S32649	
R;Jambert, B.		submitted to the EMBL Data Library, April 1993		submitted to the EMBL Data Library, April 1993	
A;Reference number: S32645		A;Accession: S32645		A;Accession: S32645	
A;Status: preliminary		A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-1174 <LAM>		A;Residues: 1-1174 <LAM>		A;Residues: 1-1174 <LAM>	
A;Cross-references: UNIPROT:Q45749; EMBL:222512; NID:g295865; PIDN:CAA80235.1; PID:g2958		A;Cross-references: UNIPROT:Q45749; EMBL:222512; NID:g295865; PIDN:CAA80235.1; PID:g2958		A;Cross-references: UNIPROT:Q45749; EMBL:222512; NID:g295865; PIDN:CAA80235.1; PID:g2958	
C;Superfamily: parasporal crystal protein		C;Superfamily: parasporal crystal protein		C;Superfamily: parasporal crystal protein	
C;Keywords: delta-endotoxin		C;Keywords: delta-endotoxin		C;Keywords: delta-endotoxin	
Query Match 39.1%; Score 1469; DB 2; Length 1174;		Query Match 39.0%; Score 1465; DB 2; Length 1155;		Query Match 39.0%; Score 1465; DB 2; Length 1155;	
Best Local Similarity 44.8%; Pred. No. 9.9e-95;		Best Local Similarity 44.5%; Pred. No. 1.8e-94;		Best Local Similarity 44.5%; Pred. No. 1.8e-94;	
Matches 325; Conservative 103; Mismatches 202; Indels 96; Gaps 17;		Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;		Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;	
QY 36 NINHE---DCLKMEYENVEPVASSTIQIGIA-GKILGTLGVPPAGQVASLYSFL 90	DB 4 NIQOCVPYNCLSNPEVELSERSTGRPLDLSLSTRFLSEFPVGVGVAFLGLDLIW 63	QY 36 NINHECLKMEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPPAGQVASLYS 87	DB 4 NPINCEIPYNCLSNPEVELGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62	QY 88 FILGELWPKGNQWEIEMEHVEEIIINOKISTYARNKALTDLKGLGDALAVYHDSLESVWG 147	DB 63 IIWGIF---GPSQWDAFLVQIEQLINRIEFARNQAIISRLGLESLNLYQIYAESFREWEA 119
QY 91 GELPKGKNQWEIEMEHVEEIIINOKISTYARNKALTDLKGLGDALAVYHDSLESVWG 150	DB 64 GFITP---SEWSLFLQIEQLRIETLERNRAITTLRGLADSVEVYLEALREWEENP 120	QY 88 FILGELWPKGNQWEIEMEHVEEIIINOKISTYARNKALTDLKGLGDALAVYHDSLESVWG 147	DB 63 IIWGIF---GPSQWDAFLVQIEQLINRIEFARNQAIISRLGLESLNLYQIYAESFREWEA 119	QY 148 NNNTRARSVKVSQYIALLELMFVQKLPSFAVSGEVPVLLPIYAQAANLHLLLRDASIFG 207	
QY 151 NTRARSVKVSQYIALLELMFVQKLPSFAVSGEVPVLLPIYAQAANLHLLLRDASIFG 210	DB 121 NAQLREDVRIRFANTDDALITAINFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQW 180				
QY 211 GLSSEISTFYNNQVERAGDSDHCWKYSTGLNNLGTNAESWVRYNQFRDMLMVL 270	DB 181 GLDIATVNNHYNRLINLHRYTHECLDYNQGLENLRGNTQWRFNFRRLTLTVD 240				
QY 271 LVALPSTQMYPIKTTAQLTREVTDAIGTVHPHPSFTSTWYNNAPS-FSAIEAAV 329	DB 241 IVALPFDYARAYPIQTSSQLTRIYTSV--IEDSP-----VSANIPIGNFPAEFG- 290				
QY 330 VRNPHLLDLEQVTIYSLSRWSNTQYMMWGKHLEFRITGTLNISTQGSTNTSINPV 389	DB 291 VRPPHLMDFVN-----SLFVTAETVRSQTVWGGHLV-----SSRNTAGNPI 331				
QY 390 TLPP-----TSRDVYRTESLAGLNLFLTQPVNGVPRVDEHMKFVTHPIAS 434	DB 332 NFPIYGFPGGAIWIADDEPRPFYRT-----LSDPV-----FVRGGFGN 371				
QY 435 DNFPYGVVIGTGTLQ-----DSENLPEATQPNVESYSHRLSHI----- 476	DB 372 PH-YVLGLRGVAFQQTGNHTRFRNSGIDSLDEIPPDNSGAPWMDYSHVLNHTFVR 430				
QY 477 --GLISASHV-KALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGG 533	DB 431 WPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIITQIPAKAHNLHSGSTVVRGPGFTGG 490				
QY 534 DILRRNTGTGDIRVNNPFAQRYRVRIRYASTDLQFHTSINGKAINQGNFSAATMNR 593	DB 491 DLLRRNTGTGADIRVNTGPLSQRYRVRIRYASTDLQFTRINGYSVQGNFQFTMNR 550				
QY 594 GEDLDYKTRFTVGTFFPFLDVQSTFTTGAWNFSSGNEGVYIDRIEFVPEVTEYAEYDF 653	DB 551 GGNLESGNFRTAGSTFPFSNAQSTFTLTGTAQFSN-QEVYIDRIEFVPAEYTFEASDL 609				
QY 654 EKAQEKVTAFTSTNPRGLKTDVHDQVSNLVESLSDEFYLDKRELFLVYKAKOL 713	DB 610 ERAQKAVNALFTSTSQGLKTNVTGVHIDQVSNLVACLSDEFCLDKRELSEKVGAKRL 669				
QY 714 HIERNM 719	DB 670 SDRKNL 675				
RESULT 11					

Db 120 DPTNPALEEMRIQFNDMNSALTITAIPLFAVQNTQVPLLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSSEISTFYNNRQVERAGDYSCHVKWYSTGLNNLRTGTAESWVRYNQFRDRTLM 267
Db 180 QRWGFDAAATINSRYNDLTRIGNYTDHARVYNTGLERVMGPDSDRWIRYNQFRRELTLT 239
Qy 268 VLDLVALFPSTYDQPIKTAQITREVYDAIGTVHPPSPFTSTTWNNAAPSF-----S 323
Db 240 VLDIVSLFPNDSTYPIRTVSQLTREIYNPV-----LENFDCSFRGSAQ 285
Qy 324 AIEAAVVRNPHLLDFEQVTIYLSLSR-----WSNTQYNNM---WGHKLEFRTIGGTINI 376
Db 286 GIEGS-IRSPHLMIDLNSITITDAHRGEYYSWGHQIMASPVGSGPFTFPLYGTWNA 344
Qy 377 STQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVPRVDFHWKVFTHPIASDN 436
Db 345 APQQRIVAQGGVVRTLSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395
Qy 437 FYYPGYGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHRLSHVSMFRSGFNSSVSIIRAPMF 453
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRV 549
Db 454 SWHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISILRV 513
Qy 550 NINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTPRTVGFTT 609
Db 514 NITAPLSQRVVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLNQLQSGSPRTVGFTT 573
Qy 610 PPSFLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQKVTALFTSTNP 669
Db 574 PNFNSGSSVFTLSAHVFNQSGNEVYIDRIEFVPAEVTAEYDLERAKAVNELFTSSNQ 633
Qy 670 RGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFVIVKYAKQLHIERNM 719
Db 634 IGLKTDVTDHYDQVNLVSLSDSEFYLDKRELFVIVKYAKQLHIERNM 683

RESULT 12
A29125
parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)
C/Species: *Bacillus thuringiensis* subsp. *kurstaki*
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29125
R/Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/technology 5, 807-813, 1987
A/Title: Insect tolerant transgenic tomato plants.
A/Reference number: A29125
A/Accession: A29125
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-1156 <PIS>
A/Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 39.0%; Score 1465; DB 2; Length 1156;
Best Local Similarity 44.5%; Pred. No. 1.9e-94;
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQG-----IGIAGKILGTGLGVFPAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIEMHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNOAISRLGLSNLYQIYAESFREWEA 119
Qy 148 NRNTRARSVVKSQYIALELMFVQKLPSFAVSGEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALEEMRIQFNDMNSALTITAIPLFAVQNTQVPLLSVYVQAANLHLSVLDRDVSFG 179

Qy 208 KEWGLSSSEISTFYNNRQVERAGDYSCHVKWYSTGLNNLRTGTAESWVRYNQFRDRTLM 267
Db 180 QRWGFDAAATINSRYNDLTRIGNYTDHARVYNTGLERVMGPDSDRWIRYNQFRRELTLT 239
Qy 268 VLDLVALFPSTYDQPIKTAQITREVYDAIGTVHPPSPFTSTTWNNAAPSF-----S 323
Db 240 VLDIVSLFPNDSTYPIRTVSQLTREIYNPV-----LENFDCSFRGSAQ 285
Qy 324 AIEAAVVRNPHLLDFEQVTIYLSLSR-----WSNTQYNNM---WGHKLEFRTIGGTINI 376
Db 286 GIEGS-IRSPHLMIDLNSITITDAHRGEYYSWGHQIMASPVGSGPFTFPLYGTWNA 344
Qy 377 STQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVPRVDFHWKVFTHPIASDN 436
Db 345 APQQRIVAQGGVVRTLSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395
Qy 437 FYYPGYGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHRLSHVSMFRSGFNSSVSIIRAPMF 453
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRV 549
Db 454 SWHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISILRV 513
Qy 550 NINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTPRTVGFTT 609
Db 514 NITAPLSQRVVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLNQLQSGSPRTVGFTT 573
Qy 610 PPSFLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQKVTALFTSTNP 669
Db 574 PNFNSGSSVFTLSAHVFNQSGNEVYIDRIEFVPAEVTAEYDLERAKAVNELFTSSNQ 633
Qy 670 RGLKTDVKDHYDQVNLVSLSDSEFYLDKRELFVIVKYAKQLHIERNM 719
Db 634 IGLKTDVTDHYDQVNLVSLSDSEFYLDKRELFVIVKYAKQLHIERNM 683

RESULT 13
A22798
parasporal crystal protein - *Bacillus thuringiensis*
C/Species: *Bacillus thuringiensis*
C/Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C/Accession: A22798
R/Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A/Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuring*
A/Reference number: A22798; MUID:85232070; PMID:2989108
A/Accession: A22798
A/Molecule type: DNA
A/Residues: 1-934 <SHI>
A/Cross-references: UNIPROT:Q9SSV8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:g551713
C/Comment: The authors translated the codon ACA for residue 264 as Ser.
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 38.8%; Score 1458.5; DB 2; Length 934;
Best Local Similarity 43.7%; Pred. No. 3.8e-94;
Matches 311; Conservative 119; Mismatches 221; Indels 61; Gaps 12;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQG-----IGIAGKILGTGLGVFPAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEIEMHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNOAISRLGLSNLYQIYAESFREWEA 119
Qy 148 NRNTRARSVVKSQYIALELMFVQKLPSFAVSGEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALEEMRIQFNDMNSALTITAIPLFAVQNTQVPLLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSSEISTFYNNRQVERAGDYSCHVKWYSTGLNNLRTGTAESWVRYNQFRDRTLM 267

Db 180 QRMGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWRYNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTAQLTRVYTDAGTGVHHPSPFTSTTWYNNAPSFSAIEA 327
Db 240 VLDLVALFNSYDSSRRYPRTVSQLTRITYNPV-----LENFDGSGFRGMAQ 285
Qy 328 AV---VRNPHLLDFLEQVTIYSLRSWSNTQVMNMWGGHKLFRFTIGGT---LNISTQGS 381
Db 286 RIEQNIROPHLMDILNRIITYTDVHRG-----FNYWSGHQITASPVGFSGPEFAFPLFGN 340
Qy 382 TNSINPVTLPFTSRDVRTESEL-----AGLNLFQTQPVNGVPRVDFHWKVFTHPI 432
Db 341 AGNAAPPVLVSLTGLGIFRTLSSPLVRRRIILGSGPN---NQELFVLDGTEFSFASLTNLT 397
Qy 433 ASDNFYFGYVGIGTQLQDSSENLPPPEATGQPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQRTV-----DSLVDIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGTGDI 547
Db 451 TFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISTL 510
Qy 548 RVNINPPFAQRYRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSQRYRVIRYASTTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRVTVGF 570
Qy 608 TTPFSFLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVYALFTST 667
Db 571 TTPFNFSNGSSVFTLSAHVFNSEVYIDRIEFVPAEVTAEYDLERAKAVNELFTSS 630
Qy 668 NPGRLKTDVXDYHIDQVSNLVSLSDFYLDKRELFVYKAKOLHIERNM 719
Db 631 NOIGLKTVDYHIDQVSNLVECLSDFECLDEKQELSEKVKHAKRLSDERNL 682

RESULT 14

JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N;Alternate names: 135K insecticidal protein
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JT0241
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
Agric. Biol. Chem. 52, 1565-1573, 1988
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A;Reference number: JT0241
A;Accession: JT0241
A;Molecule type: DNA
A;Residues: 1-1176 <SHI>
A;Cross-references: UNIPROT:P02965
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.8%; Score 1457.5; DB 2; Length 1176;
Best Local Similarity 43.7%; Pred. No. 6.4e-94;
Matches 311; Conservative 118; Mismatches 222; Indels 61; Gaps 12;
Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLVPPAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELMPKGNQWEIEMHVEEIIINOKISTYARNKALTDLKGDLAVYHDSLESWVG 147
Db 63 IIWGI---GPSQWDAFLVQIEQLNQRIEFARNQAIISRLSEGLSNLYQIYAESPREWEA 119
Qy 148 NRNNTRARSVVKSQVIALELMFVQKLPSPFVSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALITTAIPLFAVQNVQVPLLSVYVQAANLHLSVLDRVSVFG 179
Qy 208 KEWGLSSSEISTFTYNQVRAGDYSCHVCVKYSTGLNLRGTNAESWRYNQFRDMTLM 267

Db 180 QRMGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWRYNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTAQLTRVYTDAGTGVHHPSPFTSTTWYNNAPSFSAIEA 327
Db 240 VLDLVALFNSYDSSRRYPRTVSQLTRITYNPV-----LENFDGSGFRGMAQ 285
Qy 328 AV---VRNPHLLDFLEQVTIYSLRSWSNTQVMNMWGGHKLFRFTIGGT---LNISTQGS 381
Db 286 RIEQNIROPHLMDILNRIITYTDVHRG-----FNYWSGHQITASPVGFSGPEFAFPLFGN 340
Qy 382 TNSINPVTLPFTSRDVRTESEL-----AGLNLFQTQPVNGVPRVDFHWKVFTHPI 432
Db 341 AGNAAPPVLVSLTGLGIFRTLSSPLVRRRIILGSGPN---NQELFVLDGTEFSFASLTNLT 397
Qy 433 ASDNFYFGYVGIGTQLQDSSENLPPPEATGQPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQRTV-----DSLVDIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGTGDI 547
Db 451 TFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISTL 510
Qy 548 RVNINPPFAQRYRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSQRYRVIRYASTTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRVTVGF 570
Qy 608 TTPFSFLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVYALFTST 667
Db 571 TTPFNFSNGSSVFTLSAHVFNSEVYIDRIEFVPAEVTAEYDLERAKAVNELFTSS 630
Qy 668 NPGRLKTDVXDYHIDQVSNLVSLSDFYLDKRELFVYKAKOLHIERNM 719
Db 631 NOIGLKTVDYHIDQVSNLVECLSDFECLDEKQELSEKVKHAKRLSDERNL 682

RESULT 15

JC2219
parasporal crystal protein cryIAa - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2219
R;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
BioSci. Biotechnol. Biochem. 58, 830-835, 1994
A;Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an
A;Reference number: JC2219; MUID:94289859; PMID:7764972
A;Accession: JC2219
A;Molecule type: DNA
A;Residues: 1-1176 <UDA>
A;Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g53578
C;Genetics:
A;Gene: cryIA(a)
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.6%; Score 1451.5; DB 2; Length 1176;
Best Local Similarity 43.5%; Pred. No. 1.7e-93;
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps 12;
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Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELMPKGNQWEIEMHVEEIIINOKISTYARNKALTDLKGDLAVYHDSLESWVG 147
Db 63 IIWGI---GPSQWDAFLVQIEQLNQRIEFARNQAIISRLSEGLSNLYQIYAESPREWEA 119
Qy 148 NRNNTRARSVVKSQVIALELMFVQKLPSPFVSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALITTAIPLFAVQNVQVPLLSVYVQAANLHLSVLDRVSVFG 179
Qy 208 KEWGLSSSEISTFTYNQVRAGDYSCHVCVKYSTGLNLRGTNAESWRYNQFRDMTLM 267


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Db 180 QRWGFDAAATNSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRYNQFRRELTLT 239
Qy 268 VLDLVALFPSTQMYPIKTAQLTREVYTDAGTGVHPHPSFTSTTWYNNNAPSFAIEA 327
Db 240 VLDIVLAFSNVDSRRYPVRTVSQLTREIYNPV-----LENFDCSFRGMAQ 285
Qy 328 AV--VRNPHLLDFLEQVTIYSLLSRWNSNTQYMMWGGHKLFRITIGT--LNISTQGS 381
Db 286 RIEQNIRQPHLMDILNSITITVDVHRG-----FNYWSGHQITASPVGSGPEFAFPLFGN 340
Qy 382 TNSINPVTLPFTSRDVRTESL-----AGNLFLTQPVNGVPRVDFHWKFVTHPI 432
Db 341 AGNAAPPVLVSLTGLIFRTLSSPLRYRIILGSGPN--NQELFVLDGTEFSPASLTNL 397
Qy 433 ASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS-----HYKAL 487
Db 398 PSTIYRQRTV-----DSLVDIIPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGEDI 547
Db 451 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTPGQISTL 510
Qy 548 RVNINPPFAQRYRVIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGP 607
Db 511 RVNITAPLSQRYRVIRYASTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRVGP 570
Qy 608 TTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVLTFTST 667
Db 571 TTPFNFGSSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSS 630
Qy 668 NPRGLKTDVKDYHIDQVSNLVESSLDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 631 NQIGLKTVDVTDYHIDQVSNLVECLSEDEFCLDEKQELSEKVKHAKRLSDERNL 682

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Search completed: February 14, 2005, 21:00:52
Job time : 18.5835 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds
(without alignments)
3909.384 Million cell updates/sec

Title: US-10-019-823B-57
Perfect score: 3760
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELPEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	719	16	US-10-782-020-10
2	3756	99.9	719	16	US-10-782-141-8
3	3472.5	92.4	710	15	US-10-428-961-42
4	2277.5	60.6	1228	16	US-10-809-953-10
5	2264.5	60.2	1207	10	US-09-988-462-7
6	2186.5	58.2	1227	15	US-10-428-961-63
7	2171.5	57.8	1186	9	US-09-826-660-23
8	2115	56.2	1228	15	US-10-428-961-38
9	2115	56.2	1228	15	US-10-614-524-2
10	1932.5	51.4	643	9	US-09-826-660-25
11	1724.5	45.9	1167	14	US-10-089-678-1
12	1680.5	44.7	653	15	US-10-428-961-6
13	1669.5	44.4	1157	16	US-10-782-141-16

14	1510	40.2	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1510	40.2	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1510	40.2	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1494	39.7	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1494	39.7	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1494	39.7	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1487.5	39.6	1156	14	US-10-099-285-72	Sequence 72, Appli
21	1487.5	39.6	1156	15	US-10-428-961-28	Sequence 28, Appli
22	1465	39.0	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1465	39.0	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1465	39.0	1155	15	US-10-136-998A-2	Sequence 6, Appli
25	1465	39.0	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1465	39.0	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1465	39.0	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1465	39.0	1181	10	US-09-988-462-15	Sequence 15, Appli
29	1465	39.0	1181	10	US-09-988-462-17	Sequence 17, Appli
30	1465	39.0	1181	10	US-09-988-462-28	Sequence 28, Appli
31	1465	39.0	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1465	39.0	1181	15	US-10-136-998A-10	Sequence 8, Appli
33	1465	39.0	1181	15	US-10-136-998A-12	Sequence 10, Appli
34	1465	39.0	1181	15	US-10-136-998A-12	Sequence 12, Appli
35	1460	38.8	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1458	38.8	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1457	38.8	1177	14	US-10-102-469-24	Sequence 24, Appli
38	1447.5	38.5	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1424.5	37.9	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1424.5	37.9	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1398	37.2	1167	15	US-10-428-961-40	Sequence 40, Appli
42	1377	36.6	1177	9	US-09-873-873-26	Sequence 26, Appli
43	1377	36.6	1177	10	US-09-916-958A-26	Sequence 26, Appli
44	1377	36.6	1177	10	US-09-997-914-26	Sequence 26, Appli
45	1377	36.6	1177	14	US-10-365-645-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1

US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 99.9%; Score 3756; DB 16; Length 719;
Best Local Similarity 99.9%; Pred. No. 1.5e-308;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKLKNQDKHQSFSSNAKVDKISTDSLNKNTDIELQNHEDCLKMSVENVEFVSASTI	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLNKNTDIELQNHEDCLKMSVENVEFVSASTI	60
Qy	61	QTGIGTAGKILGTLGVPPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120
Db	61	QTGIGTAGKILGTLGVPPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120

QY	121	RNKALTDKGLGDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPFAVSG	180
DB	121		
QY	181	EEVPLLPYQAANLHLLLRDASIFGKDWGLSSSEISFYNNRQVERAGDYSCHVKWYS	240
DB	181		
QY	241	TGLNLRGTNAESWVRNQFRDMLMVLVDLVALPSPYDTQMPYIKTTAQLTREVTDAI	300
DB	241		
QY	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYNNMW	360
DB	301		
QY	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR	420
DB	361		
QY	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
DB	421		
QY	481	ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
DB	481		
QY	541	TGTFGDIRVNINPPAQRVRIRYASTDLOPHTSINGKAINQGNFSAATWNRGDLDYK	600
DB	541		
QY	601	TPRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
DB	601		
QY	661	TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
DB	661		
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; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.9%; Score 3756; DB 16; Length 719;			
Beat Local Similarity 99.9%; Pred. No. 1.5e-308;			
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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NAME/KEY: misc feature
LOCATION: (200)...(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 92.4%; Score 3472.5; DB 15; Length 710;
Best Local Similarity 92.4%; Pred. No. 1.4e-284;
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

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Db 52 QTGIGIAGKILGNLGVVAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 111
Qy 121 RNKALTDLKGIDALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
Db 112 RNKALADLKGIDALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG 171
Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLGSSEISSTFYNNQVERAGDSDHCHVKWYS 240
Db 172 BEVPLLPPIYAQAANLHLLLRDASIFGKWLGSSEISSTFYNNQVERAGDSDHCHVKWYN 231
Qy 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSPDYDTQMPYIKTTAQLTREYVTDAL 300
Db 232 TGLNRLMGNAESWRYNQFRDMLVLDLVALFPSPDYDTQMPYIKTTAQLTREYVTDAL 291
Qy 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 351
Qy 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVPR 420
Db 352 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVPR 411
Qy 421 VDFHWKFWVTHIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKFWVTHIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471
Qy 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 472 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531
Qy 541 TGTFTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK 600
Db 532 TGTFTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK 591
Qy 601 TPTVGTTPPSFLDQSTFTIGANWFSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
Db 592 TPTVGTTPPSFLDQSTFTIGANWFSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 651
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDEKRELFEIVKYAKQLHIERNM 719
Db 652 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDEKRELFEIVKYAKQLHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Van Mellaert, Herman
APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bc INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 60.6%; Score 2277.5; DB 16; Length 1228;
Best Local Similarity 62.7%; Pred. No. 4.5e-183;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121
Qy 131 LGDALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSGBEVPLLPPIYA 190
Db 122 LGDSFRAYQOSLEDWLENRRDARTSRVLHTQYIALELDLFLNAMPFAIRNQEVPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKWLGSSEISSTFYNNQVERAGDSDHCHVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYYERQVTRDYSDYCVWEYNTGLNLRGTN 241
Qy 251 AESWRYNQFRDMLVLDLVALFPSPDYDTQMPYIKTTAQLTREYVTDALGTVHPHPSFT 310
Db 242 AASWRYNQFRDMLVLDLVALFPSPDYDTQMPYIKTTAQLTREYVTDALGT -GVNMA 299
Qy 311 STTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMWGKLEPRTI 370
Db 300 SMWYNNNAAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMWGKLEPRTI 359
Qy 371 GGTNLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVPRVDFHWKFW 428
Db 360 GGTNLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVPRVDFHWKFW 416
Qy 429 THP-----IASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPQINISDRGTANTSQP-YESPGQLQKUSETELPPETTERPNYESYSHRLSHIGLISASH 475
Qy 484 VKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 543
Db 476 VNVVYVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 535
Qy 544 FGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK 603
Db 536 FGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYK 595
Qy 604 TVGFTTPPSFLDQSTFTIGANWFSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 663
Db 596 TVGFTTPPSFLDQSTFTIGANWFSNGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 655
Qy 664 FTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDEKRELFEIVKYAKQLHIERNM 719
Db 656 FTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDEKRELFEIVKYAKQLHIERNM 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7
Query Match 60.2%; Score 2264.5; DB 10; Length 1207;
Best Local Similarity 64.3%; Pred. No. 5.5e-182;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;
QY 40 EDCLKMEYENVEPVFVASTIQTGIGTAGKILGTGVPFAGQVASYLSPFLGELWPKGN 99
Db 10 EDSLCAEGNIDPFVASTVGTGINTAGRIILGVLGVFPAGQLASFYSLVGLWPRGRD 69
QY 100 QWEIFMEHVEEIIINQKISTYARKALTDKLGIDALAVYHDSLESVGNRNNTARSVVK 159
Db 70 QWEIFMEHVEEIIINQKISTYARKALTDKLGIDALAVYHDSLESVGNRNNTARSVVK 129
QY 160 SQYIALELMFVKLPSPFVSGEVPPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST 219
Db 130 TQYIALELDLFLNAPLFAIRNOEVLPLMVAQAANLHLLLRDASLFGSEFGLTSQEIQ 189
QY 220 FYNRQVERAGDYSCHCKVWYSTGLNLRGTNAESWYRYNQFRDMLTMDLVALPSPYD 279
Db 190 YNRQVERTRDYSYCYVEWYNTGLNLRGTNAESWYRYNQFRDMLTMDLVALPSPYD 249
QY 280 TQMPYPIKTAQLTREVTDAIGTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDPL 339

Db 250 TRTYPIINTSAQLTREVTDAIGAT--GVNMAWMYNNNAPSFSAIEAAIRSPHLLDPL 307
QY 340 EQVTIYLLSRWSNTQYMMMGCHKLEFRITGGTLNISTOGSTNTSINPVTLPTFSRDVY 399
Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFSRDVY 367
QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHKKFVTHP-----IASDNFYYPGVGIGTQLQDS 452
Db 368 RTESYAGVLLWGIYLEPIHGVPTVRNF---TNPQNISDRGTANYSQP-YESPGLQKDS 423
QY 453 ENELPPEATQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPL 512
Db 424 ETELPPEATERPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPL 483
QY 513 VKAFNLSSGAADVVRGPGFTGGDILRLRTNTGFGDIRVNIWNPFPFQARYRVRIRYASTTDLQ 572
Db 484 VKASELPQGTTVVRGPGFTGGDILRLRTNTGFGDIRVNIWNPFPFQARYRVRIRYASTVD 543
QY 573 FHTSINGKAINQGNFSATMNGEDLDYKTRTVGTTPFPFLDQVOSTFTIGAMNFFSGNE 632
Db 544 FVSRGGTTVNFRFLRTMNSGDELKYGNGFVRRAFTTPTFTQIODIIRTSIQGLSGNCE 603
QY 633 VIYDRIEFPVVEVTEAEYDEKAEKQVATLFTSTNPRGLTKVDYHIDQVSNLVESSL 692
Db 604 VIYDKIEIIPVTATFEAEYDLERAQAVNALFTNPRRLKTDVTDYHIDQVSNLVACLS 663
QY 693 DEFYLDKRELFEIVKAKQLHIERNM 719
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690
RESULT 6
US-10-428-961-63
; Sequence 63, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1227
; TYPE: PPT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-63
Query Match 58.2%; Score 2186.5; DB 15; Length 1227;
Best Local Similarity 59.2%; Pred. No. 2.2e-175;
Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;
QY 13 SSNAKVDKISTDSLKN-----ETDIELQINIHEDCLKMEYENVEPVFVASTIQTGIG 65
Db 7 NENEINALSPAVSNHSAQNMLSTDARI-----EDSLCAEGNIDPFVASTVGTGIN 61
QY 66 IAGKILGTGVPFAGQVASYLSPFLGELWPKGNQWEIEMEHEVEEIIINQKISTYARKAL 125
Db 62 IAGRIILGVLGVFPFAGQIASFYSLVGLWPRGRDPWEIEMEHEVEEIIINQKISTYARKAL 121
QY 126 TDLKLGIDALAVYHDSLESVGNRNNTARSVVKSQYIALELMFVKLPSPFVSGEVP 185

Query Match 56.2%; Score 2115; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 2.5e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;
QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHECLKSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQ 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPFAVSGEEVPLPIYA 190
DB 127 LGDSFRAYQQSLEDWLENRDARTSVLYTOYIALELDFLNAFPLFAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVIEWYNTGLNSLRGTN 246
QY 251 AESWRYNQFRDMLVLDLVALFPSTYDQYPIKTAQTREVTDAIGTVHPHPSFT 310
DB 247 AASWRYNQFRDMLVLDLVALFPSTYDQYPIKTAQTREVTDAIGTVHPHPSFT 310
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRPTI 370
DB 305 SMWYNNAPSFSAIEATAVIRSPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRPTI 370
QY 371 GGTNLNISTOGSTNTSINPVLPTFTSRDVRVYTESLAGLNLFP--LTOPVNGVPRVDFHWKVF 428
DB 365 GGLNTSTHGTNTSINPVLPTFTSRDVRVYTESLAGLNLFP--LTOPVNGVPRVDFHWKVF 428
QY 429 --THPIASDNFYYPGVYIGTQLODSENLPEATQPNVYESYSHRSLHIGLISASHVKA 486
DB 425 QNTFERGTANYSQP--YESPGLQKDSLETLPETTERPNVYESYSHRSLHIGLISASHVKA 486
QY 487 LVYSWTHRSADRNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGFGD 546
DB 484 PVSWSHRSADRNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGFGD 546
QY 547 IRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTYKTFRTVG 606
DB 544 MGLNFNTSLQRYRVRVYAAASQTMVLRTVGGSTTFDQGPSTMSANESLTSQSFRFAE 603
QY 607 FTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDYFEKAQEKVTALFTS 666
DB 604 FPVGISASGSQ--TAGISISNNAGRTQTFHFKIEFIPITATFEAEYDLERAQEAVALFTN 662
QY 667 TNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELVYKAKQLHIERNM 719
DB 663 TNPRRLKTDVTDYHIDQVSNLVESLSDSEFYLDKRELFELVYKAKQLHIERNM 715

RESULT 9

US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from *Bacillus thuringiensis*.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: *Bacillus thuringiensis*
US-10-614-524-2
Query Match 56.2%; Score 2115; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 2.5e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;
QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHECLKSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQ 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPFAVSGEEVPLPIYA 190
DB 127 LGDSFRAYQQSLEDWLENRDARTSVLYTOYIALELDFLNAFPLFAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVIEWYNTGLNSLRGTN 246
QY 251 AESWRYNQFRDMLVLDLVALFPSTYDQYPIKTAQTREVTDAIGTVHPHPSFT 310
DB 247 AASWRYNQFRDMLVLDLVALFPSTYDQYPIKTAQTREVTDAIGTVHPHPSFT 310
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRPTI 370
DB 305 SMWYNNAPSFSAIEATAVIRSPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRPTI 370
QY 371 GGTNLNISTOGSTNTSINPVLPTFTSRDVRVYTESLAGLNLFP--LTOPVNGVPRVDFHWKVF 428
DB 365 GGLNTSTHGTNTSINPVLPTFTSRDVRVYTESLAGLNLFP--LTOPVNGVPRVDFHWKVF 428
QY 429 --THPIASDNFYYPGVYIGTQLODSENLPEATQPNVYESYSHRSLHIGLISASHVKA 486
DB 425 QNTFERGTANYSQP--YESPGLQKDSLETLPETTERPNVYESYSHRSLHIGLISASHVKA 486
QY 487 LVYSWTHRSADRNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGFGD 546
DB 484 PVSWSHRSADRNTIENPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGFGD 546
QY 547 IRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTYKTFRTVG 606
DB 544 MGLNFNTSLQRYRVRVYAAASQTMVLRTVGGSTTFDQGPSTMSANESLTSQSFRFAE 603
QY 607 FTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDYFEKAQEKVTALFTS 666
DB 604 FPVGISASGSQ--TAGISISNNAGRTQTFHFKIEFIPITATFEAEYDLERAQEAVALFTN 662
QY 667 TNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELVYKAKQLHIERNM 719
DB 663 TNPRRLKTDVTDYHIDQVSNLVESLSDSEFYLDKRELFELVYKAKQLHIERNM 715

RESULT 10

US-09-826-660-25
; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05


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; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match      51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 2.6e-154;
Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3;

Qy 13 SNAKVDKISTSLKN-----ETDIELQININHEDECLMKSEYENVEPVASITQIGIG 65
Db 7 NENEINALSIPAVSHSAQNLSTDAI-----EDSLCIAEGNNIDPFVSAITVQTGIN 61

Qy 66 IAGKILGTGVFPAGVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTVARNKAL 125
Db 62 IAGRLGLVGVFPAGQIASFYSFLVGELEWPKGRDPWEIFLEHVBEIINQKISTVARNKAL 121

Qy 126 TDLKGLDALAVYHDSLESWGNNRNRNTRARSVVKSQYIALELMFVKLPSPFVSGEEVPL 185
Db 122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSVLYTQYIALELDFLNAMEPLFAIRNQEVPL 181

Qy 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNN 245
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIORYYERQVEKTRYSYDCARWNTGLNN 241

Qy 246 LRGTNABSWRYNQFRDMLTMVLVDLVALPSPYDTQMPYPIKTTAQLTREVIYTDAGTVHP 305
Db 242 LRGTNABSWLRNQFRDMLTGLVDLVALPSPYDTQMPYPIKTTAQLTREVIYTDAGTVHP 301

Qy 306 HPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKL 365
Db 302 PSGFASTNWFNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKL 361

Qy 366 EFRITIGTLNISTQGSNTSINPVLPTFRDVRVTSAGLNLELTPQVNGVPRVDFHW 425
Db 362 ESRITIGSLSTHGTNTSINPVLPTFRDVRVTSAGLNLELTPQVNGVPRVDFHW 421

Qy 426 KFVTHPIASDNFYGVYGVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 485
Db 422 RNPLNLRGSLLYTIGYGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 481

Qy 486 ALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGTFG 545
Db 482 APVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGTFG 541

Qy 546 DIRVINPPFAQRYRIRYASTDLDQFHTSINGKAINQGNFSAATMNRGDLDTFTFTV 605
Db 542 SMGLNFNTSLQRYRVRVYAASTQVLRVTVGSGTTFDQGFPSMTSANESLTSQSFRFA 601

Qy 606 GFTTTPPSFLDVOSTFTTGAMNFSNGNEVYIDRIEFVPEVYVE 648
Db 602 EFPVGISASGSQ-TAGISISNAGRQTFHFDKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

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FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1

Query Match      45.9%; Score 1724.5; DB 14; Length 1167;
Best Local Similarity 48.1%; Pred. No. 2.6e-136;
Matches 362; Conservative 125; Mismatches 220; Indels 45; Gaps 11;

Qy 1 MKLKQDKHQ---SFSSNAKVDKISTDSLKNETDIELQININHEDECLMKSEYE-----NV 51
Db 1 MSPNNQNEYELDASSSTSVSDNSVRYPLANDQTTTLQNMNFKDYLRMSEGENPELFGNP 60

Qy 52 EPFVSASTIQTGIGTAGKILGTGVFPAGVASYLSFILGELWPKGK-NQWEIFMEHVVEE 110
Db 61 ETFISSTVTGIGIGVQVIGALGVFPAGQIASFYSFIVGQLWPSSTVSVWENIMKQVED 120

Qy 111 IINQKISTYARNKALTDLKGLDALAVYHDSLESWGNNRNRNTRARSVVKSQYIALELMFV 170
Db 121 LIDQKITDVRKTAAGLQGLDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180

Qy 171 QKLPSFAVSGEEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGD 230
Db 181 AKIPSPAISGOEVPLLSVAQAANLHLLLRDASIFGAEWGTTPGEISTFYDRQVTRTAQ 240

Qy 231 YSDHCVKWYSTGLNNLRGTNAESVRYNQFRDMLTMVLVDLVALPSPYDTQMPYPIKTTAQ 290
Db 241 YSDYCVKWNLTGLDKLGTNAASWMLKYHQFRREMTLLVDLVALFPNYDTRTYPIETTAQ 300

Qy 291 LTREVTDAIGTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLS- 349
Db 301 LTREVTDPVFNRETSGFCRRWSLNSDISFSEVASVIRSPHLFDILSEIEFYTTTAG 360

Qy 350 -RWSNTQYMMWGGHKLFPRTIGTIGTLNISTQGSNTSINPVLPTFRDVRVTSAGLN-AGL 407
Db 361 LPLNTEYLEYVWGHGSIKYKNTNASSALERNYGTITSNKKIYVDLANKDIFQVRSGLADL 420

Qy 408 NLFLTQPVNGVPRVDFHWKVFTHPIASDNFYGVYGVG-----IGTQLODSENE 455
Db 421 ANYYAQ-VYGVYASF-----TLDDKNTGSGVGGFTYSKPHTTQVCTQNYNTIDE 471

Qy 456 LPPEATGQPNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRSADRTNTEPNSI 507
Db 472 IPPE--NEPLSRGYSHRLSHITSYSPKNAASSPARYGNLPVFAWTHRSADRTNTEPNSI 529

Qy 508 TQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGTFGDIRVINPPFAQRYRIRYAS 567
Db 530 TQIPVKAHTLVSGTIVIKGPGFTGGNLLKRTSSGPLAYTSVSKSPLSQRYRARIRYAS 589

Qy 568 TTDQFHTSINGKAINQGNFSAATMNRGDLDTFTFTVGTTPPSFLDVQSTFTIGANNF 627
Db 590 TTNLRLFTVITSGTRIYSINVKNTMKNKGGDLTFTNTFDLATIGTAFSTFNSYSDSLTVGADSF 649

Qy 628 SSGNEVYIDRIEFVPEVYVEAEYDFEKAQEKVATLTFTNPRGLKTDVKDHYHIDQVSNL 687
Db 650 ASGGEVYVDKELIPVNATFEAEEDLDVAKAVNGLFTSKKD-ALQTSVTDYQVNOAANL 708

Qy 688 VESLSDEFYLDKRELFEIVKAKQLHIERNM 719
Db 709 VECLSDLYPNEKRLMDVAKEAKRLVQARNL 740

RESULT 12

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Db 523 SKITQIPAVKGMILYGGVVQPGFTGGDILKRTNPSILGTFAVTNGSLSORVRRI 582
Qy 564 RYASTTDLQFHTSINGKAINQGNFSGATMNRGEDLDYKTRFTVGTTPPSFLDVQSTFTIG 623
Db 583 RYASTTDFEF-TLYLGDITIEKRFNKMTONGASLTYYETFKFASFITDQFRETQDKILLS 641
Qy 624 AWFSSGNEVYIDRIEFVPEVYEAEDFEKAEKVTAFTSTNPRGLKTDVKDHYDQ 683
Db 642 MGFSSQEVYIDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700
Qy 684 VSNLVESLSDRYLDEKRELFEIVKYAKQLHIERNM 719
Db 701 AANLVESLSDRYLDEKRELFEIVKYAKQLHIERNM 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 40.2%; Score 1510; DB 13; Length 1206;
Best Local Similarity 44.3%; Pred. No. 3.9e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFANEPTNALQNMVDYKLYKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVAVSLYSFILGELWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAIDIVGKLLSGLVFPVGPVSLYTLQIDILWPSGKESQWEIFMEQV 119
Qy 109 EEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNNYQLYLTALKEEENPNPNSRALDRVRNFEILDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 228
Db 180 FTQYMPSEFRVNFEPFLTVYAMAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 239
Qy 229 GYSDHCVKYSTGLNLRGNAESWVRNQFRDMLVLDLVALFSPYDQMPYIKTT 288
Db 240 AEYSDHCVKYETGLAKLKGTSKQWVDVYQFRREMTLAVLDVVALFPNYDTRTPMETK 299
Qy 289 AQLTREYVTDAGTVHPHPSSTSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSL 348
Db 300 AQLTREYVTDPLGAVNV--SIGSWY-DKAPSGFVIESVIRPHVFDYITGLTVYTS 355
Qy 349 SRWSNTQYMMWGGHKLFRFTIGTGLNISTQGSTNTSINPV-TLPFTSRDVRVRESLAGL 407
Db 356 RSISARYIRHWAGHOISYHRVSRGSLNQMYGTQNHLHSTSTFDFTNYDIYKTLKSDAV 415
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Qy 408 NLFLTP-----VNGVPRVDFHMKFVTHPIASDN---FVYPGVYVIGTQLODSENELEPPE 459
Db 416 LLDIVVPGYTYIFFGMEVEF---FMVQLNNTKTKLYNPVSKDIIASTRDELELPE 472
Qy 460 ATQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKAF 516
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNITVSDKITQIPAVKCM 532
Qy 517 NLSGAAVVRGPGFTGDLR-RTNTGTFGDI---RVNINPPAQRVVRIRYASTTDLQ 572
Db 533 DNLFPVVKVPGFTGGDLQYNRSTGSGVTLFLARYGLALEKAGKRVRLRYATDADIV 592
Qy 573 PHTSINGKALNQGNFSATMNRGEDLDYKTR-----TVGFTTTPFSFL-----DVQST 619
Db 593 LH--VNDQI---QMPKTNWPGEDLTSTKFKVADAITTLNLTATDSSLAKHNLGDEPNST 647
Qy 620 FTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAEKVTAFTSTNPRGLKTDVKDY 679
Db 648 LS-----GIVYVDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDY 697
Qy 680 HIDQVSNLVESLSDRYLDEKRELFEIVKYAKQLHIERNM 719
Db 698 EVNQANLVESLSDRYLDEKRELFEIVKYAKQLHIERNM 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 40.2%; Score 1510; DB 14; Length 1206;
Best Local Similarity 44.3%; Pred. No. 3.9e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFANEPTNALQNMVDYKLYKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVAVSLYSFILGELWPKG-KNOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAIDIVGKLLSGLVFPVGPVSLYTLQIDILWPSGKESQWEIFMEQV 119
Qy 109 EEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNNYQLYLTALKEEENPNPNSRALDRVRNFEILDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 228
Db 180 FTQYMPSEFRVNFEPFLTVYAMAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERA 239
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds
(without alignments)
2403.590 Million cell updates/sec

Title: US-10-019-823B-57
Perfect score: 3760
Sequence: 1 MKLKNQDKHQSPSSNAKVDK.....KRELPEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3752	99.8	719	3	US-08-286-870A-8
2	3472.5	92.4	710	4	US-09-661-322A-42
3	3394	90.3	648	3	US-08-286-870A-4
4	3373	89.7	719	2	US-09-003-217-2
5	3368	89.6	719	3	US-09-218-942-2
6	2800	74.5	535	3	US-08-286-870A-6
7	2445.5	65.0	1229	1	US-08-100-709-4
8	2445.5	65.0	1229	1	US-08-176-865-4
9	2445.5	65.0	1229	2	US-08-474-038-4
10	2445.5	65.0	1229	2	US-08-779-046-4
11	2445.5	65.0	1229	2	US-08-881-340-4
12	2340.5	62.2	488	1	US-08-448-170-10
13	2340.5	62.2	488	3	US-08-961-803-10
14	2264.5	60.2	1207	1	US-07-951-715A-7
15	2264.5	60.2	1207	2	US-08-459-448A-7
16	2264.5	60.2	1207	3	US-08-459-595A-7
17	2264.5	60.2	1207	3	US-08-459-504B-7
18	2264.5	60.2	1207	3	US-08-459-444-7
19	2264.5	60.2	1207	3	US-09-053-549-8
20	2264.5	60.2	1207	3	US-09-547-422-7
21	2264.5	60.2	1207	4	US-09-988-462-7
22	2263.5	60.2	1227	3	US-09-053-549-2
23	2195.5	58.4	1227	1	US-08-448-170-8
24	2195.5	58.4	1227	3	US-08-961-803-9
25	2186.5	58.2	1227	4	US-09-661-322A-63
26	2171.5	57.8	1186	3	US-09-178-252-23
27	2171.5	57.8	1186	4	US-09-826-660-23

28	2115	56.2	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1932.5	51.4	643	3	US-09-178-252-25	Sequence 25, Appl
30	1932.5	51.4	643	4	US-09-826-660-25	Sequence 25, Appl
31	1900	50.5	380	5	PCT-US91-02560-4	Sequence 4, Appli
32	1680.5	44.7	653	4	US-09-661-322A-6	Sequence 6, Appli
33	1669.5	44.4	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1669.5	44.4	1157	1	US-07-812-180A-2	Sequence 2, Appli
35	1669.5	44.4	1157	1	US-08-315-468-2	Sequence 2, Appli
36	1669.5	44.4	1157	3	US-07-941-650A-2	Sequence 2, Appli
37	1505.5	40.0	1176	1	US-08-257-999-2	Sequence 2, Appli
38	1494	39.7	1157	2	US-08-532-547-5	Sequence 5, Appli
39	1494	39.7	1157	2	US-08-379-656B-5	Sequence 5, Appli
40	1494	39.7	1157	3	US-08-455-838-5	Sequence 5, Appli
41	1494	39.7	1157	3	US-09-019-809-5	Sequence 5, Appli
42	1494	39.7	1157	4	US-09-471-177-5	Sequence 5, Appli
43	1494	39.7	1157	4	US-09-220-806-5	Sequence 5, Appli
44	1487.5	39.6	1156	3	US-09-002-285-72	Sequence 72, Appl
45	1487.5	39.6	1156	4	US-09-589-477-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Query Match 99.8%; Score 3752; DB 3; Length 719;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 MKLKNQKHQSSNAKVDKISTDSLKNETDIQLQNHEDCLKMSEYENVPFVSASTI 60
1 MKLKNQKHQSSNAKVDKISTDSLKNETDIQLQNHEDCLKMSEYENVPFVSASTI 60
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121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQSYIALELMFVQKLPSPFVSG 180
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661 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
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RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (200)..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 92.4%; Score 3472.5; DB 4; Length 710;
Best Local Similarity 92.4%; Pred. No. 1.9e-302;
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;
1 MKLKNQKHQSSNAKVDKISTDSLKNETDIQLQNHEDCLKMSEYENVPFVSASTI 60
1 MKLKNQKHQSSNAKVDKISTDSLKNETDIQLQNHEDCLKMSEYENVPFVSASTI 60
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61 QTGIGIAGKILGTGVFPAGQVASYLSFIIGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
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601 TFRVGTTPFSDVQSTFTIGAMNFSNGNEVIDRIEFVPEVVEYAEYDFEKAQEKV 660
601 TFRVGTTPFSDVQSTFTIGAMNFSNGNEVIDRIEFVPEVVEYAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
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RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 90.3%; Score 3394; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. No. 1.8e-295;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINIHEDCLKMSEYENVEPVSASTI 60
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Qy 181 BEVPLPIYQAANLHLLLRDASIFGKEWGLSSSEISFTFYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLPIYQAANLHLLLRDASIFGKEWGLSSSEISFTFYNQVERAGDYSCHVKWYS 240
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Db 301 GTVHPHPSFTSTTWNNNAPSFAEAADVVRNPHLLDFLEQVITYSLLSRWNSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTPVNGVPR 420
Db 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTPVNGVPR 420
Qy 421 VDFHWKFPVTHPIASDNFYYPGCVGIGTQLODSENELPPEATGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYYPGCVGIGTQLODSENELPPEATGPQNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAADVVRGPGFTGGDILARTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAADVVRGPGFTGGDILARTN 540
Qy 541 TGTGDIRVINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYE 648
Db 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYE 648
RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osmann, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.7%; Score 3373; DB 2; Length 719;
Best Local Similarity 89.7%; Pred. No. 1.7e-293;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;
Qy 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQFTLSSNAKVDKIATDSLKNETDIELKNMKNEDYLRMSEHESIDPFVSASTI 60
Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSYFLLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVPPAGQVASYLSYFLLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGGLDALAVYHDSLESWVGNRNTRARSVVKVSKQYIALELMFVQKLPSPFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWVGNRNTRARSVVKVSKQYIALELMFVQKLPSPFAVSG 180
Qy 181 BEVPLPIYQAANLHLLLRDASIFGKEWGLSSSEISFTFYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLPIYQAANLHLLLRDASIFGKEWGLSSSEISFTFYNQVERAGDYSCHVKWYS 240

Db 181 EEVPLLPYQAANLHLLLRDASIFKKNGLSSEISTFYNQVERTRDYSYHCWKNN 240
Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREVYTDAL 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREVYTDAL 300
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Db 301 GTVDPNQALRSITWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGGTLNISTQGSNTNTSINPVTLPFTSRDVTYTESLAGNLFLTQPVNGVPR 420
Db 361 GGHRLSREPIGGALNTSTQGSNTNTSINPVTLPFTSRDVTYTESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
Db 481 GSHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
Qy 541 TGTGDIRVNINPPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
Db 541 SGTFGHIRVNINPPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
Qy 601 TFRVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TFRVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Qy 719 TALFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQIHIERNM 719
Db 719 TALFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: Crv11
; CURRENT APPLICATION NUMBER: US/09/218,942
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

Query Match 89.6%; Score 3368; DB 3; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.7e-293;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDLSKNETDIELQINHDCLXMEVENVEPVSASTI 60
Db 1 MKLKNPDKHQTLSSNAKVDKIATDLSKNETDIELKNMNNEDYLRMSEHSDIPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPPAGQVASYLFGILGELWPKGNQKQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQVASYLFGILGELWPKGNQKQWEIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALTDLKGLGDALAVHDSLSWSVGNRNNTARSVVKSYIALELMFVKLPSFAVSG 180
Db 121 RNKALTDLKGLGDALAVHDSLSWSVGNRNNTARSVVKSYIALELMFVKLPSFAVSG 180

Qy 181 EEVPLLPYQAANLHLLLRDASIFKKNGLSSEISTFYNQVERAGDYSCHCVKWS 240
Db 181 EEVPLLPYQAANLHLLLRDASIFKKNGLSSEISTFYNQVERTRDYSYHCWKNN 240
Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREVYTDAL 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMYPIKTTAQLTREVYTDAL 300
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Db 301 GTVDPNQALRSITWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGGTLNISTQGSNTNTSINPVTLPFTSRDVTYTESLAGNLFLTQPVNGVPR 420
Db 361 GGHRLSREPIGGALNTSTQGSNTNTSINPVTLPFTSRDVTYTESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGHILRRTK 540
Qy 541 TGTGDIRVNINPPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
Db 541 SGTFGHIRVNINPPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
Qy 601 TFRVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TFRVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Qy 719 TALFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQIHIERNM 719
Db 719 TALFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.5%; Score 2800; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 2.6e-242;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60

Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

Qy 121 RNKALTDLKGIGDALAVYHDSLESWGNRNNTARSVKVQYIALELMFVQKLPSPFVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLESWGNRNNTARSVKVQYIALELMFVQKLPSPFVSG 180

Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240

Qy 241 TGLNNLRGTNAESWRYNQFRDMLMVLVALPSPYDTQMPYIKTTAQLTREYVTDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLMVLVALPSPYDTQMPYIKTTAQLTREYVTDAI 300

Qy 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360

Qy 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVTSIAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVTSIAGLNLFLTQPVNGVPR 420

Qy 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryETS
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

Qy 13 SSNAKVYDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSDPDARTEDSLCVAEYNNIDPVSASTVQTGINIAGRI 66

Qy 71 LGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126

Qy 131 LGDALAVYHDSLESWGNRNNTARSVKVQYIALELMFVQKLPSPFVSGEVPPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEVPPLMVA 186

Qy 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYSTGLNNLRGTN 250
Db 187 QAANLHLLLRDASIFGSEWGMASDDVNOYQEQIRYITEYSNHCVQWYNTGLNNLRGTN 246

Qy 251 AESWRYNQFRDMLMVLVALPSPYDTQMPYIKTTAQLTREYVTDAIQVHPHPSFT 310
Db 247 AESWRYNQFRDMLMVLVALPSPYDTQMPYIKTTAQLTREYVTDPIGRTNAPSQFA 306

Qy 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGHHKLEFRTI 370
Db 307 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGHHKLEFRTI 366

Qy 371 GGTTLNISTQGST-NTSINPVTLPFTSRDVRVTSIAGLNLFLTQPVNGVPRVDFHWKFTV 429
Db 367 GGTTLNISTQGST-NTSINPVTLPFTSRDVRVTSIAGLNLFLTQPVNGVPRVDFHWKFTV 422

Qy 430 HPIASDNFYPG-----YVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPETTERPNYESYSHRLSHIGLI 480

Qy 483 HVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAVYSWTHRSADRTNTEPNISITQIPLVKALNLSGAAVVRGPGFTGGDILRRNTG 540

Qy 543 TFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTF 602
Db 541 TFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTF 600

Qy 603 RTVGFTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662
Db 601 RTAGFSTPFNFLNAQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 659


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663 LFTSTNPRGLKTDVYHIDQVSNLVSDFYLDKRELFVIVKYAKQLHIERNM 719
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
660 LFTSTNPRRLKTDVYHIDQVSNMVACLSDFCLEKRELFVIVKYAKRLSDERNL 716

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-865-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 139; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDLSKN-ETDIELQ-NINHEDCLKMSEYENVEPVFVASTIQGIGIAGKI 70
DB 7 NENEIINALISPTVSNPSTQMNLSPDARIEDSLCVAEVNIDPFVFASTVQTGINIAGRI 66

QY 71 LGTIGVVPFAGQVASYLSFTILGELMPKGNQWEIFMEHVVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVFPFAGQLASFYSFLVGLMPWGRDPWEIFLEHVQELIRQOVTRNTAIARLEG 126

QY 131 LGDALAVYHDSLSWVGNNRNTARSVVKSQYIALELMFVQKLPSPFVSGSEYVPLLPITYA 190
DB 127 LGRGYRSYQQALETWLDNRDARSIIILERYVALELDITTAIFLFRINREEVPLLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEWGMASDVNOYYQEIRYRTEYSNHCVQWYNTGLNNLRGTN 246

QY 251 AESWRYNQPRFRMTLMVLDLVALFPSPDYTMQYPIKTTAQLTRVYVYTDALGTVHPHPSPT 310

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	DB	247	AESWLRYNQFRRDLTLGLVDLVALFPYSYDTRTYPINTSAQLTREIYTDPIGRNTAPSGFA	306
	QY	311	STTWYNNAPSFAIEAAVVRNPHLLDFLEOVTTISLLSRWSNTQYMMNMGGHKLERTTI	370
	Db	307	SINWFENNAPSFAIEAAIFRPPLHLDFPEQLTIYSASSRSWSSTQHMYNVWGHRNLFRPI	366
	QY	371	GGTLNISTQGST-NTSINPVTLPTFSRDVVRTESLAGLNLFLTQPVGNGVPRVDPHWKFTV	429
	Db	367	GGTINTSTOGLTNNTSINPVTLQFTSRDVVRTESNAGTNILFTTPVNGVPWARENF----	422
	QY	430	HPIASDNFYPG-----YVGIGTQLODSENELPPEATCQPNVESYSHRLSHIGLISAS	482
	Db	423	--INPQNIYERGATTYSOPYOGVGILQFDSETELPETTERPNYESYSHRLSHIGLIIGN	480
	QY	483	HVKALVYSWTHRSADRTNTEBPSNITQIPLVKAFLSSGAAVVRGPFGFTGGDIURRTWTG	542
	Db	481	TLRAPVYSWTHRSADRNTIGNRITQIPLVKALNLHSGVTVVGGPGFTGGDILARTWTG	540
	QY	543	TFGDIRVNINPPFAQRVRIRIYASTTDLOEHTSINGKAINQGNFSATMNRGEDLDYKTF	602
	Db	541	TFGDIRLVNINVLPSQRVRIRIYASTTDLOEFTRINGTTVINIGNSRTWNRGDNLERSF	600
	QY	603	RIVGFTTFPSFLDVQSFTTIGAWFNSSGNEVVIDRIEFVPVEVTYEAAYDFEQAQEKVTA	662
	Db	601	RTAGFSTPFNFLNAQSTFTLGAQSFNS-QEVYIDRVFEVFPAEVTFEAEYDLERAQXAVNA	659
	QY	663	LFTSTNPRLKTDVKDHIDQVSNLYESLSDEFYLDEKRELFKEIKVYAKOLHIERNM	719
	Db	660	LFTSTNPRLKTDVTDYHDQVSNMVACLSDFCLEKRELFKEIKVYAKRLSDERNL	716
		RESULT 9		
		US-08-474-038-4		
		; Sequence 4, Application US/08474038		
		; Patent No. 5679343		
		; GENERAL INFORMATION:		
		; APPLICANT: Donovan, William P.		
		; APPLICANT: Tan, Yiping		
		; APPLICANT: Jany, Christine S.		
		; APPLICANT: Gonzalez Jr., Jose M.		
		TITLE OF INVENTION: BACILLUS THURINGIENSIS ctyET4 AND ctyETS		
		TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS		
		NUMBER OF SEQUENCES: 5		
		CORRESPONDENCE ADDRESS:		
		ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.		
		ADDRESSEE: Nadel		
		STREET: 1601 Market Street, 36th Floor		
		CITY: Philadelphia		
		STATE: Pennsylvania		
		COUNTRY: U.S.A.		

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,038
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,865
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMEYENVEPVFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

Qy 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQLASFSYFLVGLWPSGRDPWEIFLEHVQQLIRQQVTENTRTAIARLEG 126

Qy 131 LGDALAVYHDSLESVWGNRNTRARSVKSOYIALELMFVQKLPSPFAVSGEVEPLLPYIA 190
Db 127 LGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIFLRIRNEEVPLLMYYA 186

Qy 191 QAAHLHLLLRDASIFGKHWGLSSSEISTFYNRQVERAGDYSCHVCWKYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEYSNHCYQVNTGLNNLRGTN 246

Qy 251 AESWVRYNQFRDMDTLMLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 310
Db 247 AESWLRYNQFRDMDTLMLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 306

Qy 311 STTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFRPTI 370
Db 307 STNWFNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFRPTI 366

Qy 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRVYRTESLAGLNLFLTPQVNGVPRVDFHWKFTV 429
Db 367 GGTLNISTQGST-NTSINPVTLPFTSRDVRVYRTESLAGLNLFLTPQVNGVPRVDFHWKFTV 422

Qy 430 HPIASDNFYYPG-----YVGIGTQLQDSNELPPEATGPQNPYESYSHRSLHIGLISAS 482
Db 423 --INPQNIYERGATTYSQYQGVGLQFDSSETLPETTERPNYESYSHRSLHIGLIIGN 480

Qy 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDILRRNTG 542
Db 481 TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGPGFTGGDILRRNTG 540

Qy 543 TFGDIRVNINPPFAQYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGBDLKYTF 602
Db 541 TFGDIRNLINPLSQYRVRIRYASTTDLQFFTRINGTTVNGFNFSRTWNRGDNLEYSF 600

Qy 603 RTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFYVPEVTEYAEYDFEKAQEKVTA 662
Db 601 RTAGFSTPFNFNAQSTFTLGAQSFNS-QEYVIDRVEFPAEVTFEAEYDLERAQKAVNA 659

Qy 663 LFTSTNPRGLTKDVKYHIDQVSNLVESLSDFEYLDKELFEIVKYAKQLHIERNM 719
Db 660 LFTSTNPRGLTKDVKYHIDQVSNLVESLSDFEYLDKELFEIVKYAKQLHIERNM 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jan, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYETS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```


QY 543 TFGDIRVNPPFAORYRIRYASTDLOPHTSINGKAINQNSFATMNRGDDLYKTF 602
DB 541 TFGDIRLNINPLSQRYRIRYASTDLOPHTRNGTNNIGNSFRTNWRGNLEVRSP 600
QY 603 RTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVFEVVEAEYDFEKAQKVTA 662
DB 601 RTAGFSTFNFNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFEAEYDLERAQKAVNA 659
QY 663 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 719
DB 660 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-881-340-4

Query Match 65.0%; Score 2445.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;
QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVANNIDFVSASTVQTGINIAGRI 66
QY 71 LGTLGVFPAGVASYLSFILGELWPKGNQWEIEFWEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVFPAGVASYLSFILGELWPKGNQWEIEFWEHVEEIIINQKISTYARNKALTDLKG 126
QY 131 LGDALAYHDSLSWYGNRNTRARSVKQSYIALFMFQKLPSEAVSGEEVPLPIYA 190

DB 127 LGRGYSYQOALETWLDNRDARSRIILERYVALELDITTAIPLEIRNEEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSDHCVKWKYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASIFGSEWGMASDVNQYQOIRYTEYSNHCQWYNTGLNNLRGTN 246
QY 251 AESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTAQLTREVYTDAGTVVHPHPSFT 310
DB 247 AESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTAQLTREVYTDAGTVVHPHPSFT 306
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVYIYLLSRWNTQYNNMGGHKLFRPTI 370
DB 307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVYIYLLSRWNTQYNNMGGHKLFRPTI 366
QY 371 GGTLANISTQGST-NTSINPVTLPTSRDYRTESLAGNLFLTQPVNGVPRVDFHMKFVT 429
DB 367 GGTLANISTQGST-NTSINPVTLPTSRDYRTESLAGNLFLTQPVNGVPRVDFHMKFVT 422
QY 430 HPIASDNFYYPG-----YVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPPETTERPNYESYSHRLSHIGLIGN 480
QY 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTG 542
DB 481 TLRAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTG 540
QY 543 TFGDIRVNINPPFAORYRIRYASTDLOPHTSINGKAINQNSFATMNRGDDLYKTF 602
DB 541 TFGDIRLNINPLSQRYRIRYASTDLOPHTRNGTNNIGNSFRTNWRGNLEVRSP 600
QY 603 RTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVFEVVEAEYDFEKAQKVTA 662
DB 601 RTAGFSTFNFNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFEAEYDLERAQKAVNA 659
QY 663 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 719
DB 660 LFTSTNPRGLKTDVQYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 716

RESULT 12
US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Steelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.2%; Score 2340.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 3.8e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSIKNETDIELQINHEDECLMKSEYENVEPFVSASTI 60
Db 1 MKSKNQMHQSLSNNATVDKNFTGSLNNTNTLQNFH-----EGIEPFVSASTI 51

Qy 61 QTGIGIAGKILGTGLVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGQWEIFMEHVEELINQKISTYA 111

Qy 121 RNKALTDLKGDLAVYHDSLESWVGNNRNNTRARSVVKSQYIAELMFKVQLPSPFAVSG 180
Db 112 RNKALADLKGDLAVYHESLESWIENRNNTRRSVVKSQYITLMLFVQSLPSPFAVSG 171

Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNNRQVERAGDYSCHVKWYS 240
Db 172 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNNRQSGKSKYSCHVKWYN 231

Qy 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYVTDAI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYVTDAI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 351

Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420
Db 352 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 411

Qy 421 VDFHWKFTVTHPTASDNFYYPGCVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKFTVTHPTASDNFYYPGAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 481 ASHVKALVYSWTHRSAD 497
Db 472 ASHVKALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 62.2%; Score 2340.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 3.8e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSIKNETDIELQINHEDECLMKSEYENVEPFVSASTI 60
Db 1 MKSKNQMHQSLSNNATVDKNFTGSLNNTNTLQNFH-----EGIEPFVSASTI 51

Qy 61 QTGIGIAGKILGTGLVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGQWEIFMEHVEELINQKISTYA 111

Qy 121 RNKALTDLKGDLAVYHDSLESWVGNNRNNTRARSVVKSQYIAELMFKVQLPSPFAVSG 180
Db 112 RNKALADLKGDLAVYHESLESWIENRNNTRRSVVKSQYITLMLFVQSLPSPFAVSG 171

Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNNRQVERAGDYSCHVKWYS 240
Db 172 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNNRQSGKSKYSCHVKWYN 231

Qy 241 TGLNNLRGTNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYVTDAI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMLMVLDLVALFPSTQMYPIKTTAQLTREYVTDAI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 351
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QY 361 GGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVTSTESLAGLNLFLTOPVNGVPR 420
DB 352 GGHKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVTSTESLAGLNLFLTOPVNGVPR 411
QY 421 VDFHKKFVTHPTASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
DB 412 VDFHKKFVTHPTASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 471
QY 481 ASHVKALVYSWTHRSAD 497
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-951-715A-7

Query Match 60.2%; Score 2264.5; DB 1; Length 1207;

Best Local Similarity 64.3%; Pred. No. 1.1e-193;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;
QY 40 EDCLKMSEVENVEPVFSASTIQTGIGIAGKILGTGVFPAGOVASISYFIIGELWPKGN 99
DB 10 EDSLCTIAEGNIDPFVSASTVQTGINIAGRIILGVLPVFPAGQLASFYSFLVGELWPRGRD 69
QY 100 QWEIFMEHVEEIIINQKISTYARKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVK 159
DB 70 QWEIFLEHVEQLINQOITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTSVLY 129
QY 160 SOYIALELMFVQKLPFSFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKWLSSSEIST 219
DB 130 TOYIALELDFLNAMPLEFAIRNQEVPPLIMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189
QY 220 FYNQVERAGDYSCHVCWYSTGLNNLRGTNAESWRYNQFRDRLMTLMVLDLVALFPYSYD 279
DB 190 YYERQVTRDYSDYCVIEWYNTGLNSLGTNAASWRYNQFRDRLMTLMVLDLVALFPYSYD 249
QY 280 TOMPIKTTAQLTREVYTTDAIGTGVHPHSFTSTTWNANNAPSFAIEAAVVRNPHLLDFL 339
DB 250 TRTYPINTSAQLTREVYTTDAIGAT--GVNMAWMNWNANNAPSFAIEAAAIIRSPHLLDFL 307
QY 340 EQVTIYLLSRWSNTQYMMNMGHKLFPRTIGTGLNISTQSTNTSINPVTLPFTSRDVS 399
DB 308 EQLTIESASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGAINTSINPVTLPFASRDVY 367
QY 400 RTESLAGLNL--LTPQVNGVPRVDHMKFVTHP-----IASDNFYYPGVGIGTQLODS 452
DB 368 RTESYAGVLLWGIYLEPIHGVPTVRFNF---TNPQNISDRGTANYSQP-YESFGLQKDS 423
QY 453 ENELPEATGQPNYESYSHRSLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512
DB 424 ETELPPETTERPNYESYSHRSLSHIGIILQSRVNVVYVSWTHRSADRTNTIGPNRITQIPM 483
QY 513 VKAFNLSSGAAVVRGPGFTGDDILRRNTTGTGDIRVINNPFAQRYVRIRYASTTDLQ 572
DB 484 VKASELPQGTTVVRGPGFTGDDILRRNTTGTGDIRVINNPFAQRYVRIRYASTTDLQ 543
QY 573 FHTSINGKAINQNFSAFMARGEDLDYKTRFTVGTFTTFFSFLDVQSTFTIGANFFSSGNE 632
DB 544 FVSVRGTTVNNFRFLRTMNSGDELKYNFVRAFTTPTFTTQIQTIDRTSIQGLSGNGE 603
QY 633 VYIDRIEFVPEVTVYEAEDFEKAEKVATLFTSTNPRGLKTDVKYHIDQVSNLVESLS 692
DB 604 VYIDKIEIIPVTATFEAYDLERAQEAVALFTNTNPRLKTVDYHIDQVSNLVACLS 663
QY 693 DEFYLDKRELFEIVKVKQLHIERNM 719
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.


```

1  TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE HAVING ENHANCED
2  TITLE OF INVENTION:  INSECTICIDAL ACTIVITY IN MAIZE
3  NUMBER OF SEQUENCES:  94
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  No. 5859336artis Corporation
6  STREET:  Patent & Trademark Dept., 520 White Plains
7  STREET:  Rd., POB 2005
8  CITY:  Tarrytown
9  STATE:  New York
10 COUNTRY:  USA
11 ZIP:  10591-9005
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE:  Floppy disk
14 COMPUTER:  IBM PC compatible
15 OPERATING SYSTEM:  PC-DOS/MS-DOS
16 SOFTWARE:  PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER:  US/08/459,448A
19 FILING DATE:  02-JUN-1995
20 CLASSIFICATION:  800
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER:  US 07/951,715
23 FILING DATE:  25-SEP-1992
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:  US 07/772,027
26 FILING DATE:  04-OCT-1991
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  Pace, Gary M.
29 REGISTRATION NUMBER:  40403
30 REFERENCE/DOCKET NUMBER:  CGC 1577/CIP/DIV4
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE:  (919)541-8582
33 TELEFAX:  (919)541-8689
34 INFORMATION FOR SEQ ID NO:  7:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH:  1207 amino acids
37 TYPE:  amino acid
38 TOPOLOGY:  linear
39 MOLECULE TYPE:  protein
40 US-08-459-448A-7

```

	Query Match	60.2%;	Score 2264.5;	DB 2;	Length 1207;
	Best Local Similarity	64.3%;	Pred. No. 1.1e-193;		
	Matches 442;	Conservative 78;	Mismatches 154;	Indels 13;	Gaps 5
Qy	40	EDCLKMSEYENVEBPVSASTIQTGGIAGKILGTIGVPPAGQVASLSYFILGELMPKGN	99		
Db	10	EDSLCIAEGNNIDPFVSATVQTGINIAGRILGVLGVPPAGQLASFYSLVIGELWPRGR	69		
Qy	100	QWEIFMEHVVEEII NQKISYIYARNKALTDLKGGLDALAVTHDSLESWVGNNRNNTRARSVK	159		
Db	70	QWEIFLEHVEQLINQOITENARNALARLQGLGDSFRAYQQSLEDWLENRDDARTSVLY	129		
Qy	160	SQYIALELMFVQKLPFAVSGEEVPLPIYAAQANLHLLLRDASIFGKRWGLSSSEIST	219		
Db	130	TOYIALELDFLNAMPFLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEFGLTSQEIQR	189		
Qy	220	FYNQVERAGDYSDBCVKWYSTGLNNLRGTNAESWRYNQFRDDMTLMVLDLVALFPSYD	279		
Db	190	YYERQVERTRDYSYCVWEYNTGLNSLRGTNAASWRYNQFRDULTGLVLDLVALFPSYD	249		
Qy	280	TQMYPKTTAQLTREVVYDAIGTVHHPSETSTTWYNNNAPSFSAIEAAVVRNPHLLDFL	339		
Db	250	TRTYPINTSAQLTREVVYDAIGAT--GVNMASMNWYNNNAPSFSAIEAAAIRSPHLLDFL	307		
Qy	340	EQVTIYSLRSWNTQYNNMWGGHKLFRITIGGTILNISTOGSTNTSINPVTLPFTSRDVI	399		
Db	308	EQLTIFSSRSWNRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDVI	367		
Qy	400	RTESLAGLNLF--LTQPVNGVPRVDPHKVEVTHP-----IASDNFYYPGVIGIGTQLQDS	452		
Db	368	RTESYAGVLLWGIYLEIPHGVTYRFNF---TNPONISDRGTANTYTOP--YESPGLOLKDS	423		

453	Qy	ENELPPEATGQPNVYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL	512
424	Db	ETELPPETTERPNVYESYSHRLSHIGIILQSRVNVVPVYSWTHRSADRTNTIGPNRITQIPM	483
513	Qy	VKAFNLSSGAAVVRGPGTGGDILRRNTGTFTGDIRVNINPPFAQRYRVIRYASTTDLQ	572
484	Db	VKASELPQGTTVVRGPGTGGDILRRNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFD	543
573	Qy	FHTSINGKAINQGNFSAWMNGBDLDYKTFRTVGTTPPSFLDVQSTFTTGAWNFSSGNE	632
544	Db	FFVSRGGTTVNNRFLRTMNSGDELKYGNFVRRAFTTPFTTQDIIRTSIQGLSGNGE	603
633	Qy	VYIDRIEVPVVEVYEAEDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLS	692
604	Db	VYIDKIEIIPVTATFEAYDRLERAQEAVALFTNTNPRELKTDVTDYHIDQVSNLVACLS	663
693	Qy	DEPYLDEKRELFPIVKYAKQLHIERNM	719
664	Db	DEPCLDEKRELFKVKYAKRLSDERNL	690

Search completed: February 14, 2005, 20:59:06
Job time : 25.3302 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds
(without alignments)
2827.419 Million cell updates/sec

Title: US-10-019-823B-57
Perfect score: 3760
Sequence: 1 MKLKQDKHQSFSSNAKVDK.....KRELFEIVYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	4	Aab66910 Insectici
2	3760	100.0	719	6	Aae36274 B. thurin
3	3756	99.9	719	4	Aab66908 Insectici
4	3756	99.9	719	6	Aae36272 B. thurin
5	3756	99.9	719	8	Adr89421 cryIIa.1
6	3747	99.7	719	4	Aau02095 Bacillus
7	3745	99.6	719	4	Aab66911 Insectici
8	3745	99.6	719	6	Aae36275 B. thurin
9	3739	99.4	719	4	Aab66909 Insectici
10	3739	99.4	719	6	Aae36273 B. thurin
11	3735	99.3	719	2	Aar08041 81 kD end
12	3724.5	99.1	718	6	Aae36271 B. thurin
13	3718.5	98.9	718	4	Aab66907 Insectici
14	3547	94.3	719	7	Adm74717 B. thurin
15	3516	93.5	719	4	Aab66912 Insectici
16	3516	93.5	719	6	Aae36276 B. thurin
17	3472.5	92.4	710	4	Aau02041 B. thurin
18	3393	90.2	719	3	Abb07073 Bacillus
19	3373	89.7	719	2	Aaw49089 Bacillus
20	3287	87.4	1217	4	Aau02092 Bacillus
21	2730	72.6	1208	4	Aau02093 Bacillus
22	2447	65.1	1230	8	Adk98484 B thuring
23	2447	65.1	1230	8	Adk98489 B thuring
24	2447	65.1	1230	8	Adk98481 B thuring
25	2447	65.1	1230	8	Adk98491 B thuring

26	2447	65.1	1230	8	ADK98487	Adk98487 B thuring
27	2445.5	65.0	1229	2	AAR54074	Aar54074 CryET5. 2
28	2445.5	65.0	1229	2	AAW35259	Aaw35259 Bacillus
29	2445.5	65.0	1229	2	AAW17699	Aaw17699 CryET5. 3
30	2445.5	65.0	1229	2	AAW87633	Aaw87633 CryET5 pr
31	2445.5	65.0	1229	2	AAW30923	Aaw30923 B. thurin
32	2445.5	65.0	1229	8	ADK98479	Adk98479 B thuring
33	2340.5	62.2	488	2	AAW44322	Aaw44322 Bacillus
34	2340.5	62.2	488	4	AAW19947	Aaw19947 Bacillus
35	2277.5	60.6	1228	2	AAR50955	Aar50955 Bacillus
36	2272.5	60.4	1209	4	AAU02094	Aau02094 Bacillus
37	2263.5	60.2	1227	4	AAW31990	Aaw31990 Chimeric
38	2195.5	58.4	1227	2	AAW44321	Aaw44321 Bacillus
39	2195.5	58.4	1227	4	AAW19950	Aaw19950 Bacillus
40	2186.5	58.2	1227	4	AAU02046	Aau02046 B. thurin
41	2171.5	57.8	1186	2	AAW16796	Aaw16796 Amino aci
42	2155.5	57.3	1221	4	AAU00421	Aau00421 B. thurin
43	2141.5	57.0	1221	4	AAU00420	Aau00420 B. thurin
44	2115	56.2	1228	4	AAB84628	Aab84628 Amino aci
45	2115	56.2	1228	4	AAU02039	Aau02039 B. thurin

ALIGNMENTS

RESULT 1
AAB66910
ID AAB66910 standard; protein; 719 AA.
XX
AC AAB66910;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa4.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
(ZENE) ZENECA LTD.
Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
Vincent JL, Lee MD;
WPI; 2001-123015/13.
Novel insecticidal protein obtained from species of Paecilomyces for
controlling insects, and for insect-resistant transgenic plant
production.
Claim 14; Page 60-62; 72pp; English.
The present invention relates to novel insecticidal proteins obtained
from Paecilomyces sp. (see AAB66999 to AAB6901 and AAB6913). The
insecticidal proteins can be used to produce transgenic plants, which are
insect-resistant. Also, the insecticidal proteins are useful for
controlling insects by providing them at a locus where insects feed

Query Match 100.0%; Score 3760; DB 4; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.3e-290;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSYENVEPFSASTI	60
Db	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSYENVEPFSASTI	60
QY	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
QY	121	RNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG	180
Db	121	RNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG	180
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSHCVKWYS	240
Db	181	EEVPLLPYIAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSHCVKWYS	240
QY	241	TGLNNLRTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
Db	241	TGLNNLRTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
QY	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTSINGKAINQGNFSATMNRGDLDYK	360
Db	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTSINGKAINQGNFSATMNRGDLDYK	360
QY	361	GGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPR	420
Db	361	GGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPR	420
QY	421	VDFHWKFTVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHWKFTVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTEPNISITQPLVKAFNLSGAAVVRGPGTGGDLRRTN	540
Db	481	ASHVKALVYSWTHRSADRTNTEPNISITQPLVKAFNLSGAAVVRGPGTGGDLRRTN	540
QY	541	TGTFGDIRVNINPFPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK	600
Db	541	TGTFGDIRVNINPFPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK	600
QY	601	TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	660
Db	601	TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 2			
AAE36274			
ID	AAE36274 standard; protein; 719 AA.		
AC	AAE36274;		
XX	26-JUN-2003 (first entry)		
DT	B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.		
DE	Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.		
XX	Bacillus thuringiensis.		
OS	WO200298911-A2.		
XX	12-DEC-2002.		
PD	30-MAY-2002; 2002WO-GB002666.		
XX	07-JUN-2001; 2001GB-00013900.		
XX	(SYGN) SYNGENTA LTD.		
PA			
XX			

PI	Vincent JL, Viner R;
XX	WPI; 2003-175137/17.
DR	
XX	
PPT	New insecticidal protein comprising an X-glycine motif at the amino-
XX	terminus, useful as an active ingredient of a pesticide.
XX	
PFS	Claim 12; Page 50-53; 67pp; English.
XX	
CC	The invention relates to insecticidal protein comprising an X-glycine
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
CC	sequence is used in the invention
XX	
SQ	Sequence 719 AA;
	Query Match 100.0%; Score 3760; DB 6; Length 719;
	Best Local Similarity 100.0%; Pred. No. 1.3e-290;
	Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEPFSASTI 60
Db	1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEPFSASTI 60
QY	61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db	61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY	121 RNKALTDLKGLGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
Db	121 RNKALTDLKGLGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
QY	181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
Db	181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
QY	241 TGLNNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
Db	241 TGLNNLRGTNAESWVRYNQFRDRTLMLVDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
QY	301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMNW 360
Db	301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYMNW 360
QY	361 GGHKLEFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPR 420
Db	361 GGHKLEFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPR 420
QY	421 VDFHWKFTVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db	421 VDFHWKFTVTHPIASDNFYYPGVYIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY	481 ASHKVALLVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGTGGDLRRTN 540
Db	481 ASHKVALLVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGTGGDLRRTN 540
QY	541 TGTFGDIRVNINPFPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db	541 TGTFGDIRVNINPFPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY	601 TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
Db	601 TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY	661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db	661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
AAB66908
ID AAB66908 standard; protein; 719 AA.
XX
AC AAB66908;
AC
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa2.
XX
KW Insecticide; transgenic plant; insect-resistance.
OS
XX Paecilomyces sp.
XX WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
PS Claim 14; Page 55-57; 72pp; English.
XX
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 719 AA;
Query Match 99.9%; Score 3756; DB 4; Length 719;
Best Local Similarity 99.9%; Pred. No. 2.7e-290;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVVEIINQKISTYA 120
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSFAVSG 180
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSCHVKWYS 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSCHVKWYS 240
Qy 241 TGLNNLRGTNAESWRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300
Qy 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360

Qy 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPTTSRDVYRTESLAGLNLFLTPQVNGVPR 420
Db 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPTTSRDVYRTESLAGLNLFLTPQVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFFYPYGVIGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFFYPYGVIGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTGDIRVNNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVNNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 660
Db 601 TFRVTGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
RESULT 4
AAE36272
ID AAE36272 standard; protein; 719 AA.
XX
AC AAE36272;
XX
DT 26-JUN-2003 (first entry)
XX
DB B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 44-47; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 719 AA;
Query Match 99.9%; Score 3756; DB 6; Length 719;
Best Local Similarity 99.9%; Pred. No. 2.7e-290;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFIIGELWPKGNQWEIFMEHVVEIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFIIGELWPKGNQWEIFMEHVVEIINQKISTYA 120
QY 121 RNKALTDLKGDLAVYHDSLESWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180
Db 121 RNKALTDLKGDLAVYHDSLESWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDI 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVPHLLDLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVPHLLDLEQVTIYSLLSRWSTQYMNW 360
QY 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRPESLAGLNLFLTQPVNGVPR 420
Db 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRPESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHVKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHVKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRPGFTGGDILRRTN 540
QY 541 TGTGDIRVNINPPFAQRVRYRYASTDLOPHTSNGKAINQGNFSATWNRGDDLYK 600
Db 541 TGTGDIRVNINPPFAQRVRYRYASTDLOPHTSNGKAINQGNFSATWNRGDDLYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFAKAEKV 660
Db 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFAKAEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
ADR89421
ID ADR89421 standard; protein; 719 AA.
XX
AC ADR89421;
XX
DT 18-NOV-2004 (first entry)
XX
DE cryIIa.
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
PN W02004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX

PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
FI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
XX
CC New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
CC and polypeptides, useful for killing lepidopteran or coleopteran pests or
CC for producing organisms with pesticide resistance.
XX
CC Example 6; SEQ ID NO 33; 178pp; English.
CC
CC This sequence represents a delta-endotoxin crystal protein. This protein
CC was included in the scope of the invention as a comparison to the delta-
CC endotoxins of the invention. Some of the delta-endotoxin coding sequences
CC of the invention have alternative start codons, producing more than one
CC protein from a single open reading frame. The nucleic acid sequences for
CC the invention are useful in DNA constructs or expression cassettes for
CC transformation and expression in plants and bacteria. The nucleic acids
CC and corresponding polypeptides are useful for killing lepidopteran or
CC coleopteran pests. Compositions containing the delta-endotoxins of the
CC invention, and methods for their production, are useful for the
CC production of organisms with pesticide resistance, specifically bacteria
CC and plants. These organisms are useful for generating altered or improved
CC delta-endotoxin or delta-endotoxin-associated proteins that have
CC pesticidal activity, or for detecting the presence of delta-endotoxin or
CC delta-endotoxin-associated proteins or nucleic acids in products or
CC organisms.
XX
SQ Sequence 719 AA;
Query Match 99.9%; Score 3756; DB 8; Length 719;
Best Local Similarity 99.9%; Pred. No. 2.7e-290;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFIIGELWPKGNQWEIFMEHVVEIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFIIGELWPKGNQWEIFMEHVVEIINQKISTYA 120
QY 121 RNKALTDLKGDLAVYHDSLESWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180
Db 121 RNKALTDLKGDLAVYHDSLESWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDI 300
Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYPIKTTAQLTREVYTDI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVPHLLDLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVPHLLDLEQVTIYSLLSRWSTQYMNW 360
QY 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRPESLAGLNLFLTQPVNGVPR 420

Db 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNGEDLDYK 600
Qy 601 TFRVTGFTTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
Db 601 TFRVTGFTTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6
AAU02095
ID AAU02095 standard; protein; 719 AA.

AC AAU02095;
XX
XX
DT 07-SEP-2001 (first entry)

DE Bacillus thuringiensis partial mutant CryIIa.

XX Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;
KW mutant; mutcin.

XX Bacillus thuringiensis.

XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..719
FT /label= Mature_CryIIa

XX EP1099760-A1.

XX 16-MAY-2001.

PD 09-NOV-1999; 99EP-00203723.

XX 09-NOV-1999; 99EP-00203723.

PR (CPRO-) CPRO-DLO CENT PLANTENVERDEBELINGS REPROD.

XX De Maagd RA, Bosch HJ;

XX WPI; 2001-337141/36.

DR N-PSDB; AAS04855.

XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT domains derived from at least 2 different crystal proteins, such as
PT CryIIa and CryIIa, and having insecticidal activity, useful for combating
PT insects.

XX Example; Page 30-32; 43pp; English.

XX The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
CC encoding which was mutated to allow cloning of domain III or domains I
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins
CC of the invention, having structural domains I, II and III in this order
CC starting from the N-terminal derived from at least 2 different crystal
CC proteins, are useful for protecting plants against pest insects, e.g.

CC moths, butterflies and Colorado potato beetle or for combating insects
SQ Sequence 719 AA;

Query Match 99.7%; Score 3747; DB 4; Length 719;
Best Local Similarity 99.7%; Pred. No. 1.4e-289;
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCLKNQDKHQSFSNAKVDKISTDLSKNETDIELQINIHEDCLKMSEYENVEFVSASTI 60
Db 1 MCLKNQDKHQSFSNAKVDKISTDLSKNETDIELQINIHEDCLKMSEYENVEFVSASTI 60
Qy 61 QTGIGIAGKILGTGLGVPPAGQVASYLSFTLGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGLGVPPAGQVASYLSFTLGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALTDLKGLDALAVYHDSLESWVGNNTRARSVVKSOYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGLDALAVYHDSLESWVGNNTRARSVVKSOYIALELMFVQKLPFAVSG 180
Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240
Qy 241 TGLNLRGTNAESWVRYNOFRDMTLMVLDLVALFPSPYDTQMPYIKTTAQLTREYVTDAL 300
Db 241 TGLNLRGTNAESWVRYNOFRDMTLMVLDLVALFPSPYDTQMPYIKTTAQLTREYVTDAL 300
Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNGEDLDYK 600
Qy 601 TFRVTGFTTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
Db 601 TFRVTGFTTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 7
AAB66911
ID AAB66911 standard; protein; 719 AA.

XX AAB66911;

AC AAB66911;

DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa5.

DE Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

QY 241 TGLNLRGTAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
DB 241 TGLNLRGTAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYPGVVGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYPGVVGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TERTVGFTTTPSFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEKV 660
DB 601 TERTVGFTTTPSFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 9

AAB66909 standard; protein; 719 AA.

AC AAB66909;

DT 12-APR-2001 (first entry)

DE Insecticidal protein cryIIa3.

KW Insecticide; transgenic plant; insect-resistance.

OS Paecilomyces sp.

PN WO200100841-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-GB002457.

PR 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

PA (ZENE) ZENECA LTD.

PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

PI Vincent JL, Lee MD;

DR WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

PT production.

XX Claim 14; Page 57-59; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66909 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;
SQ
Query Match 99.4%; Score 3739; DB 4; Length 719;
Best Local Similarity 99.4%; Pred. No. 6e-289;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKLKNQDKHOSFSSNAKVDKISTOSLKNETDIELQNIHEDCLKNSEYENVEPVSASTI 60
DB 1 MKLKNQDKHOSFSSNAKVDKISTOSLKNETDIELQNIHEDCLKNSEYENVEPVSASTI 60
QY 61 QTGIGTAGKILGTLGVPPAQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120
DB 61 QTGIGTAGKILGTLGVPPAQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMPVQKLPSFAVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMPVQKLPSFAVSG 180
QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISSTFYNRQVERAGDYSYHCVKWS 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISSTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGTAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
DB 241 TGLNLRGTAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYPGVVGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYPGVVGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TERTVGFTTTPSFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEKV 660
DB 601 TERTVGFTTTPSFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 10

AAE36273 standard; protein; 719 AA.

AC AAE36273;

DT 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.

KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

OS Bacillus thuringiensis.

PN WO200298911-A2.

XX

PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-GB002666.
XX PR 07-JUN-2001; 2001GB-00013900.
XX PA (SYGN) SYNGENTA LTD.
XX PI Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
XX Claim 12; Page 47-50; 67pp; English.
XX
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 6; Length 719;
Best Local Similarity 99.4%; Pred. No. 6e-289;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHDCLKNSEYENVEPVFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHDCLKNSEYENVEPVFSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEIFMEHVEIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEIFMEHVEIINOKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVQKLPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240

QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREYVYTDI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREYVYTDI 300

QY 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360

QY 361 GGHKLEFRTIGTGLNISTQGSNTSINPVTLPFTSRDVRATESLAGNLFQTPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSNTSINPVTLPFTSRDVRATESLAGNLFQTPVNGVPR 420

QY 421 VDFHWKVFTHPIASDNFYYPYGVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKVFTHPIASDNFYYPYGVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540

QY 541 TGTGDIRVWNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDDLYK 600
DB 541 TGTGDIRVWNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDDLYK 600

QY 601 TERTVGFTTPTSFSLDVQSTFTIGANFSSGNEVYIDRIEFVVPVVEYAEYDFEKAQEKV 660
DB 601 TERTVGFTTPTSFSLDVQSTFTIGANFSSGNEVYIDRIEFVVPVVEYAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEYLDKRELFEIVKYAKOLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEYLDKRELFEIVKYAKOLHIERNM 719

RESULT 11
AAR08041
ID AAR08041 standard; protein; 719 AA.
XX AAR08041;
AC AAR08041;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-FEB-1991 (first entry)
XX
DE 81 kD endotoxin deduced from DNA carried on pJH12.
XX Crystal; insecticide; toxin; delta endotoxin.
XX Bacillus thuringiensis; JHCC 4353 and 4835.
XX WO9013651-A.
XX 15-NOV-1990.
XX
XX 09-MAY-1989; 89GB-00010624.
XX 09-MAY-1989; 89GB-00010624.
XX
XX (ICIL) IMPERIAL CHEM IND PLC.
PI Blenk RG, Ely S, Tailor RH, Tippet JM;
XX
DR WPI; 1990-361486/48.
DR N-PSDB; AAQ06636.
XX
PT Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.
XX
PS Claim 5; Fig 5-10; 66pp; English.
XX
CC The sequence carried on pJH12 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can be used to produce transformants E. coli strain MC12022/pJH12 (NCIB 40278, or bacteriophage EMBL4 vector (NCIB 40279) or E. coli strain BL21/pJH11 (NCIB 40275). The delta-endotoxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 719 AA;

Query Match 99.3%; Score 3735; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.3e-288;
Matches 715; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHDCLKNSEYENVEPVFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHDCLKNSEYENVEPVFSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEIFMEHVEIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEIFMEHVEIINOKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTTRARSVVKSQYIALELMFVQKLPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240

|||||
Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSYHCVKWS 240
Qy 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALFPSPDYDTQMPYIKTTAQLTREYVYDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALFPSPDYDTQMPYIKTTAQLTREYVYDAI 300
Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYPGYVIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYPGYVIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12

AAE36271
ID AAE36271 standard; protein; 718 AA.
XX
AC AAE36271;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIaI.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT
XX
PS Claim 12; Page 42-44; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as

CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 718 AA;

Query Match 99.1%; Score 3724.5; DB 6; Length 718;

Best Local Similarity 99.4%; Pred. No. 8.6e-288;

Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Qy 61 QTGIGTAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGTAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMPVQKLPSFAVSG 180
Db 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMPVQKLPSFAVSG 180
Qy 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSYHCVKWS 240
Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSYHCVKWS 240
Qy 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALFPSPDYDTQMPYIKTTAQLTREYVYDAI 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALFPSPDYDTQMPYIKTTAQLTREYVYDAI 300
Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN - VPR 419
Qy 421 VDFHWKFVTHPIASDNFYPGYVIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 480
Db 420 VDFHWKFVTHPIASDNFYPGYVIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 479
Qy 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539
Qy 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 540 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599
Qy 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
Db 600 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 659
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 13

AAB66907
ID AAB66907 standard; protein; 718 AA.
XX
AC AAB66907;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIaI.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX

OS Paecilomyces sp.
XX WO200100841-A1.
XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
XX 29-JUN-1999; 99GB-00015215.
XX 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX Claim 14; Page 53-55; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX Sequence 718 AA;
SQ

Query Match 98.9%; Score 3718.5; DB 4; Length 718;
Best Local Similarity 99.3%; Pred. No. 2.6e-287;
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFILGELWPKGNQWEIFMEHVEELINQISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVAVSLYFILGELWPKGNQWEIFMEHVEELINQISTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVKQLPSFAVSG 180
DB 121 RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSDHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSDHCVKWYS 240
QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFSPYDTQWPIKTAQLTREVYTDAL 300
DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFSPYDTQWPIKTAQLTREVYTDAL 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMW 360
QY 361 GGHKLEFRITIGTGLNISTOGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
DB 361 GGHKLEFRITIGTGLNISTOGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVN-VPR 419
QY 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 420 VDFHWKFVTHPIASDNFYYPGVYIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 479
QY 481 ASHVKALVSWTHRSADRNTIENSITQIPLVKAFNLSGGAAVRGPFGTGGDILLRRTN 540
DB 480 ASHVKALVSWTHRSADRNTIENSITQIPLVKAFNLSGGAAVRGPFGTGGDILLRRTN 539
QY 541 TGTGDIRVNNPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600

DB 540 TGTGDIRVNNPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
QY 601 TFRVTGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDFEKAQEKV 660
DB 600 TFXTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAAYDFEKAQEKV 659
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 660 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 14
ADM74717
ID ADM74717 standard; protein; 719 AA.
XX ADM74717;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
DE B. thuringiensis cryIIel SEQ ID NO:2.
XX
XX cryI; toxicity; lepidoptera; cryIAb; cryIbA; coleoptera; diptera;
KW cryIIel.
KW
XX Bacillus thuringiensis.
XX OS
XX CN1401772-A.
PN
XX 12-MAR-2003.
PD
XX 20-AUG-2001; 2001CN-00124163.
PF
XX 20-AUG-2001; 2001CN-00124163.
PR
XX (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.
PA
XX Song F, Zhang J, Huang D;
PI WPI; 2003-442339/42.
XX N-PSDB; ADM74716.
DR
XX Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence
PT with high-toxicity to lepidoptera pests, encoded protein, primer
PT sequences and the shuttle vector pSXY422b, useful as a pesticide.
XX
XX Example 3; SEQ ID NO 2; 29pp; Chinese.
XX The invention relates to a novel Bacillus thuringiensis cryI gene, gene
CC combination, expression vector, nucleotide sequence of the B
CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the
CC amino acid sequence of the protein encoded by it, cooperative use of the
CC cryI gene with the expression product of cryIAb or cryIbA, primer
CC sequences for expressing the genes, and the constructed shuttle vector
CC pSXY422b. The gene in combination with the cryIAb or cryIbA genes
CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.
CC The present sequence represents the cryIIel protein.
SQ Sequence 719 AA;
Query Match 94.3%; Score 3547; DB 7; Length 719;
Best Local Similarity 93.5%; Pred. No. 1.2e-273;
Matches 672; Conservative 26; Mismatches 21; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFILGELWPKGNQWEIFMEHVEELINQISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVAVSLYFILGELWPKGNQWEIFMEHVEELINQISTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVKQLPSFAVSG 180

Db 121 RNIALADLKGLGDALAVHESLESWTNRNARATSVKSYIALELLFVQKLPSPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLDASIFGKESSEISTFYNNROVERAGDYSCHVKWYS 240
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Qy 241 TGLNNLGTNAESWRYNQPRDMLMVLDLVALPSPSYDTOMYDIKTTAQLTREVYTDAL 300
Db 241 TGLNNLGTNAESWRYNQPRDMLMVLDLIALPSPYDTLVYPIKTTSLTREVYTDAL 300
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLSRWSNTQYMNW 360
Db 301 GTVHPNASFASTWYNNAPSFSAIESAVVRNPHLLDFLEQVTTYSLSRWSNTQYMNW 360
Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHRLERTIGGVLTNTSQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKPEATLPASDNFYYPGVAGVGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TERTVGFTTPESFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660
Db 601 TERTVGFTTPESFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719

RESULT 15

AAB66912 ID AAB66912 standard; protein; 719 AA.

XX AAB66912;

AC 12-APR-2001 (first entry)

XX Insecticidal protein cry1b1.

DE Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

PN 04-JAN-2001.

XX 23-JUN-2000; 2000WO-CB002457.

XX 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

PT production.

XX
PS
XX

Claim 14; Page 64-66; 72pp; English.

The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB6901 and AAB6913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

SQ Sequence 719 AA;

Query Match 93.5%; Score 3516; DB 4; Length 719;

Best Local Similarity 92.8%; Pred. No. 3.7e-271;

Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHOSFSSNAKVDKISTOSLKNKNTDIELQNIHEDCLKMSEYENVEPVSASTI 60

Db 1 MKLKNPDKHOSLSSNAKVDKIATDSLKNKNTDIELKNMNEYLRMSEHESIDPFVSASTI 60

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISYYA 120

Db 61 QTGIGIAGKILGTGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120

Qy 121 RNKALFDLKGDLALAVYHDSLESWGVNRRNTRRSVVKSYIALELMFVQKLPSPFAVSG 180

Db 121 RNKALSDLRGLGDALAVYHESLESWVENNTRRSVVKVQYIALELMFVQKLPSPFAVSG 180

Qy 181 EEPVLLPIYAQAANLHLLLDASIFGKESSEISTFYNNROVERAGDYSCHVKWYS 240

Db 181 EEPVLLPIYAQAANLHLLLDASIFGKESLSASEISTFYNNQVERTSDYSDCHIKWYN 240

Qy 241 TGLNNLGTNAESWRYNQPRDMLMVLDLVALPSPSYDTOMYDIKTTAQLTREVYTDAL 300

Db 241 TGLNNLGTNAESWRYNQPRDMLMVLDLVALPSPYDTLVYPIKTTSLTREVYTDAL 300

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Db 301 GTVHPNQAFASFTWYNNAPSFSAIEAAVVRSPHLLDFLEKVTIYSLSRWSNTQYMNW 360

Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420

Db 361 GGHRLERSPIGGALNTSQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420

Qy 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

Db 421 VDFHWKFPPTLPASDNFYYPGVAGVGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

Db 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

Qy 601 TERTVGFTTPESFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660

Db 601 TERTVGFTTPESFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719

Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719

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Job time : 102.351 secs

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OM protein - protein search, using sw model

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(without alignments) (without alignments)
3350.901 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	3756	99.9	719	16	US-10-782-020-10	Sequence 10, Appl	
2	3756	99.9	719	16	US-10-782-141-8	Sequence 8, Appl	
3	3472.5	92.4	710	15	US-10-428-961-42	Sequence 42, Appl	
4	2277.5	60.6	1228	16	US-10-809-953-10	Sequence 10, Appl	
5	2264.5	60.2	1207	10	US-09-988-462-7	Sequence 7, Appl	
6	2186.5	58.2	1227	15	US-10-428-961-63	Sequence 63, Appl	
7	2171.5	57.8	1186	9	US-09-826-660-23	Sequence 23, Appl	
8	2115	56.2	1228	15	US-10-428-961-38	Sequence 38, Appl	
9	2115	56.2	1228	15	US-10-614-524-2	Sequence 2, Appl	
10	1932.5	51.4	643	9	US-09-826-660-25	Sequence 25, Appl	
11	1724.5	45.9	1167	14	US-10-089-678-1	Sequence 1, Appl	
12	1680.5	44.7	653	15	US-10-428-961-6	Sequence 6, Appl	
13	1659.5	44.4	1157	16	US-10-782-141-16	Sequence 16, Appl	

ALIGNMENTS

RESULT 1

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US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin (
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

```

	Query Match	99.9%	Score 3756;	DB 16;	Length 719;
	Best Local Similarity	99.9%;	Pred. No. 1.2e-308;		
	Matches 718; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEVENVPFVSASTI	60			
Dd	1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEVENVPFVSASTI	60			
Qy	61 OTGIGIAGKI LGTGLVPPFAGOVASLSYFILGELWPKGNQWEIFMEHV EIIINQKIS TYA	120			
Dd	61 OTGIGIAGKI LGTGLVPPFAGOVASLSYFILGELWPKGNQWEIFMEHV EIIINQKIS TYA	120			

QY	121	RNKALTDLKGIGDALAVYHDSLESWVGNRNTRARSVVKSOYIALELMFVQKLPSPAVSG	180
DB	121	RNKALTDLKGIGDALAVYHDSLESWVGNRNTRARSVVKSOYIALELMFVQKLPSPAVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNNQVERAGDYSCHVKWYS	240
DB	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNNQVERAGDYSCHVKWYS	240
QY	241	TGLNNLRGTNAESWVRYNQFRDMLTMVLDLVALPSPYDTQMPYIKTTAQLTREVYTDAL	300
DB	241	TGLNNLRGTNAESWVRYNQFRDMLTMVLDLVALPSPYDTQMPYIKTTAQLTREVYTDAL	300
QY	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYMNW	360
DB	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYMNW	360
QY	361	GGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFTQPVNGVPR	420
DB	361	GGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFTQPVNGVPR	420
QY	421	VDHFWKVFTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
DB	421	VDHFWKVFTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540
DB	481	ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	600
DB	541	TGTFGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	600
QY	601	TFRTVGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
DB	601	TFRTVGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
DB	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.9%; Score 3756; DB 16; Length 719;			
Best Local Similarity 99.9%; Pred. No. 1.2e-308;			
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDLSKNETDIELQNIHEDCLMKSEYENVEPVSASTI	60

NAME/KEY: misc feature
LOCATION: (200) (200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 92.4%; Score 3472.5; DB 15; Length 710;
Best Local Similarity 92.4%; Pred. No. 1.2e-284;
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFSASTI 60
DB 1 MKSKNQNMHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPFILGELWPKGKNQWEIFMEHVEEIIINQISTYA 120
DB 52 QTGIGIAGKILGNLGVFPAGQVASYLSPFILGELWPKGKSQWEIFMEHVEEIIINQISTYA 111
QY 121 RNKALTDLKGDLALAVHDSLESWVGNNRNTARSVVKSQYIALELMFVQKLPSPAVSG 180
DB 112 RNKALADLKGDLALAVHDSLESWVGNNRNTARSVVKSQYITLLELMFVQSLPSPAVSG 171
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKRWGLSSSEISTFYNRQVERAGDSDHCVKWS 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKRWGLSSSEISTFYNRQSGKSKEYSDHCVKWN 231
QY 241 TGLNLRGNTAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDI 300
DB 232 TGLNLRMGNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDI 291
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYNNMW 360
DB 292 GTVHPHPSFTSTWYNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYNNMW 351
QY 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPR 420
DB 352 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPR 411
QY 421 VDFHWKFTVTHPIASDNFYGYGIGTOLQDSNELPPEATGPNVESYSHRLSHIGLIS 480
DB 412 VDFHWKFTVTHPIASDNFYGYGIGTOLQDSNELPPEATGPNVESYSHRLSHIGLIS 471
QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 472 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRKN 531
QY 541 TGTGDIRVNPFPFAQRVRIYASTDLOFHTSINGKAINQGNFSAWMNRGDDLYK 600
DB 532 TGTGDIRVNPFPFAQRVRIYASTDLOFHTSINGKAINQGNFSAWMNRGDDLYK 591
QY 601 TERTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEV 660
DB 592 TERTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEV 651
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 652 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 710

RESULT 4

US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Van Mellaert, Herman
APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bc INSECT
TITLE OF INVENTION: CRYSTAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 60.6%; Score 2277.5; DB 16; Length 1228;
Best Local Similarity 62.7%; Pred. No. 4e-183;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEVENVEPFSVASTIQTGIGIAGKI 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFSVASTVQTGINIAGRI 61
QY 71 LGTLGVFPAGQVASYLSPFILGELWPKGKNQWEIFMEHVEEIIINQISTYARNKALTDLKG 130
DB 62 LGVLGVFPAGQVASYLSPFILGELWPKGRDQWEIFLEHVEQLINQOITENARTALARLQ 121
QY 131 LGDALAVHDSLESWVGNNRNTARSVVKSQYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 122 LGDSFRAYQOQSLDLEWLNDRDARTSRVLHTQYIALELDLFLNAMPLFAIRNQEVPLLMVYA 181
QY 191 QAANLHLLLRDASIFGKRWGLSSSEISTFYNRQVERAGDSDHCVKWSYSLGNNLRGTN 250
DB 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSYCVWEYNTGLNSLRTN 241
QY 251 AESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDIAGTVHPHPSFT 310
DB 242 AASWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDIAGT--GVNMA 299
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYNNMWGKHLEPRTI 370
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLRSWNTQYNNMWGKHLEPRTI 359
QY 371 GGTNLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPRVDFHWK 428
DB 360 GGLNTSTHGATNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPRVDFHWK 416
QY 429 THP-----IASDNFYGYGIGTOLQDSNELPPEATGPNVESYSHRLSHIGLISASH 483
DB 417 TNPQNISDRGTANYSQP--YESPGQLQKDSSETLPPETTERPNVESYSHRLSHIGLIS 475
QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 543
DB 476 VNPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 535
QY 544 FGDIRVNPFPFAQRVRIYASTDLOFHTSINGKAINQGNFSAWMNRGDDLYK 603
DB 536 FGPVIRVNGPLTQRYRIGFRYASTVDFVSRGGTNNFRFLRFLMNSGDELKYNFV 595
QY 604 TVGFTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEV 663
DB 596 RRAFTTPFTTQIQTIDIRTSIQGLSGNEVYIDKIEIIPVTATFEAYDLERAQEA 655
QY 664 FTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 5

US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.

Thu Mar 10 14:26:05 2005

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689

SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7
Query Match 60.2%; Score 2264.5; DB 10; Length 1207;
Best Local Similarity 64.3%; Pred. No. 4.9e-182;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;
40 EDCLMKSEYNEVPEFVSASTIQTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGN 99
10 EDLSCIAEGNIDFVSASTVQTGINAGRIILGVLGVPFAGQVASYLSFILGELMPGRGD 69
100 QWEIEMFHEVBEIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNNRNRARSVK 159
70 QWEIEMFHEVBEIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNNRNRARSVK 129
160 SQYIALELMFVKLPSPFASVGEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEIST 219
130 TQYIALELDFLNAELFAIRNQEVPLLMVYQAANLHLLLRDASIFGSEGLTSQEIQR 189
220 FYNQVERAGYSDHCVKYSTGLNLRGTNAESWVRNQRDRMTLMLVLDLVALFPSPYD 279
190 YVERQVERTRYSYDCEWYNTGLNLRGTNAESWVRNQRDRMTLMLVLDLVALFPSPYD 249
280 TQMPYIKTKTAQLTREYVTDAGTVHPHPSFTSTWYNNNAPSPSAIEAAVVRNPHLLDEL 339

Db 250 TRTPINTSAQLTREYVTDAGT--GVNMMASNNWNNNAPSPSAIEAAIRSHLLDEL 307
Qy 340 EQVTIYLLSRWNTQYMMWGGHLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDYY 399
Db 308 EQLTIFSSASSRWSNTRHMTYRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDYY 367
Qy 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKVFVTHP-----IASDNFYYPGVYVIGTQLODS 452
Db 368 RTESYAGVLLWGIYLEPIHGVPTRFNF--TNPNQISDRGTANYSQP-YESPGQLQKDS 423
Qy 453 ENELPPEATQPNYESYSHRLSHIGLISASHKALVYSWTHRSADRTNTTIEPNSITQIPL 512
Db 424 ETELPPEPTERRPNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTTIGPNRITQIPM 483
Qy 513 VKAFNLSSGAAGVVRGPGFTGGDILRRRTNTGTGDIRVNNINPPFAQRYRVRIRYASTDLQ 572
Db 484 VKASELPQGTTVVRGPGFTGGDILRRRTNTGCGPIRVTVNGPLTQRYRIGFRYASTVDFD 543
Qy 573 PHTSINGKAINQGNFSATMNRGEBLDYKTRFTVGTFTTTPFSLDVQSTFTIGAMNFSGNE 632
Db 544 PFVSRGGTTVNNFRFLRTMNSGDELKYGNVFRAFTTPTFTQIQDIIRTSIQGLSGNGE 603
Qy 633 VYIDRIEFVPEVTEAEYDFEKAQEKYALFTSTNPRGLKTDVYKHIDQVSNLVESLS 692
Db 604 VIDKIEIIPVTATPEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663
Qy 693 DEFYLDKRELFEIVKYAKOLHIERNM 719
Db 664 DEFLDKRELLEKVKYAKRLSDERNL 690

RESULT 6
US-10-428-961-63
Sequence 63, Application US/10428961
Publication No. US2003023711A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
REFERENCE: MECO201--1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63
LENGTH: 1227
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 15; Length 1227;
Best Local Similarity 59.2%; Pred. No. 2e-175;
Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;
13 SSNAKVDKISTDLKN-----ETDIELQNIHEDCLKMSEYNEVPEFVSASTIQTGIG 65
7 NENEIINALSPAVSNHSAQMNLSLDARI-----EDSLCIAEGNIDPFVSASTVQTGIN 61
66 IAGKILGTGVPFAGQVASYLSFILGELMPKGNQWELFMEHVEEIIINQKISTYARNKAL 125
62 IAGRILGVLGVPFAGQVASYLSFILGELMPGRDPWEIFLEHVEHLIRQQVTRNTOTAL 121
126 TDLKGLGDALAVYHDSLESWVGNNRNRARSVKSYQYIALELMFVKLPSPFASVGEVPL 185

Query Match 56.2%; Score 2115; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 2.3e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;
13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70
7 NENEIINALSPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
71 LGTIGVPPAGOVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNATALARLQ 126
131 LGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVQKLPFAVSGEEVPLPIYA 190
127 LGDSFRAYQOSLEDWLENRDDARTSVLYTQYIALELDFLNAMEPLFAIRNQEVPPLMVA 186
191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTN 250
187 QAANLHLLLRDASIFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN 246
251 AESWRYNQFRDMLVLDLVALFPSPDYTPYPIKTTAQLTREYVTDATGTVHPHPSFT 310
247 AASWRYNQFRDMLVLDLVALFPSPDYTPYPIKTTAQLTREYVTDATGTVHPHPSFT 304
311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNMGHKLFRFTI 370
305 SMWYNNAPSFSAIEAVIRSPHLLDFLEQVITYSLSRWSNTQYMNMGHKLFRFTI 364
371 GGTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFF--LTQPVNGVPRVDFHMKFV 428
365 GGGTNTSTHGSTNTSINPVLSPFSDRVYWTESYAGVLLWGIYLEPIHGVTFRFNRNP 424
429 --THPIASDNFYYPGVIGITQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVKA 486
425 QNTFERGTANYSQP--YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISASHVKA 483
487 LVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPFTGGDILRRTNTGTFGD 546
484 PVSWSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPFTGGDILRRTNTGTFGD 543
547 IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVG 606
544 MGLNFNNTSLQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVG 603
607 FTTPPSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFTS 666
604 FPGVGSASGSQ--TAGISISNAGRQTFHFQKIEFIPITATFEAYDLEAQAQAVNALFTN 662
667 TNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 719
663 TNPRRLKTDVTDYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 715

RESULT 10
US-10-614-524-2
Sequence 25, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 2001-04-05

Query Match 56.2%; Score 2115; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 2.3e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;
13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70
7 NENEIINALSPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
71 LGTIGVPPAGOVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNATALARLQ 126
131 LGDALAVYHDSLESVGNRNTRARSVVKSOYIALELMFVQKLPFAVSGEEVPLPIYA 190
127 LGDSFRAYQOSLEDWLENRDDARTSVLYTQYIALELDFLNAMEPLFAIRNQEVPPLMVA 186
191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTN 250
187 QAANLHLLLRDASIFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN 246
251 AESWRYNQFRDMLVLDLVALFPSPDYTPYPIKTTAQLTREYVTDATGTVHPHPSFT 310
247 AASWRYNQFRDMLVLDLVALFPSPDYTPYPIKTTAQLTREYVTDATGTVHPHPSFT 304
311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNMGHKLFRFTI 370
305 SMWYNNAPSFSAIEAVIRSPHLLDFLEQVITYSLSRWSNTQYMNMGHKLFRFTI 364
371 GGTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFF--LTQPVNGVPRVDFHMKFV 428
365 GGGTNTSTHGSTNTSINPVLSPFSDRVYWTESYAGVLLWGIYLEPIHGVTFRFNRNP 424
429 --THPIASDNFYYPGVIGITQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVKA 486
425 QNTFERGTANYSQP--YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISASHVKA 483
487 LVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPFTGGDILRRTNTGTFGD 546
484 PVSWSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPFTGGDILRRTNTGTFGD 543
547 IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVG 606
544 MGLNFNNTSLQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVG 603
607 FTTPPSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFTS 666
604 FPGVGSASGSQ--TAGISISNAGRQTFHFQKIEFIPITATFEAYDLEAQAQAVNALFTN 662
667 TNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 719
663 TNPRRLKTDVTDYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 715

RESULT 9
US-10-614-524-2
Sequence 2, Application US/10614524
Publication No. US20040016020A1
GENERAL INFORMATION:
APPLICANT: Arnaut, Greta
APPLICANT: Boets, Annemie
APPLICANT: Damme, Nicole
APPLICANT: Mathieu, Eva
APPLICANT: Vanneste, Stijn
APPLICANT: Van Rie, Jeroen
TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
FILE REFERENCE: NEWBTSUS2
CURRENT APPLICATION NUMBER: US/10/614,524
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/173387
PRIOR FILING DATE: 1999-12-28


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; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match      51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 2.3e-154;
Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTDSLKN-----ETDIELQNIHEDCLKMSEYENVEPFVSASTIQTGIG 65
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 NENEIINALSIPAVSNHSAQMNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTLGVFPAGQVASYFLIGELMPKGNQWEIEMHEVBEIINQKISTYARNKAL 125
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 IAGRLGVLPFPAGQIASFYSLVGLMPGRDPWEIPLFHEVBEIINQKISTYARNKAL 121

QY 126 TDLKGLGDALAVYHDSLESVGNRNTRARSVVKVSYQYIALELMFVQKLPSPAVSGEEVPL 185
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 ARLOGLNSFRAYQOSLEDWLENRRDARTSRVLYTQYIALELDLFLNAPLFAIRNQEVPL 181

QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWSYTGILNN 245
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 LMVYAQAANLHLLLRDASIFGSEFGLTQSEIQRYERQVEKTRREYSDYCARWYNTGLNN 241

QY 246 LRGTNAESWRYNQPRRDMLVLDLVALFPSPYDTQMPYIKTTAQLTRVYTDATIGTVHP 305
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 LRGTNAESWRYNQPRRDMLVLDLVALFPSPYDTQMPYIKTTAQLTRVYTDATIGTVHP 301

QY 306 HPSFTSTWYNNNAPSFAAEEAAYVRNPHLLDLEQVITYSLLSRWSNTQYNNMVGSHKL 365
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 PSGFASTNWFNNNAPSFAAEEAAYVRNPHLLDLEQVITYSLLSRWSNTQYNNMVGSHKL 361

QY 366 EFRITGGLNISTQSTNTSINPVLPTFSRDVYRTESLAGNLFLTPQVNGVPRVDFHW 425
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 362 ESRTIRGSLSTHGTNTSINPVLPTFSRDVYRTESLAGNLFLTPQVNGVPRVDFHW 421

QY 426 KFTVTHPIASDNFYYPGYGIGTQDSENELPPEATGPNYSYSHRLSHGLISASHVK 485
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 422 RNPLNSLRGSLLYTIGYGTQQLFDSETELPETTERPNYSYSHRLSNIRLISGNTLR 481

QY 486 ALVYSWTHRSADRTNTIENPSITQIPLVKAFNLSSGAAYVRGPGFTGGDILRRNTGTFG 545
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 482 APVYSWTHRSADRTNTIENPSITQIPLVKAFNLSSGAAYVRGPGFTGGDILRRNTGTFG 541

QY 546 DIRVNIPTPAQRVRYRYASTDLOQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTV 605
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 542 SMGLNFNTSLQVRVRYRYAASQTMLVLTVCGSTTDDQGPSTMSANESLTSQSFRA 601

QY 606 GFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYE 648
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 602 EFPVGISASGSQ-TAGISISNNACRQTFHFDKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
```

```
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1

Query Match      45.9%; Score 1724.5; DB 14; Length 1167;
Best Local Similarity 48.1%; Pred. No. 2.4e-136;
Matches 362; Conservative 125; Mismatches 220; Indels 45; Gaps 11;

QY 1 MKLKQDKHQ--SFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYB-----NV 51
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSPNNQNEYILDASSSTVSNDNSVRYPLANDQTTLLQNMNKKDYLRMSEGENPELFGNP 60

QY 52 EPPFVSASTIQTGIGIAGKILGTLGVFPAGQVASYFLIGELMPKGNK-NQWEIEMHEVVEE 110
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ETFISSSTVQTGIGIAGKILGTLGVFPAGQVASYFLIGELMPKGNK-NQWEIEMHEVVEE 120

QY 111 IINOKISTYARNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKVSYQYIALELMFV 170
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 LIDOKITSDVRKKTALAGLQGLDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180

QY 171 QKLPFAVSGEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGD 230
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 AKIPSAISGQEVPLLSVYAQAANLHLLLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240

QY 231 YSDHCVKVYSTGLNLRGTAESWRYNQPRRDMLVLDLVALFPSPYDTQMPYIKTTAQ 290
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 YSDYCVKWTGDLKLGTAASWLVKQFRREMTLLVLDLVALFPYDTRTYPIETTAQ 300

QY 291 LTREYVYTDIGTVHPHPSFTSTWYNNNAPSFAAEEAAYVRNPHLLDLEQVITYSLLS- 349
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 LTREYVYTDIVFNRETSGFCRRWSLSDISFSEVESAVIRSPHLPDILSEIEFYTRAG 360

QY 350 -RWSNTQYNNMVGSHKLFPRTIGTTLNISTQSTNTSINPVLPTFSRDVYRTESL-AGL 407
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 LPLANNTEYLEYVWGHSHIKYKNTNASSALERNYGTITSNKIKYYDLANKDIFQVRSGLADL 420

QY 408 NLFLTQPVNGVPRVDFHWKFTVTHPIASDNFYYPGYVG-----IGTQLQDSENE 455
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 ANYYAQ-VYGVPYASF-----TLDDKNTGSGSVGFTYSKPHHTMQVCTQNYNTIDE 471

QY 456 LPPEATGPNYSYSHRLSHGLIS-----ASHVKALVYSWTHRSADRTNTIENPSI 507
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 472 IPPE--NEPLSRGYSHRLSHITSYFSKXNASSPARYGNLPAFWATHRSADVTNTVYSDKI 529

QY 508 TQIPLVKAFNLSSGAAYVRGPGFTGGDILRRNTGTGDIRVNIPTPAQRVRYRYAS 567
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 530 TQIPLVKAFNLSSGAAYVRGPGFTGGDILRRNTGTGDIRVNIPTPAQRVRYRYAS 589

QY 568 TTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTFFSFLDVQSTFTIGAWNF 627
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 590 TTNLRLFWISGTRIYSINVNKTMKGGDLTFNTFDLATIGTFTFNSYSDSLTVGADSF 649

QY 628 SSGNEVYIDRIEFVPEVTVYEYDFEKAQEKVATLTSTNPRGLKTDVYKHIDQVSNL 687
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 650 ASGGEVYDKFELIPVNATFEAEDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNOAANL 708

QY 688 VESLSDEFYLDKRELFELVYKAKQLHIERNM 719
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 709 VECLSDLEYFNEKRMMLDAVKEAKRLVQARNL 740

RESULT 12
```



```

US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MFC0201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match          44.7%; Score 1680.5; DB 15; Length 653;
Best Local Similarity 51.5%; Pred. No. 5.1e-133;
Matches 146; Conservative 106; Mismatches 173; Indels 47; Gaps 14;

```

QY	13	SSNAKVDK1STDLSKN---ETDIELQNINHHEDCLKMSYENVEFVVSASTIQTGIGIACK	69
DB	2	NENEIINALSIPAVSNHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINIAGR	60
QY	70	ILGTLGVPPAGQVQASLYSFILGELWPKGNQWEIPEHVEEIIINQKISYARNKALTDLK	129
DB	61	ILGVLGVPPAGQLASFYSFLVGELWPSGRDPWEIFLEYVEQLIRQQVTENTRTAIRLE	120
QY	130	GLGDALAVYHDSLESVWGNRRNTRARSVVKSQYIALELMPVQKLPFSAVSGEEVPLPIY	189
DB	121	GLGRGYSYQQALETWLDNDRANDARSIIILERYVALELDITTAIPLFRIRNEEVEPLLMVY	180
QY	190	AQAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGT	249
DB	181	AQAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYETEYSNHCQWYNTGLNNLRGT	240
QY	250	NAESWRYNQFRDDMTLWLDLVALFPSTQMPYIKTTAQLTREYVTDAGTVHPHPSF	309
DB	241	NAESWLRYNQFRDLTLGVLDLVALFPSTRTYPTINTSAQLTREIYTDPIGRTNAPSGF	300
QY	310	TSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNQYMNMGHKLERT	369
DB	301	ASTNWFNNNAPSFAIEAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVGHRLNFRP	360
QY	370	IGGTLNISTQGST-NTSINPVTLPF-TSRDQVYRTESLAGNLFLTQPVNGVPRVDFHWKF	427
DB	361	IGGTLNTSTQGLTNNTSINPVLTHVYSSRDVYRTESNAGTNILFTTPVNGVPWAREN--F	418
QY	428	VTHPIASDNFYYP-----GYVGIGTQLODSENELPPEATQGPYVESYSHRLSHIG--	477
DB	419	ITLRFMKEARPLPTVNRIRELGFNYLIQKLNHYQK-----QQNDQIMNHIVIDISYR	470
QY	478	LISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGDILR	537
DB	471	LIIGNTLRAPVYSWTHRSADRTNTEIGNRITQIPAVKGRFLENG-SVIGSGFTGDDVVR	529
QY	538	-RTNCTGF---GDIRVYNIN-PFFAQYRVRYRYASTTDLOPHTSINGKAINQGNFSATMN	592
DB	530	LNRNNGNIQNRGYIEVPIQFTSTSTRYRVRYRYASTYSIELNVNLGNSSITPNTLPATAA	589
QY	593	RGEDLDYKTRFTVGTTFPFSFLDVQSTFT-----IGAWNPFSSGNEWYIDRIEFVVEVT	646
DB	590	SLDNLO-----SGDFGYGEINNAFTSATGNIVGARNFSAEYIIDRFEPFIPVTAT	640

Qy	647 YEAEYDFEKAQE 658
	: : :
Db	641 FEVEYDLERAQK 652

RESULT 13

US-10-782-141-16

; Sequence 16, Application US/10782141

; Publication No. US20040197917A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Kozziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMT-014, A Delta-Endotoxin Gene and

; TITLE OF INVENTION: Methods for Its Use

; FILE REFERENCE: 045600/274143

; CURRENT APPLICATION NUMBER: US/10/782,141

; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,632

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 1157

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-782-141-16

Query Match	44.4%;	Score 1669.5;	DB 16;	Length 1157;
Best Local Similarity	49.1%;	Pred. No. 1.1e-131;		
Matches 371;	Conservative 98;	Mismatches 230;	Indels 57;	Gaps 18;
QY	1	MLKLNODHQSPSSNAKVDKISTDS	---	LKNETDIEIQNHEDCLKMSEYE-----N 50
DB	1	MSPNNQNEYIIDATPST-SVSSDSNRYPFANEPTDALQNMVYKDYLKMSGGENPELFGN	59	
QY	51	VEPVASASITQTGIGIAGKILGTIGVPAGOVASLYSFLIGELWP-KGKNQWEIFMEHVE	109	
DB	60	PETFISSSTIQTGIGIVGRILGALGVPPASQIASFYSPFVQGLWPSKSVDIWGEIMERVE	118	
QY	110	EIINQKISITYARNKALTDLKGGLDALAVYHDSLESVGNRNNTFARSVVKVSOYIALELMF	169	
DB	120	ELVDQKIEKYVKDXALAEIKGLGNALDVYQOSLEDWLENRDARTSRVSVNQFIADLINF	179	
QY	170	VQKLPSFAVSGEEVPLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAG	229	
DB	180	VSSIPSFVSGHEVLLLVAYQAQVNLHLLLRDASIFGEWGGFTFGEISRFYNRQVQLTA	239	
QY	230	DYSDHCVKWYSTGLNNLRCTNAESWVRVYQFRDWTMLVLDLVALFPSYDTQMPIKTTA	289	
DB	240	EYSDYCVKWYKIGLDKLGKTTSKWLNHYQFRREMTLLVLDLVALFPNYDTHMYPietta	299	
QY	290	QLTREVVYTAIGTVHPHPGFTST----	TWVNNAPSPSAIEAAVVRNPHLLDLEQVTIY 345	
DB	300	QLTRDVTYTPIA-----FNIVTSTGFCNPWSTHSGILFYEVENNVRPPHLLFDILLSSVEIN	355	
QY	346	SLLSR-----WSNTQYMMWGGHKLEFR-----	TIGGLTNIISTQGSTNTSINPVTLPFTSR 396	
DB	356	T-SRGGITLNDAXINYSGHTLKYRRRTADSTVITYTANYGRIITSEKNS-----	FALEDR 408	
QY	397	DVYRRESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFY-----	YPGVYIGTQLQD 451	
DB	409	DIFEINSTVANLANYQKAYGVPGSWFH--	MVKRGTSTSTAYLYSKTHHALQGC-TQVYE 465	
QY	452	SENEUPPEATQOPNYESYSHRLSHI-----	GLISASHVKALVYSWTHRSADRNTTIE 503	
DB	466	SSDEIPLDRT-VPVAESYSHRLSHITSHSFSKNG--	SAYYGSFPFVFWTHTSADLNTIY 522	
QY	504	PNSTITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFDIRVNIINPPFAQRYVRVI	563	

Db 523 SDKITQIPAVKMDLYLGGSVVQPGFTGCDILKRTNPSILGTFVAVTVNGSLSQRYRVI 582

Qy 564 RYASTTDLOPHTSINGKAINQGNFSATMNRGDLDYKTRTGVGTTTPSFSLDVQSTFTIG 623

Db 583 RYASTTDFEF-TLYIGDTIEKNRENKTMWNGASLTYEFKFSFITDFQFRETQDKILLS 641

Qy 624 AMNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEKVATLFTSTNPRGLKTDVVDYHIDQ 683

Db 642 MGDFSSGQEVYIDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700

Qy 684 VSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719

Db 701 AANLVECLSDLLYPNEKRLFLDAVREAKRLSGARNL 736

RESULT 14

US-10-032-717-2

; Sequence 2, Application US/10032717

; Publication No. US20020151709A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Nicholas B. Duck

; APPLICANT: Xiang Feng

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Theodore W. Kahn

; APPLICANT: Lynn E. Sims

; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With

; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

; FILE REFERENCE: 35718/237005

; CURRENT APPLICATION NUMBER: US/10/032,717

; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: 60/242,838

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1206

; TYPE: PR

; ORGANISM: Bacillus thuringiensis

US-10-032-717-2

Query Match 40.2%; Score 1510; DB 13; Length 1206;

Best Local Similarity 44.3%; Pred. No. 3.6e-118;

Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MMLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNIHEDCLKM-----SEYE-N 50

Db 1 MSPNNQNEVEIIDATPST-SVNSDNSRYPFANPTNALQNDYKDYKMSAGNASSEYPGS 59

Qy 51 VEPFYSA-STIQTGIGIAGKILGTLPVFPAGQVAVSLYSFILGELWPKG-KNOWEIEFMEHV 108

Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVPFVGPVSLYTLQIDILWPSGEKSQWEIEMEY 119

Qy 109 BEINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNNTNRARSVVKSQYIALELM 168

Db 120 EELNQKIAEYARNKALSLEGLGNNYQLYLTALAEENPNNGSRALRDVRNRFELDLSL 179

Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERA 228

Db 180 FTQYMPFRVTNFEVPLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYDQMKLT 239

Qy 229 GDYSDHCVKWYSTGLNNLRGTNAESVVRNQFRDMLTAVLDLVALPSPYDTQMYPIKTT 288

Db 240 AEYSDHCVKWYETGLAKRGTSKQWVDYNGQFRREMTLAVLDVVALPFPNYDRTYPMETK 299

Qy 289 AOLTRVYTDAGTVHPHPSFTSTTWYNNAPSATAEAAVVRNPHLLDFLEQVITYSL 348

Db 300 AOLTRVYTDPLGAVNVS---SIGSWY-DKAPSGFVIESSVIRPPHVDYITGLTYVTQS 355

Qy 349 SRWSNTQYMMWGGHKLFPRTIGTGLNISTQGSTNTSINPV-TLPFTSRDYVRYTESLAGL 407

Db 356 RSISARYIRHWAGHQISYHRVSRGSLNQOQMYGTNQNLHSTSTFDFTNYDIYKTLSDAV 415

Qy 408 NLFLTQP-----VNGVPRVDFHFKFVTHPIASDN---FYYPGYVGIGTQLQDSENELPPE 459

Db 416 LLDIVYPGYTYIFFGMPEVEF---FMVQNLNTRKTLKYNPVSODIIASTRSELELPE 472

Qy 460 ATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHESADRTNTIEPNSITQIPLVKAF 516

Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCW 532

Qy 517 NLSSGAAYVRGPGTGGDILR-RTNTGTFGDI---RVNINPPFAQRYRVRIRYASTTDLQ 572

Db 533 DNLFPVVPVKGPGHTGGDLLQYNRSTGSGTFLARYGLALEKAGKYRVRRLRYATDADIV 592

Qy 573 FHTSINGKAINQGNFSATMNRGDLDYKTR-----TVGFTTTPFSFL-----DVQST 619

Db 593 LH--VNDQI---QMPKTNWPGEDLTSKTFKVADAITTLNLATDSSALKHNLGDEPNST 647

Qy 620 FTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKVATLFTSTNPRGLKTDVKDY 679

Db 648 LS-----GIVYVDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDY 697

Qy 680 HIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719

Db 698 EVNQAANLVECLSDLLYPNEKRLFLDAVREAKRLSEARNL 737

RESULT 15

US-10-414-637-2

; Sequence 2, Application US/10414637

; Publication No. US20030177528A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Nicholas B. Duck

; APPLICANT: Xiang Feng

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Theodore W. Kahn

; APPLICANT: Lynn E. Sims

; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With

; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

; FILE REFERENCE: 35718/237005

; CURRENT APPLICATION NUMBER: US/10/414,637

; CURRENT FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: US/10/032,717

; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: 60/242,838

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1206

; TYPE: PR

; ORGANISM: Bacillus thuringiensis

US-10-414-637-2

Query Match 40.2%; Score 1510; DB 14; Length 1206;

Best Local Similarity 44.3%; Pred. No. 3.6e-118;

Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MMLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNIHEDCLKM-----SEYE-N 50

Db 1 MSPNNQNEVEIIDATPST-SVNSDNSRYPFANPTNALQNDYKDYKMSAGNASSEYPGS 59

Qy 51 VEPFYSA-STIQTGIGIAGKILGTLPVFPAGQVAVSLYSFILGELWPKG-KNOWEIEFMEHV 108

Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVPFVGPVSLYTLQIDILWPSGEKSQWEIEMEY 119

Qy 109 BEINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNNTNRARSVVKSQYIALELM 168

Db 120 EELNQKIAEYARNKALSLEGLGNNYQLYLTALAEENPNNGSRALRDVRNRFELDLSL 179

Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERA 228

Db 180 FTQYMPFRVTNFEVPLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYDQMKLT 239

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds
(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-57
Perfect score: 3760
Sequence: 1 MLLKNQDKHQSFSSNAKVDK.....KRELFIVKYAKQLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3752	99.8	719	3 US-08-286-870A-8	Sequence 8, Appli
2	3472.5	92.4	710	4 US-09-661-322A-42	Sequence 42, Appl
3	3394	90.3	648	3 US-08-286-870A-4	Sequence 4, Appli
4	3373	89.7	719	2 US-09-003-217-2	Sequence 2, Appli
5	3368	89.6	719	3 US-09-218-942-2	Sequence 2, Appli
6	2800	74.5	535	3 US-08-286-870A-6	Sequence 6, Appli
7	2445.5	65.0	1229	1 US-08-100-703-4	Sequence 4, Appli
8	2445.5	65.0	1229	1 US-08-176-865-4	Sequence 4, Appli
9	2445.5	65.0	1229	1 US-08-474-038-4	Sequence 4, Appli
10	2445.5	65.0	1229	2 US-08-779-046-4	Sequence 4, Appli
11	2445.5	65.0	1229	2 US-08-881-340-4	Sequence 4, Appli
12	2340.5	62.2	488	1 US-08-448-170-10	Sequence 10, Appl
13	2340.5	62.2	488	3 US-08-961-803-10	Sequence 10, Appl
14	2264.5	60.2	1207	1 US-07-951-715A-7	Sequence 7, Appli
15	2264.5	60.2	1207	2 US-08-459-449A-7	Sequence 7, Appli
16	2264.5	60.2	1207	3 US-08-459-595A-7	Sequence 7, Appli
17	2264.5	60.2	1207	3 US-08-459-504B-7	Sequence 7, Appli
18	2264.5	60.2	1207	3 US-08-459-444-7	Sequence 7, Appli
19	2264.5	60.2	1207	3 US-09-053-549-8	Sequence 8, Appli
20	2264.5	60.2	1207	3 US-09-547-422-7	Sequence 7, Appli
21	2264.5	60.2	1207	4 US-09-988-462-7	Sequence 7, Appli
22	2264.5	60.2	1227	3 US-09-053-549-2	Sequence 2, Appli
23	2195.5	58.4	1227	1 US-08-448-170-8	Sequence 8, Appli
24	2195.5	58.4	1227	3 US-08-961-803-9	Sequence 9, Appli
25	2186.5	58.2	1227	4 US-09-661-322A-63	Sequence 63, Appl
26	2171.5	57.8	1186	3 US-09-178-252-23	Sequence 23, Appl
27	2171.5	57.8	1186	4 US-09-826-660-23	Sequence 23, Appl

28	2115	56.2	1228	4 US-09-661-322A-38	Sequence 38, Appl
29	1932.5	51.4	643	3 US-09-178-252-25	Sequence 25, Appl
30	1932.5	51.4	643	4 US-09-826-660-25	Sequence 25, Appl
31	1900	50.5	380	5 PCT-US91-02560-4	Sequence 4, Appli
32	1680.5	44.7	653	4 US-09-661-322A-6	Sequence 6, Appli
33	1669.5	44.4	1157	1 US-07-876-280-30	Sequence 30, Appl
34	1669.5	44.4	1157	1 US-07-812-180A-2	Sequence 2, Appli
35	1669.5	44.4	1157	1 US-08-315-468-2	Sequence 2, Appli
36	1669.5	44.4	1157	3 US-07-941-650A-2	Sequence 2, Appli
37	1505.5	40.0	1176	1 US-08-257-999-2	Sequence 2, Appli
38	1494	39.7	1157	2 US-08-532-547-5	Sequence 5, Appli
39	1494	39.7	1157	2 US-08-379-656B-5	Sequence 5, Appli
40	1494	39.7	1157	3 US-08-455-838-5	Sequence 5, Appli
41	1494	39.7	1157	3 US-09-019-809-5	Sequence 5, Appli
42	1494	39.7	1157	4 US-09-471-177-5	Sequence 5, Appli
43	1494	39.7	1157	4 US-09-220-806-5	Sequence 5, Appli
44	1487.5	39.6	1156	3 US-09-002-285-72	Sequence 72, Appl
45	1487.5	39.6	1156	4 US-09-589-477-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Thu Mar 10 14:26:05 2005

Query Match 99.8%; Score 3752; DB 3; Length 719;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPVSASTI 60
1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPVSASTI 60
61 QTGTGAGKILGTLGVPPAGQVASYLSFIIGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120
61 QTGTGAGKILGTLGVPPAGQVASYLSFIIGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120
121 RNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVKSQYIALELMFVKLPSFAVSG 180
121 RNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVKSQYIALELMFVKLPSFAVSG 180
181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHCVKWS 240
181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHCVKWS 240
241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300
241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300
301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNW 360
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361 GGHKLEPRTIGTTLNISTQSTNTSINPVTLPPTSVDYRTESLAGLNLFLTQPVNGVPR 420
361 GGHKLEPRTIGTTLNISTQSTNTSINPVTLPPTSVDYRTESLAGLNLFLTQPVNGVPR 420
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421 VDFHWKFWTHPIASDNFYYPGYAGIGTQODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
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541 TGTFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
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601 TFRVGTFTPFSDVQSTFTIGAMNFSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660
661 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719
661 TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupa, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 92.4%; Score 3472.5; DB 4; Length 710;
Best Local Similarity 92.4%; Pred. No. 1.9e-302;
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;
1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPVSASTI 60
1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPVSASTI 60
61 QTGTGAGKILGTLGVPPAGQVASYLSFIIGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120
61 QTGTGAGKILGTLGVPPAGQVASYLSFIIGELWPKGNQWEIIPMEHVEEIIINQKISTYA 120
121 RNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVKSQYIALELMFVKLPSFAVSG 180
121 RNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVKSQYIALELMFVKLPSFAVSG 180
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241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300
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301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNW 360
361 GGHKLEPRTIGTTLNISTQSTNTSINPVTLPPTSVDYRTESLAGLNLFLTQPVNGVPR 420
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421 VDFHWKFWTHPIASDNFYYPGYAGIGTQODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
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RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 90.3%; Score 3394; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. No. 1.8e-295;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKVQVIALELMFVQKLPSPAVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKVQVIALELMFVQKLPSPAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKWYS 240
QY 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFSDYDQYPIKTAQTREVTDAI 300
DB 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFSDYDQYPIKTAQTREVTDAI 300
QY 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTRSDVRYTESLAGNLFLTQPNVGVPR 420
DB 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTRSDVRYTESLAGNLFLTQPNVGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGYVIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYYPGYVIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TERTVGTTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTYE 648
DB 601 TERTVGTTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTYE 648
RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 89.7%; Score 3373; DB 2; Length 719;
Best Local Similarity 89.7%; Pred. No. 1.7e-293;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYA 120
QY 121 RNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKVQVIALELMFVQKLPSPAVSG 180
DB 121 RNKALTDLKGLGDALAVYHDSLESVGNRNTRARSVVKVQVIALELMFVQKLPSPAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKWYS 240

Db 181 EEVPLLPYQAANLHLLLRDASIFEKNGGLSASEISFTFYNQOVERTRDYSYHCVKWN 240
Qy 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFSPSYDTQMPYIKTTAQLTREYVTDI 300
Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFSPSYDTQMPYIKTTAQLTREYVTDI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNW 360
Db 301 GTVDPNQALRSITWYNNAPSPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNW 360
Qy 361 GGHKLEFRITGGTINISQGSNTSINPVTLPFTSRDVRITESLAGNLFLTQPVNGVPR 420
Db 361 GGHLESRRPIGGALNTSQGSNTSINPVTLPFTSRDVRITESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPTLPPIASDNFYYPGVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 GSHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTK 540
Qy 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600
Db 541 SGTFGHIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600
Qy 601 TFRVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TFRVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDELYLDEKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDELYLDEKRELFEIVKYAKQIHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: CRY11
; CURRENT APPLICATION NUMBER: US/09/218,942
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2
Query Match 89.6%; Score 3368; DB 3; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.7e-293;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;
Qy 1 MKLNQDQKHQSFSSNAKVDKISTDLSLKNEDTIELQINHEDCLKMSYEYENVEPVSASTI 60
Db 1 MKLNQDQKHQSFSSNAKVDKISTDLSLKNEDTIELQINHEDCLKMSYEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINOKISITVA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINOKISITVA 120
Qy 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVVKSVQVIALELMFVKQLPSFAVSG 180
Db 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVVKSVQVIALELMFVKQLPSFAVSG 180

Qy 181 EEVPLLPYQAANLHLLLRDASIFEKNGGLSASEISFTFYNQOVERTRDYSYHCVKWN 240
Db 181 EEVPLLPYQAANLHLLLRDASIFEKNGGLSASEISFTFYNQOVERTRDYSYHCVKWN 240
Qy 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFSPSYDTQMPYIKTTAQLTREYVTDI 300
Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFSPSYDTQMPYIKTTAQLTREYVTDI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNW 360
Db 301 GTVDPNQALRSITWYNNAPSPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNW 360
Qy 361 GGHKLEFRITGGTINISQGSNTSINPVTLPFTSRDVRITESLAGNLFLTQPVNGVPR 420
Db 361 GGHLESRRPIGGALNTSQGSNTSINPVTLPFTSRDVRITESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFVTHPIASDNFYYPGVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPTLPPIASDNFYYPGVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTK 540
Qy 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600
Db 541 SGTFGHIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600
Qy 601 TFRVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
Db 601 TFRVTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDELYLDEKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDELYLDEKRELFEIVKYAKQIHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989


```

; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.5%; Score 2800; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 2.6e-242;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDQKHQSPSSNAKVDKISTDSLKNETDIEQLQINHEDECLKMSYENVEPFVSASTI 60
Db 1 MKLNQDQKHQSPSSNAKVDKISTDSLKNETDIEQLQINHEDECLKMSYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTLGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSVQYIALELMFVKQLPSFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSVQYIALELMFVKQLPSFAVSG 180

QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
Db 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240

QY 241 TGLNLRGNTNAESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300
Db 241 TGLNLRGNTNAESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI 300

QY 301 GTVHPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
Db 301 GTVHPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360

QY 361 GGKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPR 420
Db 361 GGKLEPRTIGTGLNISTQSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPR 420

QY 421 VDFHWKFTVHPHPIASDNFYPGYVIGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVHPHPIASDNFYPGYVIGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 481 ASHKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Jan, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
```

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-100-709-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIEQLQ-NINHEDECLKMSYENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVANNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARKNALTDLKG 130
Db 67 LGVLGVFPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLESWGNRNNTARSVVKSVQYIALELMFVKQLPSFAVSGEEVPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRDARSIIILRYVALELDITTAIPLRIRNEEVPLLMVYA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
Db 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSHNCVQWYNTGLNNLRGTN 246

QY 251 AESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDIAGTVHPHPSFT 310
Db 247 AESWLRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDIPIGRTNAPSFGA 306

QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNWGGHKLERTI 370
Db 307 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNWGGHKLERTI 366

QY 371 GGTGLNISTQGST-NTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPRVDFHWKFTV 429
Db 367 GGTGLNISTQGST-NTSINPVTLPFTSRDVRYESLAGLNFLTQPVNGVPRVDFHWKFTV 422

QY 430 HPIASDNFYPG-----YVIGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTSYQPYQGVIGIQLFDSSETLPPTTERPENYESYSHRLSHIGLIIGN 480

QY 483 HVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOQNFSTMTNRGDLDYKTF 602
Db 541 TFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOQNFSTMTNRGDLDYKTF 600

QY 603 RTVGFTTPESFLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKVTA 662
Db 601 RTAGFSTPPFNFLNAQSTFTTIGAWNFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKVTA 659
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QY 663 LFTSTNPRGLTKDVKYHIDQVSNLVESLDEFLVDEKRELFEIVKYAKQLHIERNM 719
Db 660 LFTSTNPRGLTKDVKYHIDQVSNLVESLDEFLVDEKRELFEIVKYAKQLHIERNM 716

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-865-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity. 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHECLKMEYENVEPVFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPVSNPSTQMLSPDARIEDSLCVAENVNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIFMHEVEELINQKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQVASYLSFILGELWPKGNQWEIFMHEVEELINQKISTYARNKALTDLKG 126

QY 131 LGDALAVVHDSLSWGVNRRNTRARSVVKSQYIALBELMVQKLPSFVSGEEVPLPIYA 190
Db 127 LGRGYSYQOALETWLDNRNDRSRIILERVVALELDITTAIPFIRNEEVPLMWYA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSLSSTFFYNQVRAGDYSCHCKWYSTGLNLRGTN 250
Db 187 QAANLHLLLRDASIFGKEWGLSSLSSTFFYNQVRAGDYSCHCKWYSTGLNLRGTN 246

QY 251 AESWRYNQPRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVVYDAIGTVHPSPFT 310

Db 247 AESWRYNQPRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVVYDAIGTVHPSPFT 306
QY 311 STTWYNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMWGGHKLFRFI 370
Db 307 STWYNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMWGGHKLFRFI 366

QY 371 GGTNLNISTOGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPVNGVPRVDFHFKFVT 429
Db 367 GGTNLNISTOGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPVNGVPRVDFHFKFVT 422

QY 430 HPIASDNFYYPG-----YVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQYQGVGIGLQFDETELPPETTERENYESYSHRLSHIGLIGN 480

QY 483 HVKALVSWTHRSADRTNTEPNISITQIPLVAFNLSSGAADVVRGPGFTGGDLRRTNTG 542
Db 481 TLRAPVSWTHRSADRTNTEPNISITQIPLVAFNLSSGAADVVRGPGFTGGDLRRTNTG 540

QY 543 TFGDIRVNIWPPFAQRYRVRIRYASTTDLQFHTSINGKAINQCNFSATMNGEDLDYKTF 602
Db 541 TFGDIRVNIWPPFAQRYRVRIRYASTTDLQFHTSINGKAINQCNFSATMNGEDLDYKTF 600

QY 603 RTVGFTTFFSFLDVOSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVT 662
Db 601 RTAGFSTPFNFELNAQSTFTLGAQFSN-QEYVIDRVEFVPAEVTFEAYDLEAKAVNA 659

QY 663 LFTSTNPRGLTKDVKYHIDQVSNLVESLDEFLVDEKRELFEIVKYAKQLHIERNM 719
Db 660 LFTSTNPRGLTKDVKYHIDQVSNLVESLDEFLVDEKRELFEIVKYAKQLHIERNM 716

RESULT 9
US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDECLMSYENVEPFVSASTQTGTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSDPDIEDSLCAEVNNDPFFVSASTVQTGINIAGRI 66

QY 71 LGTIGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMFVQKLPSPAVSGEVPPLPIYA 190
Db 127 LGRGYRSYQQALETWLDNRDARSRIILERYVALELDITTAIPFRIRNEEVPPLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
Db 127 LGRGYRSYQQALETWLDNRDARSRIILERYVALELDITTAIPFRIRNEEVPPLMVYA 186

QY 251 AEWVRYNQFRDMTLMVLDLVALPSPYDTOMYPIKTAQLTREVYTDAGTGVHPHPSFT 310
Db 247 AESWLRYNQFRDRLTLGVLDLVALPSPYDTRYPINTSAQLTREIYDPIGRTNAPSGFA 306

QY 311 STTWNNNAPSFAIEAAVVRNPRLDLEQVTIYSLRSWNTQYMMWGHGKLEFRTI 370
Db 307 STWNNNAPSFAIEAAVVRNPRLDLEQVTIYSLRSWNTQYMMWGHGKLEFRTI 366

QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHKKFVT 429
Db 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHKKFVT 422

QY 430 HPIASDNFYYPG-----YVGIGTQLQDSENELEPPATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQYQGVGIQFDSETELPPTTERPNYESYSHRLSHIGLIIGN 480

QY 483 HVKALVYSWTHRSADRTNTIENSIITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542
Db 481 TLRAPVYSWTHRSADRTNTIGNRIITQIPLVKALNLHSGVTWVGPGFTGGDILRRTNTG 540

QY 543 TFGDIRVNPFPAPQVRVRIYASTDLOFHTSINGKAINQGNFSATMARGEDLDYKFT 602
Db 541 TFGDIRLINVPLSQRYVRIRYASTDLOFHTSINGKAINQGNFSATMARGEDLDYKFT 600

QY 603 RTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQEKVTA 662
Db 601 RTAGFSTFNFNLNAQSTFTLGAQSFN-QEVVIDRVEFVPAEVTFAEYDLERAQKAVNA 659

QY 663 LFTSTNPRGLKTDVKDHIDQVSNLVESLSDEFYLDKRELFEIVKAKOLHIERNM 719
Db 660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEIVKAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      65.0%; Score 2445.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDECLMSYENVEPFVSASTQTGTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSDPDIEDSLCAEVNNDPFFVSASTVQTGINIAGRI 66

QY 71 LGTIGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLESVGNRNTRARSVVKSQYIALELMFVQKLPSPAVSGEVPPLPIYA 190
Db 127 LGRGYRSYQQALETWLDNRDARSRIILERYVALELDITTAIPFRIRNEEVPPLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEYSNHCYQWYNTGLNNLRGTN 246

QY 251 AEWVRYNQFRDMTLMVLDLVALPSPYDTOMYPIKTAQLTREVYTDAGTGVHPHPSFT 310
Db 247 AESWLRYNQFRDRLTLGVLDLVALPSPYDTRYPINTSAQLTREIYDPIGRTNAPSGFA 306

QY 311 STTWNNNAPSFAIEAAVVRNPRLDLEQVTIYSLRSWNTQYMMWGHGKLEFRTI 370
Db 307 STWNNNAPSFAIEAAVVRNPRLDLEQVTIYSLRSWNTQYMMWGHGKLEFRTI 366

QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHKKFVT 429
Db 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPRVDFHKKFVT 422

QY 430 HPIASDNFYYPG-----YVGIGTQLQDSENELEPPATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQYQGVGIQFDSETELPPTTERPNYESYSHRLSHIGLIIGN 480

QY 483 HVKALVYSWTHRSADRTNTIENSIITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542
Db 481 TLRAPVYSWTHRSADRTNTIGNRIITQIPLVKALNLHSGVTWVGPGFTGGDILRRTNTG 540
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.2%; Score 2340.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 3.8e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFSASTI 60
Db 1 M KSKNQNMHQSLSNNATVDKFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSYFSLGELWPKGNQWEIFMEHVEEINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSYFSLGELWPKGKQWEIFMEHVEEINQKISTYA 111

Qy 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNRARSVVKSOYIALELMFVQKLPSFAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWIEENRNRTRSVVKSQYITLELMFVQSLPSFAVSG 171

Qy 181 EEVPLLPPIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
Db 172 EEVPLLPPIAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKYSYSDHCVKWYN 231

Qy 241 TGLNLRGTNAESWVRYNQFRDMLMVLVDLVALFPSYDTQMPIKTTAQLTREVTDAI 300
Db 232 TGLNRLMGNAESWVRYNQFRDMLMVLVDLVALFPSYDTQMPIKTTAQLTREVTDAI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSTNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSTNTQYNNMW 351

Qy 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRRTSLAGNLFLTQPVNGVPR 420
Db 352 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRRTSLAGNLFLTQPVNGVPR 411

Qy 421 VDFHWKFTVTHPIASDNFYYPGYVIGTQLOQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLOQDSENELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 481 ASHKALVYSWTHRESAD 497
Db 472 ASHKALVYSWTHRESAD 488
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RESULT 13

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US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. P5158C2, Active Against Lepidopteran Pests, and Genes
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; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10
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Query Match 62.2%; Score 2340.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 3.8e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFSASTI 60
Db 1 M KSKNQNMHQSLSNNATVDKFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSYFSLGELWPKGNQWEIFMEHVEEINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSYFSLGELWPKGKQWEIFMEHVEEINQKISTYA 111

Qy 121 RNKALTDLKGDLALAVYHDSLESWVGNNRNRARSVVKSOYIALELMFVQKLPSFAVSG 180
Db 112 RNKALADLKGDLALAVYHDSLESWIEENRNRTRSVVKSQYITLELMFVQSLPSFAVSG 171

Qy 181 EEVPLLPPIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
Db 172 EEVPLLPPIAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKYSYSDHCVKWYN 231

Qy 241 TGLNLRGTNAESWVRYNQFRDMLMVLVDLVALFPSYDTQMPIKTTAQLTREVTDAI 300
Db 232 TGLNRLMGNAESWVRYNQFRDMLMVLVDLVALFPSYDTQMPIKTTAQLTREVTDAI 291

Qy 301 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSTNTQYNNMW 360
Db 292 GTVHPHPSFTSTTWYNNAPSFAIEAAVVRNPHLLDPLEQVTIYSLLSRWSTNTQYNNMW 351
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QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVLPTFTSRDVRTESLAGLNLFLTOPVNGVPR 420
DB 352 GGHKLEFRTIGTGLNISTQGSTNTSINPVLPTFTSRDVRTESLAGLNLFLTOPVNGVPR 411
QY 421 VDFHFKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 412 VDFHFKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471
QY 481 ASHKVALVYSWTHRSAD 497
DB 472 ASHKVALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
Sequence 7, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-951-715A-7

Query Match 60.2%; Score 2264.5; DB 1; Length 1207;

Best Local Similarity 64.3%; Pred. No. 1.1e-193;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;
QY 40 EDCLKMSYENVEPVSASTIOTGIGTAGKILGTGVPFAGQVASYFSLGELWPKGN 99
DB 10 EDCLKMSYENVEPVSASTIOTGIGTAGKILGTGVPFAGQVASYFSLGELWPKGN 69
QY 100 QWEIFMEHVEEIIINQKISTYARNKALTDLKGIGDALAVHDSLESWVGNNRNTARSVVK 159
DB 70 QWEIFMEHVEEIIINQKISTYARNKALTDLKGIGDALAVHDSLESWVGNNRNTARSVVK 129
QY 160 SQYIALELMFVQKLPSFVSGEEVPLPIYAQAANLHLLLRDASIEGKWSLSSEIST 219
DB 130 TOYIALELMFVQKLPSFVSGEEVPLPIYAQAANLHLLLRDASIEGKWSLSSEIST 189
QY 220 FYNQVERAGDSDHCVKWTSTGLNNRGTNAESWRYNQFRDRLMVLVLPSPSYD 279
DB 190 YFERQVERTRDYSYCVWEWNTGLNSLRGTNAESWRYNQFRDRLMVLVLPSPSYD 249
QY 280 TOMYPIKTTAQLTREVYTDAGTGVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFL 339
DB 250 TRTYPIKTTAQLTREVYTDAGTGVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFL 307
QY 340 EQVTIYLLSRWSNTQYMNMGHKLERTTIGTGLNISTQGSTNTSINPVLPTFTSRDVT 399
DB 308 EQVTIYLLSRWSNTQYMNMGHKLERTTIGTGLNISTQGSTNTSINPVLPTFTSRDVT 367
QY 400 RTESLAGLNLFLTOPVNGVPRVDFHWKVFTHP-----IASDNFYYPGVGIGTQLOD 452
DB 368 RTESLAGLNLFLTOPVNGVPRVDFHWKVFTHP-----IASDNFYYPGVGIGTQLOD 423
QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNIEPNSITQIPL 512
DB 424 ETELPPETTERENYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNIEPNSITQIPL 483
QY 513 VKAFNLSSGAUVVRPGFTGGDILRRNTGTGPDIRVNINPPFAQRYVRIRYASTTDLQ 572
DB 484 VKAFNLSSGAUVVRPGFTGGDILRRNTGTGPDIRVNINPPFAQRYVRIRYASTTDLQ 543
QY 573 FHTSINGKAINQGNFSATMNGEDLDYKTFRTVGTFTPSFLDVQSTFTIGANFSSGNE 632
DB 544 FVSRGGTNNFRFLRTMNSGDELKYNFVRRAFTTPTFTQIQTIRTSIQGLSGNGE 603
QY 633 VYIDRIEFPVVEVTEYAEYDFEKAQKVTALFTSTNPRGLTKDVKDYHIDQVSNLVSLS 692
DB 604 VYIDRIEFPVVEVTEYAEYDFEKAQKVTALFTSTNPRGLTKDVKDYHIDQVSNLVSLS 663
QY 693 DEFYLDKRELFVIVKAKQLHIERNM 719
DB 664 DEFYLDKRELFVIVKAKQLHIERNM 690

RESULT 15
US-08-459-448A-7
Sequence 7, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-7

Query Match 60.2%; Score 2264.5; DB 2; Length 1207;
Best Local Similarity 64.3%; Pred. No. 1.1e-193;
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;
Qy 40 EDCLKMSYENVEPVFASTIQTGIGIAGKILGTGVFPFAGQVASYLSFILGELMPKGN 99
Db 10 EDSLCIAEGNNIDFVSASTVQGINIAGRIILGVLPFAGQVASYLSFILGELMPGRD 69
Qy 100 QWEIFMEHVEEIIINOKISTYARNKALTDLKLGDALAVYHDSLESWVGNRNNTARSVK 159
Db 70 QWEIFLEHVEQLINQITENARTALRLQGLGDSFRAYQQSLEDWLENRDDARTRSVLY 129
Qy 160 SOYIALELMFVQKLPSFAVSGEEVPLPIYAAQANLHLLLRDASIFCKEWGLSSSEIST 219
Db 130 TQYIALELDFLNPALFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEFGLTSQEIQR 189
Qy 220 FYNQVERAGDYSCHVKWYSTGLNNLGTNAESWRYNQFRDMLMVLDLVALFPSSYD 279
Db 190 YERQVERTDYSYCVENWYNTGLNSLGTNAASWRYNQFRDLTLGLVLDLVALFPSSYD 249
Qy 280 TOMYPIKTTAQLTRREVYTDAGTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDPL 339
Db 250 TRTYPINTSAQLTRREVYTDAGTAT--GVNMAAMNWNPNAPSFAIEAAAIIRSPHLLDPL 307
Qy 340 EQVTIYSLSRWSNTQYMNWGGHKLFRPTIGTGLNLTSTQGSTNTSINPVTLPFTSRDNY 399
Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDNY 367
Qy 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFTVHP-----IASDNFYYPYGVIGTQLQDS 452
Db 368 RTESYAGVLLWGIYLEPIHGVPVTRFNF---TNPQNISDRGTANYSQP-YESPGLOLKDS 423

Qy 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512
Db 424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVVPVYSWTHRSADRTNTIGPNRIITQIPM 483
Qy 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPPAQRVRYRYASTTDLQ 572
Db 484 VKASELPQGTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFD 543
Qy 573 FHTSINGKAINQGNFSAWNRGEBLDYKTFRTVGTFTTTPPSFLDVQSTFTTIGAWNPFSSGNE 632
Db 544 FVSRGGTTVNNFRFLRTMNSGDELKYGNFVRAFTTPTFTTQIQDIIRTSIQGLSGNGE 603
Qy 633 VYIDRIEFVPEVETYEAEYDFEKAQEKVLTALFTSTNPRGLKTDVYHIDQVSNLVESLS 692
Db 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFNTNPRRLKTDVYHIDQVSNLVACL 663
Qy 693 DEFYLDKRELFETVVKYAKQLHIERNM 719
Db 664 DEFCLDKRELEKVKYAKRLSDERNL 690

Search completed: March 9, 2005, 17:27:45
Job time : 25.1512 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds
(without alignments)
4539.261 Million cell updates/sec

Title: US-10-019-823B-58
Perfect score: 3761
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3724	99.0	719	1 C1IA_BACTK	Q45752 bacillus th
2	3724	99.0	719	2 Q6X181	Q6x181 bacillus th
3	3719	98.9	719	2 Q33NJ5	Q93nj5 bacillus th
4	3718	98.9	719	2 Q85796	O85796 bacillus th
5	3589	95.4	719	2 Q8KY61	O8ky61 bacillus th
6	3517	93.5	719	2 Q9F0P8	Q9fop8 bacillus th
7	3484	92.6	719	1 C1IB_BACTE	Q45709 bacillus th
8	3363	89.4	719	1 C1ID_BACTU	O9xdl1 bacillus th
9	3341	88.8	719	1 C1IC_BACTU	O87404 bacillus th
10	2417.5	64.3	1229	1 C1BB_BACTU	Q45739 bacillus th
11	2417.5	64.3	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2250.5	59.8	1228	2 Q33T75	Q93t75 bacillus th
13	2248.5	59.8	1228	1 C1BA_BACTK	P05517 bacillus th
14	2240.5	59.6	1228	2 Q33NM5	O93nm5 bacillus th
15	2166.5	57.6	849	2 Q6PYW8	Q6pyw8 bacillus th
16	2166.5	57.6	1227	1 C1BE_BACTU	O85805 bacillus th
17	2083.5	55.4	1231	2 Q8KNY2	O8kny2 bacillus th
18	2078.5	55.3	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
19	1971.5	52.4	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1876	49.9	381	2 Q45740	Q45740 bacillus th
21	1643.5	43.7	1157	1 C8AA_BACUK	Q45704 bacillus th
22	1630	43.3	1144	2 Q8KZL7	Q8kz17 bacillus th
23	1466	39.0	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1460.5	38.8	1169	1 C8BA_BACUK	Q45705 bacillus th
25	1458.5	38.8	1166	1 C1GA_BACTU	Q45746 bacillus th
26	1455	38.7	1169	1 C1FB_BACTM	O66377 bacillus th
27	1451	38.6	1167	1 C1JA_BACTU	Q45738 bacillus th
28	1449	38.5	1174	2 Q45749	Q45749 bacillus th
29	1443	38.4	1155	1 C1AB_BACTK	P06578 bacillus th
30	1443	38.4	1155	2 Q7BE98	Q7be98 bacillus th
31	1443	38.4	1155	2 Q9F296	Q9f296 bacillus th

RESULT 1

ID	C1IA_BACTK	STANDARD;	PRT;	719 AA.
AC	Q45752; P71092; Q45750; Q45751; Q45756;			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
GN	Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryV1;			
OS	Bacillus thuringiensis (subsp. kurstaki).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=29339;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSIR732;			
RX	MEDLINE=93298009; PubMed=8517758;			
RA	Gleave A.P., Williams R., Hedges R.J.;			
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes and characterization of a cryV gene cloned from B. thuringiensis subsp. kurstaki.";			
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=JHCC4835;			
RX	MEDLINE=92269582; PubMed=1588820;			
RA	Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RT	"Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";			
RL	Mol. Microbiol. 6:1211-1217(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HD-1;			
RX	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus.";			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AB88;			
RX	MEDLINE=96178985; PubMed=8606196;			
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,			
RT	Craig J.A., Koziel M.G., Estruch J.J.;			
RT	"Cloning of a cryV-type insecticidal protein gene from Bacillus thuringiensis: the cryV-encoded protein is expressed early in stationary phase.";			
RL	J. Bacteriol. 178:2141-2144(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=61;			

ALIGNMENTS

32	1441	38.3	1118	2	Q9AM83	Q9am83 bacillus th
33	1438	38.2	1156	2	Q6GUA7	Q6gua7 bacillus th
34	1433	38.1	1177	2	Q6EIX3	Q6eix3 bacillus th
35	1431	38.0	1155	2	Q93T21	Q93t21 bacillus th
36	1430.5	38.0	793	2	Q6PYW7	Q6pyw7 bacillus th
37	1430.5	38.0	1180	2	Q9S5V8	Q9s5v8 bacillus th
38	1429.5	38.0	1176	2	Q7WZT9	Q7wzt9 bacillus th
39	1425.5	37.9	1181	1	C1AE_BACTL	O03748 bacillus th
40	1423.5	37.8	1176	2	Q45736	Q45736 bacillus th
41	1419.5	37.7	1176	1	C1AA_BACTK	P02965 bacillus th
42	1419.5	37.7	1176	2	Q9RC30	Q9rc30 bacillus th
43	1411.5	37.5	1169	2	Q8GHE8	Q8ghe8 bacillus th
44	1407.5	37.4	1179	1	C1AD_BACTA	Q03744 bacillus th
45	1404.5	37.3	1169	1	C1GB_BACTZ	Q9zaz6 bacillus th

Tue Feb 15 10:07:56 2005

RA Selvapandiyan A., Bhatnagar R.K.;
 RT "Isolation, cloning and expression of cryV gene.";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Promotes colloidsomic lysis by binding to the midgut
 CC epithelial cells of certain coleopteran and lepidopteran species.
 CC Active on Plutella xylostella and Bombyx mori.
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; M98544; AAA22354.1; -;
 CC EMBL; X62821; CAA44633.1; -;
 CC EMBL; L36338; AAC36999.1; -;
 CC EMBL; L49391; AAB00958.1; -;
 CC EMBL; Y08920; CAA70124.1; -;
 CC PIR; I39815; I39815.
 CC PIR; S25383; S25383.
 CC HSSP; P02965; ICIV.
 CC InterPro; IPR001178; Endotoxin.
 CC InterPro; IPR005638; Endotoxin_C.
 CC InterPro; IPR005639; Endotoxin_N.
 CC InterPro; IPR008979; Gal_bind_like.
 CC Pfam; PF03944; Endotoxin_C; 1.
 CC Pfam; PF00555; Endotoxin_M; 1.
 CC Pfam; PF03945; Endotoxin_N; 1.
 CC Sporulation; Toxin.
 KW VARIANT 159 159 K -> R (in strain 61).
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-
 FT VARIANT 233 233 1).
 FT VARIANT 443 443 A -> V (in strain AB88).
 FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).
 SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C2SDAFF5 CRC64;

 Query Match 99.0%; Score 3724; DB 1; Length 719;
 Best Local Similarity 99.3%; Pred. No. 5.1e-252;
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60

 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

 QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPFAVS 179
 DB 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPFAVS 179

 QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWY 239
 DB 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWY 239

 QY 240 STGLNLRGTNAESWVRNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREVYTD 299
 DB 240 STGLNLRGTNAESWVRNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREVYTD 299

 QY 300 IGVHPHPSFTSTWYNNAPPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMM 359
 DB 300 IGVHPHPSFTSTWYNNAPPSAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMM 359

 QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419

DB 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419
 QY 420 RVDPHWKFTVHTPIASDNFYPCYAGITQLODSENELPPATGQPNYESYSHRLSHIGLI 479
 DB 420 RVDPHWKFTVHTPIASDNFYPCYAGITQLODSENELPPATGQPNYESYSHRLSHIGLI 479
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRT 539
 DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRT 539
 QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLDY 599
 DB 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDLDY 599
 QY 600 KTFRTVGTTPFPFLDVQSTFTIGAMNFFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
 DB 600 KTFRTVGTTPFPFLDVQSTFTIGAMNFFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
 QY 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFVIVKAKQLHIERNM 719
 DB 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFVIVKAKQLHIERNM 719

 RESULT 2
 Q6X181 ID Q6X181 PRELIMINARY; PRT; 719 AA.
 AC Q6X181;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CryII.
 GN Name=CryII;
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY262167; AAP86782.1; -;
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal_bind_like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 DR SEQUENCE 719 AA; 81216 MW; 3627E5A6C2SDAFF5 CRC64;
 SQ

 Query Match 99.0%; Score 3724; DB 2; Length 719;
 Best Local Similarity 99.3%; Pred. No. 5.1e-252;
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60

 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

 QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPFAVS 179
 DB 120 ARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPFAVS 179

 QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWY 239
 DB 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWY 239

Qy	240	STGLNLRGNTAESWVRYNQFRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD	299
Db	240	STGLNLRGNTAESWVRYNQFRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD	299
Qy	300	IGTVHHPSPFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNM	359
Db	300	IGTVHHPSPFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNM	359
Qy	360	WGGHKLFRFTIGGTINISTQGSTNTSINPVTLPFTSRDVRTSLAGLNFLTQPVNGVP	419
Db	360	WGGHKLFRFTIGGTINISTQGSTNTSINPVTLPFTSRDVRTSLAGLNFLTQPVNGVP	419
Qy	420	RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI	479
Db	420	RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI	479
Qy	480	SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRT	539
Db	480	SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRT	539
Qy	540	NTGTFGDIRVNINPPPAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDY	599
Db	540	NTGTFGDIRVNINPPPAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDY	599
Qy	600	KTFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK	659
Db	600	KTFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK	659
Qy	660	VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM	719
Db	660	VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM	719
RESULT 3			
Q93NJ5	PRELIMINARY; PRT; 719 AA.		
ID	Q93NJ5		
AC	Q93NJ5		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	CryIIa.		
GN	Name=cryIIa;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Song F., Zhang J., Gu A., Huang D., Li G.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF373207; AAK66742.1; -		
DR	HSSP; P02965; 1CIY.		
DR	GO; GO:0005102; P:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal_bind_like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;		
Query Match			
Best Local Similarity 98.9%; Score 3719; DB 2; Length 719;			
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;			
Qy	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLXKSEYENVEPVSASTI	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLXKSEYENVEPVSASTI	60
Qy	61	QTGIGIAGKILGTGVPFAGQVASLYSFILGELWPKGNQWEILFMEHVEE-INQKISTY	119

Db	61	QTGIGIAGKILGTGVPFAGQVASLYSFILGELWPKGNQWEI-FMEHVEEINQKISTY	119
Qy	120	ARNKALTDLKGLGDALAVYHDSLESWVGNNRNNTRARSVVRISOYIALELMFVQKLPSFAVS	179
Db	120	ARNKALTDLKGLGDALAVYHDSLESWVGNNRNNTRARSVVRISOYIALELMFVQKLPSFAVS	179
Qy	180	GEVPLLLPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY	239
Db	180	GEVPLLLPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY	239
Qy	240	STGLNLRGNTAESWVRYNQFRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD	299
Db	240	STGLNLRGNTAESWVRYNQFRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTD	299
Qy	300	IGTVHHPSPFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
Db	300	IGTVHHPSPFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
Qy	360	WGGHKLFRFTIGGTINISTQGSTNTSINPVTLPFTSRDVRTSLAGLNFLTQPVNGVP	419
Db	360	WGGHKLFRFTIGGTINISTQGSTNTSINPVTLPFTSRDVRTSLAGLNFLTQPVNGVP	419
Qy	420	RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI	479
Db	420	RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI	479
Qy	480	SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRT	539
Db	480	SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRT	539
Qy	540	NTGTFGDIRVNINPPPAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDY	599
Db	540	NTGTFGDIRVNINPPPAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDY	599
Qy	600	KTFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK	659
Db	600	KTFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK	659
Qy	660	VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM	719
Db	660	VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM	719
RESULT 4			
O85796	PRELIMINARY; PRT; 719 AA.		
ID	O85796		
AC	O85796		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Insecticidal protein.		
GN	Name=cryVI01;		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OC	Plasmid large plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SI01;		
RA	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF076953; AAC26910.1; -		
DR	HSSP; P02965; 1CIY.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal_bind_like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;		

KW	Plasmid.	719 AA;	81230 MW;	42746D478359BBA7	CRC64;
SQ	SEQUENCE				
	Query Match	98.9%;	Score 3718;	DB 2;	Length 719;
	Best Local Similarity	99.2%;	Pred. No. 1.3e-251;		
	Matches 714;	Conservative	2;	Mismatches 2;	Indels 2;
					Gaps 2;
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLMKSEYENVEFPVSASTI	60		
DB	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLMKSEYENVEFPVSASTI	60		
QY	61	QTGIGIAGKILGTIGVPPAGQVASLYSIFILGELWPKGNQWEILFMEHVEE-INQKISTY	119		
DB	61	QTGIGIAGKILGTIGVPPAGQVASLYSIFILGELWPKGNQWEILFMEHVEE-INQKISTY	119		
QY	120	ARNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVRSQYIALELMFVKQLPSFAVS	179		
DB	120	ARNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVRSQYIALELMFVKQLPSFAVS	179		
QY	180	GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKMY	239		
DB	180	GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKMY	239		
QY	240	STGLNNLRCTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTTDA	299		
DB	240	STGLNNLRCTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTTDA	299		
QY	300	IGTVHPHPGFTSTTWYNNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTQYMMN	359		
DB	300	IGTVHPHPGFTSTTWYNNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTQYMMN	359		
QY	360	WGGHKLEFRTIGGTNLINISQGSTNTSINPVTLPFTSRDVVRATESLAGLNLFLTQPVNGVP	419		
DB	360	WGGHKLEFRTIGGTNLINISQGSTNTSINPVTLPFTSRDVVRATESLAGLNLFLTQPVNGVP	419		
QY	420	RVDFHWKFVTHPIASDNFYFPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI	479		
DB	420	RVDFHWKFVTHPIASDNFYFPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI	479		
QY	480	SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539		
DB	480	SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539		
QY	540	NTGTGDIRVNNINPPAQRVYRIRIYASTTDLQFHTSINGKAINQGNFSAATWNRGDBLDY	599		
DB	540	NTGTGDIRVNNINPPAQRVYRIRIYASTTDLQFHTSINGKAINQGNFSAATWNRGDBLDY	599		
QY	600	KTFRTVGFTTTPSFLDVQSTTTIGAWNFSSGNEVIYDRIEFVPVEVYEAEDFEKAQEK	659		
DB	600	KTFRTVGFTTTPSFLDVQSTTTIGAWNFSSGNEVIYDRIEFVPVEVYEAEDFEKAQEK	659		
QY	660	VTALFTSTNPRGLKTDVKYHIDQVGNLVLESDFVLDEKRELFEIVKYANELHIERNM	719		

```

RESULT 5
Q8KY61
ID Q8KY61 PRELIMINARY; PRT; 719 AA.
AC Q8KY61;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278797; AAM73516.1; -.
DR PIR; B42459; B42459.

```

HSP; P02965; 1CIY.
DR GO: 0005102; F:receptor binding; IEA.
DR GO: 0006952; P:defense response; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;
SO

Query Match	95.4%;	Score 3589;	DB 2;	Length 719;
Best Local Similarity	95.6%;	Pred. No. 1.5e-242;		
Matches 688; Conservative	14;	Mismatches 16;	Indels 2;	Gaps 2;

QY	1	MLKKNQKHQS	FSSNAKVDKISTD	SLKNETDI	ELQINNHEDCL	KMSYEN	VEPVSASTI	60			
DB	1	MLKNPDKHQS	FSSNAKVDKISTD	SLKNETDI	ELQINNHEDCL	KISEYEN	VEPVSASTI	60			
QY	61	QTGIGIAGK	ILGTGLVPFAGQ	VASLYSFI	LGBELWPK	GKNQWEIL	FMEHVEE-INQ	ISTY 119			
DB	61	QTGIGIAGK	ILGTGLVPFAGQ	VASLYSFI	LGBELWPK	GKNQWEI-FMEHVEE	IINQKISTY	119			
QY	120	ARNKALTDL	KGLGDALAVYHDS	LESWGVRN	NTRARS	VYVR	SQYIALELMFVQKL	PSFAVS 179			
DB	120	ARNKALTDL	KGLGDALAVYHDS	LESWGVRN	KNTRARS	VVK	SQYIALELMFVQKL	PSFAVS 179			
QY	180	GEEVPLPI	YQAANLHLLLRD	ASIFGKEW	GLSSSEISTE	FYNRQ	VERAGDYS	DHCVKWMY 239			
DB	180	GEEVPLPI	YQAANLHLLLRD	ASIFGKEW	GLSSSEISTE	FYNRQ	VERAGDYS	DHCVKWMY 239			
QY	240	STGLNNL	RGTNAESWRYNQ	FRDMTMLV	LDVALP	SYDTOM	YPIKTAQL	TREVYTDA 299			
DB	240	STGLNNL	RGTNAESWRYNQ	FRDMTMLV	LDVALP	SYDTOM	YPIKTAQL	TREVYTDA 299			
QY	300	IGTVHP	PHSPSTTWTYNN	NAPSAIEA	AVVRNPH	LLDFE	QVTIYSL	LSRWSNTQYMM 359			
DB	300	IGTVHP	PNASFSTWTYNN	NAPSFSTIE	SAVRNPH	LLDFE	QVTIYSL	LSRWSNTQYMM 359			
QY	360	WGCHKLE	FRPTIGGTLN	ISQGSTNTS	INPVTLP	FTSRD	VYRTESLAGLNL	FLTQPVNGVP 419			
DB	360	WGHRLE	FRPTIGGMLNT	ISQGSTNTS	INPVTLP	FTSRD	VYRTESLAGLNL	FLTQPVNGVP 419			
QY	420	RVD	FHWKFVTHPI	ASDNFYYP	GYAGIGTQ	LQDSE	NELPPEAT	GQPNYESYSHRLSHIGLI 479			
DB	420	RVD	FHWKFVTHPI	ASDNFYYP	GYAGIGTQ	LQDSE	NELPPEAT	GQPNYESYSHRLSHIGLI 479			
QY	480	SASHVKAL	VYSWTHRS	ADRNTIEB	NSITQIPL	VKA	FNLSGGA	AVRPGPFTGGDILRRT 539			
DB	480	SASHVKAL	VYSWTHRS	ADRNTIEB	NSITQIPL	VKA	FNLSGGA	AVRPGPFTGGDILRRT 539			
QY	540	NTGTFGD	IRVNINPP	FAQRVRYR	IRYASTTD	LQFHTS	INGKAINQ	GNFSATMNRG	EDLDY 599		
DB	540	NTGTFGD	IRVNINPP	FAQRVRYR	IRYASTTD	LQFHTS	INGKAINQ	GNFSATMNRG	EDLDY 599		
QY	600	KTFRTVG	FTTFFS	FLDVQSTFT	IGAWN	FSSGNEV	IDRIEF	VPVEVTYEA	EDYD	FEKAQEK 659	
DB	600	KTFRTVG	FTTFFS	FLDVQSTFT	IGAWN	FSSGNEV	IDRIEF	VPVEVTYEA	EDYD	FEKAQEK 659	
QY	660	VTALFTST	NPRLKTDV	KOYHIDQ	VSNL	VSLS	DEFLD	KE	RELFI	VKYANELH	IERNM 719
DB	660	VTALFTST	NPRLKTDV	KOYHIDQ	VSNL	VSLS	DEFLD	KE	RELFI	VKYANELH	IERNM 719

RESULT 6
Q9F0P8
ID Q9F0P8 PRELIMINARY; PRT; 719 AA.
AC Q9F0P8;
DT 01-MAR-2001 Created
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)


```
DE CryII.
GN Name=cryII;
OS Bacillus thuringiensis.
OG Plasmid pBtC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007;
RX MEDLINE=22837682; PubMed=12957903;
RY DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
RA Hu Y., Li G., Huang D.;
RT "Identification of cryII-type genes from Bacillus thuringiensis
RT strains and characterization of a novel cryII-type gene.";
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 93.5%; Score 3517; DB 2; Length 719;
Best Local Similarity 93.1%; Pred. No. 1.6e-237;
Matches 670; Conservative 27; Mismatches 21; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNKNETDIELQNKSEYENVEPFSASTI 60
Db 1 MKLKNQDKHOSLSSNAKVDKISTDSLKNETDIELQNKNETDIELQNKSEHESIDPFSASTI 60

Qy 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTLGVFPAGQIASLYSFILGELWPKGKSQWEI-FMEHVEELIDQKISTY 119

Qy 120 ARNKALTDLKGIDALAVYHDSLESVGNPNTRARSVRSQYIALELMFVQKLPSFAVS 179
Db 120 ARNIALADLKGIDALAVYHDSLESWKNNRNARATSVVKSQYIALELLFVQKLPSFAVS 179

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSDDHCKWY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASVFGKEWGLSNSQISTFYNNQVVERTSDYSDHCKWY 239

Qy 240 STGLNNLRGTNAESWRYNORFRDMTLMVLDLVALFPSSYDTQMPYIKTTAQLTREVYTD 299
Db 240 STGLNNLRGTNAESWRYNORFRDMTLMVLDLIALFPSSYDTLVYPIKTTSQLTREVYTD 299

Qy 300 ICTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWNTQYMMN 359
Db 300 ICTVHPNASFASTTWYNNNAPSFAIESAVVRNPHLLDFLEQVITYSLLSRWNTQYMMN 359

Qy 360 WGHKLEFRFTGGTLNISTQSTNTSINPVTLPFTSRDVRRTESLAGNLFQTQVNGVP 419
Db 360 WGHRLFRFTGGVLTNSTQSTNTSINPVTLPFTSRDVRRTESLAGNLFQTQVNGVP 419

Qy 420 RYDFHWKVFTHPIASDNFYYPGAGIGTQLQDSSENLPEATGPNYSEYSHRLSHIGLI 479
Db 420 RYDFHWKVFTHPIASDNFYYPGAGIGTQLQDSSENLPEATGPNYSEYSHRLSHIGLI 479

Qy 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539

Qy 540 NTGTFGDIRVNINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
Db 540 NTGTFGDIRVNINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599

540 NTGTFGDIRVNINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
600 KTFRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPVEVYEAAYDEKAQEK 659
600 KTFRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPVEVYEAAYDEKAQEK 659
660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFVVKYANELHIERNM 719
660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFVVKYAKOIHIERNM 719

RESULT 7
CLIB_BACTE STANDARD; PRT; 719 AA.
AC Q45709;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticial crystal protein cryIIb (Insecticidal delta-endotoxin
DE CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U07642; AAA82114.1; -.
CC PIR; I40590; I40590.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_Like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81295 MW; B8210ABEAE97688E CRC64;

Query Match 92.6%; Score 3484; DB 1; Length 719;
Best Local Similarity 92.2%; Pred. No. 3.3e-235;
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNKNETDIELQNKSEYENVEPFSASTI 60
Db 1 MKLKNQDKHOSLSSNAKVDKISTDSLKNETDIELQNKNETDIELQNKSEHESIDPFSASTI 60
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QY	61	QTGIGIACKILGTGVPAGQVASYLSFILGELWPKGKQWEILFMEHVEE-INQKISTY	119
Db	61	QTGIGIACKILGTGVPAGQVASYLSFILGELWPKGKQWEILFMEHVEE-INQKISTY	119
QY	120	ARNKALTDKGLDALAVYHDSLESWGNRNTRARVRSQYIALELMFVQKLPSPFAVS	179
Db	120	ARNKALSULRGLDALAVYHDSLESWGNRNTRARVRSQYIALELMFVQKLPSPFAVS	179
QY	180	GEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISFYNNRQVERAGDYSCHCVKWY	239
Db	180	GEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISFYNNRQVERTRDYSCHCVKWY	239
QY	240	STGLNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVYTDA	299
Db	240	NTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVYTDA	299
QY	300	IGTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
Db	300	IGTVHPNQAFASTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
QY	360	WGCHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTOPVNGVP	419
Db	360	WGCHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTOPVNGVP	419
QY	420	RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENLPPATGQPNYESYSHRLSHIGLI	479
Db	420	RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENLPPATGQPNYESYSHRLSHIGLI	479
QY	480	SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
Db	480	SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
QY	540	NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY	599
Db	540	NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY	599
QY	600	KTFRTVGTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEK	659
Db	600	KAPRTVGTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM	719
Db	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM	719
RESULT 8			
CLID_BACTU	CLID_BACTU	STANDARD;	PRT; 719 AA.
AC	Q9XDL1;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Pesticidal crystal protein cryIIId (Insecticidal delta-endotoxin		
DE	CryII(d) (Crystaline entomocidal protoxin) (81 kDa crystal protein).		
GN	Name=cryIIId; Synonyms=cryII(d), NRcrv;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RP	[1]_TaxID=1428;		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=BR30;		
RX	MEDLINE=20374042; PubMed=10919402;		
RA	Choi S.-K.; Shin B.-S.; Kong E.-M.; Rho H.M.; Park S.-H.;		
RT	"Cloning of a new Bacillus thuringiensis cryII-type crystal protein		
RT	gene."		
RL	Curr. Microbiol. 41:65-69 (2000).		
CC	- - FUNCTION: Promotes colloidsmotic lysis by binding to the midgut		
CC	epithelial cells of many lepidopteran larvae. Active on Plutella		
CC	xylostella and on Bombyx mori.		
CC	- - DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	- - MISCELLANEOUS: Toxic segment of the protein is located in the N-		

CC	terminus.		
CC	- - SIMILARITY: Belongs to the delta endotoxin family.		
CC	-----		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF047579; AAD44366.1; -.		
DR	HSSP; P02965; 1CIY.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
KW	Sporulation; Toxin.		
SQ	SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;		
Query Match 89.4%; Score 3363; DB 1; Length 719;			
Best Local Similarity 89.3%; Pred. No. 9.8e-227;			
Matches 643; Conservative 36; Mismatches 39; Indels 2; Gaps 2;			
QY	1	MKLKQDKHQFSSNAKVDKISTSLKNETDIELQINIHEDCLKXSEYENVEPVSASTI	60
Db	1	MKSKQNMYSFSSNATVDKSTDPLEHNTNMELQNSHEDCLKXSEYEVSPVSVSTI	60
QY	61	QTGIGIACKILGTGVPAGQVASYLSFILGELWPKGKQWEILFMEHVEE-INQKISTY	119
Db	61	QTGIGIACKILGTGVPAGQVASYLSFILGELWPKGKQWEILFMEHVEE-INQKISTY	119
QY	120	ARNKALTDKGLDALAVYHDSLESWGNRNTRARVRSQYIALELMFVQKLPSPFAVS	179
Db	120	ARNKALADKGLDALAVYHDSLESWGNRNTRARVRSQYIALELMFVQKLPSPFAVS	179
QY	180	GEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISFYNNRQVERAGDYSCHCVKWY	239
Db	180	GEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISFYNNRQVERAGDYSCHCVKWY	239
QY	240	STGLNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVYTDA	299
Db	240	NTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVYTDA	299
QY	300	IGTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
Db	300	IGTVHPNAPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
QY	360	WGCHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTOPVNGVP	419
Db	360	WGCHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTOPVNGVP	419
QY	420	RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENLPPATGQPNYESYSHRLSHIGLI	479
Db	420	RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENLPPATGQPNYESYSHRLSHIGLI	479
QY	480	SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
Db	480	SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
QY	540	NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY	599
Db	540	NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY	599
QY	600	KTFRTVGTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEK	659
Db	600	KAPRTVGTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM	719
Db	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM	719


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Db 660 ITAMFTSTNLRKLTNVDCHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLNIERNM 719

RESULT 9
ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidial crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC -----
DR EMBL; AF056933; AAC62933.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
DR KQ Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 88.8%; Score 3341; DB 1; Length 719;
Best Local Similarity 89.2%; Pred. No. 3.4e-225;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVDK1STDSIKNETDIELQNHEDCLKMSYENVEPVFSASTI 60
Db 1 MKLNQDKHQTLSSNAKVDK1ATDSIKNETDIELKMNEDYLRMSHESIDPFVSASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTGVFPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119

QY 120 ARNKALTDLKGGLDALAVYHDSLESVWGNRNTRARSQVYALFELMFVQKLPSPAVS 179
Db 120 ARNKALTDLKGGLDALAVYHDSLESVWGNRNTRARSQVYALFELMFVQKLPSPAVS 179

QY 180 GBEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWY 239
Db 180 GBEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWY 239

QY 240 STGLNLRGTNAESWRYNQPRDMTLMVLDLVALFPSPYDTQMPIKTAQLTREVYTD 299
Db 240 STGLNLRGTNAESWRYNQPRDMTLMVLDLVALFPSPYDTQMPIKTAQLTREVYTD 299

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Db 240 NTGLNLRATNGQSVRYNQPRKDIELMVLDLVRVFPSTYDTPYPIKTTSQLTREVYTD 299

QY 300 IGTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDLEQVTIYISLLSRWNTQYNNM 359
Db 300 IGTVDNQALRSTTWTNNNAPSFAIEAAVVRNPHLLDLEQVTIYISLLSRWNTQYNNM 359

QY 360 WGGHKLFRITGGTLNI STQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPQVNGVP 419
Db 360 WGGHKLFRITGGTLNI STQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPQVNGVP 419

QY 420 RVDPHKFWTHPIASDNFYPGYAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDPHKFWTHPIASDNFYPGYAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539

QY 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDDY 599
Db 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDDY 599

QY 600 KTFRTVGFTTTPFSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Db 600 KTFRTVGFTTTPFSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659

QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLNIERNM 719
Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLNIERNM 719

RESULT 10
C1BB_BACTU STANDARD; PRT; 1229 AA.
ID C1BB_BACTU STANDARD; PRT; 1229 AA.
AC 045739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidial crystal protein cryIIB (Insecticidal delta-endotoxin
DE CryIIB(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIIB; Synonyms=cryET5, cryIIB(b);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L32020; AAA22344.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.

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Qy 542 GTFGDIRVNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNGEDLDYKT 601
Db 540 GTFGDIRLNVPLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNGEDLDYKT 599
Qy 602 FRTVGTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQSKVT 661
Db 600 FRTAGSTPFNPLAQSTFTLGAQSPN-QEVIYIDRVEFVPAEFTFEAYEDLERAQKAVN 658
Qy 662 ALFTSTNPRGLKTDVKYHIDQVSNLVESLDEFYLDKRELFELFVYKVELHIERNM 719
Db 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDKRELFELFVYKVELHIERNM 716

RESULT 12
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=HD-9;
RM Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; Endotoxin_C.
DR InterPro; IPR005639; Endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match
Best Local Similarity 62.5%; Pred. No. 1.8e-148;
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

Qy 23 TDSLKNETDIELQININ-----EDCLKMSEVENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRRKNEININAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINAGRI 61
Qy 71 LGTLGVFPAGQVASYSLFILGELWPKGNQWEILFMEHVEE-INQXISTYARKNALTDLK 129
Db 62 LGVLGVFPAGQLASFYSFLVGLWPRGRDQWEI-FLEHVEQLINQITENARNALTALRLQ 120
Qy 130 GLGDALAVYHDSLESVGNRRNRRARSVVRVSQYIALEMFVQKLPSPAVSGEVPLPIY 189
Db 121 GLGDSFRAYQOSLEWLENRDARTSRVLHTQYIALELDFLNAMPLFAIRNQEVPLLMVY 180
Qy 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCVKWYSTGLNNLRGT 249
Db 181 AQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSQVWYNTGLNSLRGT 240
Qy 250 NAESWRYNQPRRDMTLMVLVDLVALFPSTQMPYIKTAQLTREVTDAIGTVHPHPSF 309
Db 241 NAASWRYNQPRRDLTLGLVDLVALFPSYDTRTPINISQALTRREVTDAIGAT--GVNM 298
Qy 310 TSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMGHKLFRFT 369
Db 299 ASMNWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSSRRWSNTRNTMYWRGHTIQSRP 358

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Qy 370 IGGTLNISTOGSTNTSINPVTLPFTSRDYVVTESLAGNLFF--LTQPVNGVPRVDRHWKF 427
Db 359 IGGGLNTSTHGATNTSINPVTLPFTSRDYVVTESLAGNLFF--LTQPVNGVPRVDRHWKF 416
Qy 428 VTHP-----IASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482
Db 417 -TNPQNSIDRGSTANYSQP-YESPLQKQDSETELPPETTERPNYESYSHRLSHIGIILQS 474
Qy 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAPNLSSGAADVVRGPGFTGGDILRRNTG 542
Db 475 RVNVPVYSWTHRSADRTNTEPNSITQIPLVKAPNLSSGAADVVRGPGFTGGDILRRNTG 534
Qy 543 TFGDIRVNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNGEDLDYKT 602
Db 535 GFGPIRVTVNGPLTQRYRIGFRYASTVDFVFSRGGTNNFRFLRTMNSGDLEKYGNF 594
Qy 603 RTVGTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQSKVT 662
Db 595 VRRATFTPTFTQIDIRTSIQGLSGNGEVYIDKIEIPVTATFEAYEDLERAQEAUNA 654
Qy 663 LFTSTNPRGLKTDVKYHIDQVSNLVESLDEFYLDKRELFELFVYKVELHIERNM 719
Db 655 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDKRELFELFVYKVELHIERNM 711

RESULT 13
C1BA BACTK
ID C1BA BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1998 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
DE CryIIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIIa; Synonyms=cryA4, cryII(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RC SEQUENCE FROM N.A.
RA SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RC SEQUENCE FROM N.A.
RA SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X06711; CAA29898.1; -
DR EMBL; X95704; CAA65003.1; -
DR PIR; S00873; S00873.
DR HSSP; P07130; 1DLC.

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DR	InterPro; IPR001178; Endotoxin.	OS	Bacillus thuringiensis.
DR	InterPro; IPR005638; endotoxin_C.	OC	Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
DR	InterPro; IPR005639; endotoxin_N.	OX	NCBI_TaxID=1428;
DR	InterPro; IPR008979; Gal_bind_Like.	RN	[1]
DR	Pfam; PF03944; Endotoxin_C; 1.	RP	SEQUENCE FROM N.A.
DR	Pfam; PF00555; Endotoxin_M; 1.	RA	Zhang J., Song F., Huang D.;
DR	Pfam; PF03945; Endotoxin_N; 1.	RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
KW	Sporulation; Toxin.	DR	EMBL; AF368257; AAK63251.1; -.
FT	VARIANT 150 Y -> H (in strain HD-110).	DR	HSSP; P07130; 1DLC.
SQ	SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;	DR	GO; GO:0005102; F:receptor binding; IEA.
		DR	GO; GO:0006952; P:defense response; IEA.
		DR	GO; GO:0009405; P:pathogenesis; IEA.
		DR	InterPro; IPR001178; Endotoxin.
		DR	InterPro; IPR005638; endotoxin_C.
		DR	InterPro; IPR005639; endotoxin_N.
		DR	InterPro; IPR008979; Gal_bind_Like.
		DR	Pfam; PF03944; Endotoxin_C; 1.
		DR	Pfam; PF00555; Endotoxin_M; 1.
		DR	Pfam; PF03945; Endotoxin_N; 1.
		SQ	SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;
			Query Match 59.6%; Score 2240.5; DB 2; Length 1228;
			Best Local Similarity 62.3%; Pred. No. 8.9e-148;
			Matches 447; Conservative 78; Mismatches 165; Indels 27; Gaps 8;
QY	23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70	QY	23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
Db	2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61	Db	2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
QY	71 LGTLGVPPAGQVASYLFIIGELMPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129	QY	71 LGTLGVPPAGQVASYLFIIGELMPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
Db	62 LGVLGVPPAGQLASFYSLVGLMWRGRDQWEI-FLEHVEQLINQOITENARNTALARLQ 120	Db	62 LGVLGVPPAGQLASFYSLVGLMWRGRDQWEI-FLEHVEQLINQOITENARNTALARLQ 120
QY	130 GLGDALAVYHDSLESWVGNNRNRARSVRSQYIALELMFVQKLPSFAVSGEEVPLPIY 189	QY	130 GLGDALAVYHDSLESWVGNNRNRARSVRSQYIALELMFVQKLPSFAVSGEEVPLPIY 189
Db	121 GLGDSFRAYQOSLEDWLENRDDARTRSVLTQYIALELDFLNAMPLFAIRNQEVPLLMVY 180	Db	121 GLGDSFRAYQOSLEDWLENRDDARTRSVLTQYIALELDFLNAMPLFAIRNQEVPLLMVY 180
QY	190 AQANLHLLLRDASIFGKEWGLSSSISTFYNQVERAGDYSCHVKWYSTGLNNLRGT 249	QY	190 AQANLHLLLRDASIFGKEWGLSSSISTFYNQVERAGDYSCHVKWYSTGLNNLRGT 249
Db	181 AQANLHLLLRDASLFGSEFGLTSQIORYYERQVTRDYSDYCVIEWNTGLNSLRGT 240	Db	181 AQANLHLLLRDASLFGSEFGLTSQIORYYERQVTRDYSDYCVIEWNTGLNSLRGT 240
QY	250 NAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTRVYTTDAIGTVHPHPSF 309	QY	250 NAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTRVYTTDAIGTVHPHPSF 309
Db	241 NAASWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTRVYTTDAIGAT--GVNM 298	Db	241 NAASWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTRVYTTDAIGAT--GVNM 298
QY	310 TSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFPRT 369	QY	310 TSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFPRT 369
Db	299 ASMNWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFPRT 358	Db	299 ASMNWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFPRT 358
QY	483 HVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542	QY	483 HVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
Db	475 RVNVVPVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 534	Db	475 RVNVVPVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 534
QY	543 TFGDIRVNIWPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELKYTF 602	QY	543 TFGDIRVNIWPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELKYTF 602
Db	535 GFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNF 594	Db	535 GFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNF 594
QY	603 RTVGTTTPSFLDVQSTFTIGAWNFSSGNEVVDRIEFVPEVTVYEAEDFEKAQEKVTA 662	QY	603 RTVGTTTPSFLDVQSTFTIGAWNFSSGNEVVDRIEFVPEVTVYEAEDFEKAQEKVTA 662
Db	595 VRRFTTPTFTQIIDIIRTSIQGLSGNGEYIDKIEIIPVATFEAEYDLERAQEAUNA 654	Db	595 VRRFTTPTFTQIIDIIRTSIQGLSGNGEYIDKIEIIPVATFEAEYDLERAQEAUNA 654
QY	663 LFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719	QY	663 LFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db	655 LFTNTNPRRLKTDVTDYHDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711	Db	655 LFTNTNPRRLKTDVTDYHDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 14
Q93NM5
ID Q93NM5 PRELIMINARY; PRT; 1228 AA.
AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry1Ba.
GN Name=cry1Ba;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds
(without alignments)
4171.616 Million cell updates/sec

Title: US-10-019-823B-58
Perfect score: 3761
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELPEIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3724	99.0	719	2 I39814	insecticidal prote
2	3724	99.0	719	2 I39815	insecticidal prote
3	3715	98.8	719	2 S25383	parasporal crystal
4	3484	92.6	719	2 I40590	cryv465 protein -
5	2248.5	59.8	1228	2 S00873	parasporal crystal
6	1872	49.8	380	2 B42459	hypothetical prote
7	1466	39.0	1157	1 S49247	parasporal crystal
8	1458.5	38.8	1166	2 S32645	parasporal crystal
9	1450	38.6	1155	2 A26513	parasporal crystal
10	1449	38.5	1174	2 S32649	parasporal crystal
11	1443	38.4	1155	2 JD0002	parasporal crystal
12	1443	38.4	1156	2 A29125	parasporal crystal
13	1434	38.1	1155	2 I39838	parasporal crystal
14	1430.5	38.0	934	2 A22798	parasporal crystal
15	1429.5	38.0	1176	2 JT0241	parasporal crystal
16	1426	37.9	1155	2 S02134	parasporal crystal
17	1425.5	37.9	1181	2 A41052	parasporal crystal
18	1423.5	37.8	1176	2 JC2219	parasporal crystal
19	1419.5	37.7	1176	2 A22617	parasporal crystal
20	1419.5	37.7	1176	2 S02215	parasporal crystal
21	1338	35.6	1174	2 A42459	parasporal crystal
22	1324	35.2	1138	2 A48944	parasporal crystal
23	1315.5	35.0	1156	2 A29838	parasporal crystal
24	1304.5	34.7	823	2 S04181	parasporal crystal
25	1295.5	34.4	1189	2 S00944	parasporal crystal
26	1281	34.1	1154	2 S39536	parasporal crystal
27	1248	33.2	1171	2 I40572	parasporal crystal
28	1248	33.2	1171	2 A37829	parasporal crystal
29	1235	32.8	1176	2 A48970	parasporal crystal

30 1208 32.1 1160 2 S32647 parasporal crystal
31 1193.5 31.7 1165 2 S11446 parasporal crystal
32 1188.5 31.6 655 2 JC7140 protoxin - Bacillu
33 1172 31.2 1172 2 S32689 parasporal crystal
34 1154 30.7 1160 2 I40589 parasporal crystal
35 1139.5 30.3 1178 1 USBSXH parasporal crystal
36 1139 30.3 1177 2 A49785 parasporal crystal
37 1137 30.2 652 2 A27323 parasporal crystal
38 1113 29.6 659 2 S10228 parasporal crystal
39 1080.5 28.7 652 2 I39811 parasporal crystal
40 966 25.7 649 1 JH0261 parasporal crystal
41 917 24.4 618 2 S11445 parasporal crystal
42 881 23.4 1156 2 S19306 parasporal crystal
43 800 21.3 1136 1 USBS8I parasporal crystal
44 693.5 18.4 934 2 B29838 parasporal crystal
45 645 17.1 1180 2 I39870 parasporal crystal

insecticidal protein cryvI - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: I39814
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I39814
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: GB:L36338; NID:G540281; PIDN:AAC3699.1; PID:G540282
C;Genetics:
A;Gene: cryvI
C;Superfamily: parasporal crystal protein

ALIGNMENTS

RESULT 1

Query Match 99.0%; Score 3724; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 2.4e-254;
Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

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Qy 61 QTGIGTAGKILGTGVPFAGQVASLYSFTLGEIWPCKGNQWEILFMEHVEE-INQIKISTY 119
Db 61 QTGIGTAGKILGTGVPFAGQVASLYSFTLGEIWPCKGNQWEI-FMEHVEEINQIKISTY 119

Qy 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTFRSRRSVRSQYIALELMFVQKLPSPAVS 179
Db 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTFRSRRSVRSQYIALELMFVQKLPSPAVS 179

Qy 180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMY 239
Db 180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMY 239

Qy 240 STGLNLRGNTAESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTD 299
Db 240 STGLNLRGNTAESWRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTD 299

Qy 300 IGTVPHPSPSTTTWYNNAPSFSAIEAAVVRPHLLDFLEQVTIYSLSRWNTQYMM 359
Db 300 IGTVPHPSPSTTTWYNNAPSFSAIEAAVVRPHLLDFLEQVTIYSLSRWNTQYMM 359

Qy 360 WGGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFITQPVNGVP 419
Db 360 WGGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFITQPVNGVP 419

Tue Feb 15 10:07:55 2005

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DB 420 RVDPHWKFTVHTPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
DB 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
QY 600 KTFRTVGFTHPPFSLDVOSTFTTGAMNFSNGNEVYIDRIEFVFPVEVYEAEDYDEKAQEK 659
DB 600 KTFRTVGFTHPPFSLDVOSTFTTGAMNFSNGNEVYIDRIEFVFPVEVYEAEDYDEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2
I39815
insecticidal protein cryV - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39815
R:Gleave, A.P.; Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1993
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for
iensis subsp. kurstaki.
A:Reference number: I39815; MUID:93298009; PMID:8517758
A:Accession: I39815
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA23354.1; PID:g142768
C:Genetics:
A:Gene: cryV
C:Superfamily: parasporal crystal protein

Query Match 99.0%; Score 3724; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 2.4e-254;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKGGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPFAVS 179
DB 120 ARNKALTDLKGGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
QY 240 STGLNNLRGTNAESWVRYNQFRDMLMWLDLVALPSPDYDTQMPYIKTTAQLTREVTDA 299
DB 240 STGLNNLRGTNAESWVRYNQFRDMLMWLDLVALPSPDYDTQMPYIKTTAQLTREVTDA 299
QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
DB 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVNGVP 419
DB 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVNGVP 419
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QY 420 RVDPHWKFTVHTPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RVDPHWKFTVHTPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
DB 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
QY 600 KTFRTVGFTHPPFSLDVOSTFTTGAMNFSNGNEVYIDRIEFVFPVEVYEAEDYDEKAQEK 659
DB 600 KTFRTVGFTHPPFSLDVOSTFTTGAMNFSNGNEVYIDRIEFVFPVEVYEAEDYDEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3
S25383
parasporal crystal protein cryIIa1 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV
C:Species: Bacillus thuringiensis
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S25383
R:Taylor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A:Reference number: S25383; MUID:92269582; PMID:1588820
A:Accession: S25383
A:Molecule type: DNA
A:Residues: 1-719 <TAI>
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290
C:Genetics:
A:Gene: cryV
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 98.8%; Score 3715; DB 2; Length 719;
Best Local Similarity 99.2%; Pred. No. 1.1e-253;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKGGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPFAVS 179
DB 120 ARNKALTDLKGGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
QY 240 STGLNNLRGTNAESWVRYNQFRDMLMWLDLVALPSPDYDTQMPYIKTTAQLTREVTDA 299
DB 240 STGLNNLRGTNAESWVRYNQFRDMLMWLDLVALPSPDYDTQMPYIKTTAQLTREVTDA 299
QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
DB 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVNGVP 419
DB 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVNGVP 419
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Qy 420 RYDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 479
Db 420 RYDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNNPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATWNRGEDLDY 599
Db 540 NTGTFGDIRVNNPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATWNRGEDLDY 599
Qy 600 KTRFTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEAYDFEKAQEK 659
Db 600 KTRFTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEAYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
RESULT 4
140590
cryV465 protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140590
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: 140590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g467234
C;Genetics:
A;Gene: cryV465
C;Superfamily: parasporal crystal protein

Query Match 92.6%; Score 3484; DB 2; Length 719;
Best Local Similarity 92.2%; Pred. No. 2e-237;
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVFVSASTI 60
Db 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKMNEDYLRMSEHESIDPVFVSASTI 60
Qy 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKILTY 119
Qy 120 ARNKALTDKGLGDALAVYHDSLESWVGNNRNTRRSVRSQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALSDRLGDLALAVYHDSLESWVENNTRRSVVKNQYIALELMFVQKLPSFAVS 179
Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSASEISTFYNRQVERTRDYSCHCIKWY 239
Qy 240 STGLNLRGTNAESWRYNQPRRDMTLMVLDLVALFPSYDTQMPYIKTAAQLTREVTDA 299
Db 240 NTGLNLRGTNAESWRYNQPRKDMTLMVLDLVALFPSYDTLVYPYIKTTSQLTREVTDA 299
Qy 300 ICTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
Db 300 ICTVHPNQAFSTWNNNAPSFAIEAAVIRSPLHLLDFLEKVTIYSLLSRWNTQYNNM 359
Qy 360 WGGHKLFRITCGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVP 419
Db 360 WGGHRLSRIPGGALNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVP 419

Qy 420 RYDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 479
Db 420 RYDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNNPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATWNRGEDLDY 599
Db 540 NTGTFGDIRVNNPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATWNRGEDLDY 599
Qy 600 KTRFTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEAYDFEKAQEK 659
Db 600 KTRFTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEAYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
RESULT 5
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g580941
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 59.8%; Score 2248.5; DB 2; Length 1228;
Best Local Similarity 62.5%; Pred. No. 5.7e-150;
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;
Qy 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
Db 62 LGVLGVFPAGQVASYLSFILGELWPRGRDQWEI-FLEHVEQLINQITENARNALTALRLQ 120
Qy 130 GLGDALAVYHDSLESWVGNNRNTRRSVRSQYIALELMFVQKLPSFAVSGEEVPLPIY 189
Db 121 GLGDSFRAYQOQSLDLEWLNKRDADRSLVLYQYIALELDFLNAMPLFAIRNQEVPLLMVY 180
Qy 190 AQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWYSTGLNNLRGT 249
Db 181 AQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSYCVWEYNTGLNSLRGT 240
Qy 250 NABSWRYNQPRRDMTLMVLDLVALFPSYDTQMPYIKTAAQLTREVTDAIGTVHPHPSF 309
Db 241 NAASWRYNQPRRDLTLGLVDLVALFPSYDTRTYPINTSAQLTREVTDAIGAT--GVNM 298
Qy 310 TSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMGGHKLERT 369
Db 299 ASMNWNNNAPSFAIEAAVIRSPLHLLDFLEQLTIFSSASRWNTNRHNTYWRGHTIQSRP 358
Qy 370 IGGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPRVDEHMKF 427
Db 359 IGGGLNSTHGATNTSINPVTLPFTSRDVRVRESYAGVLLWGIYLEPIHGVTVRNF-- 416

parasporal crystal protein crylPa3 - *Bacillus thuringiensis*
C:/Species: *Bacillus thuringiensis*
C:/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:/Accession: S32649
R:/Lambert, B.
submitted to the EMBL Data Library, April 1993
A:/Reference number: S32645
A:/Accession: S32649
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-1174 <LAM>
A:/Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PID:g295865
C:/Superfamily: parasporal crystal protein
C:/Keywords: delta-endotoxin

JD0002

N;Alternative names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal protein
C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A>Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from
A;Reference number: A90025
A;Accession: A90025
A:Molecule type: mRNA
A;Residues: 1-1155 <KON>
A;Cross-references: UNIPROT:P06578
A;Experimental source: subsp. kurstaki
R;Geiser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A>Title: The hypervariable region in the genes coding for entomopathogenic crystal proteins
A;Reference number: A91560; MUID:87163505; PMID:3557124
A;Accession: A91560
A:Molecule type: DNA
A;Residues: 1-1155 <GEI>
A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A;Experimental source: subsp. kurstaki
R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA 15, 305-314, 1986
A>Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product analysis
A;Reference number: A90955; MUID:86300092; PMID:3743328
A;Accession: A90955
A:Molecule type: DNA
A;Residues: 1-1155 <WAB>
A;Cross-references: GB:M13898; NID:g142719; PIDN:AA22330.1; PID:g142720
A;Experimental source: subsp. berliner
R;Chak, K.F.; Jen, J.C.
submitted to the EMBL Data Library, October 1990
A>Description: Complete nucleotide sequence and expression in Escherichia coli of a cry
A;Reference number: S14555
A;Accession: S14555
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-1155 <CHA>
A;Cross-references: ENBL:X54939; NID:g40272; PIDN:CXA38701.1; PID:g40273
R;Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerckhofe,
Eur. J. Biochem. 161, 273-280, 1986
A>Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thurin
A;Reference number: A26461; MUID:87054026; PMID:3023091
A;Accession: A26461
A:Molecule type: DNA
A;Residues: 1-730,'L',732-784,'R',786-1155 <HOF>
A;Cross-references: GB:X04598; NID:g40254; PIDN:CXA28405.1; PID:g40255
A;Experimental source: strain berliner 1715
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C;Genetics:
A;Gene: cry-1-2; bt2
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
F:82-586/Product: toxic peptide #status predicted <TXP>
F:82-300/Region: toxic #status predicted
F:300-586/Region: insecticidal #status predicted

	Query Match	Score 1443;	IDB 2;	Length 1155;
	Best Local Similarity	44.2%;	Pred. No.	3.1e-93;
	Matches 314;	Conservative 109;	Mismatches 231;	Indels 56; Gaps 13;
QY	36	NNHHEDCLKMSEVNVZ-PFFVSASTIQTG-----IGIAHKILGTGLGVPPAGQVASLYS	87	
Dd	4	NNINECIPYNCLSNPEVEVLGGERITGYTPIDISLSLTQFLLEFP-VPGAGFVLGLVD	62	
QY	88	FILGELMPKGKNQWEILLMEHVEEINKISTYARNKALTDLKGLDALAVYHDSLVWG	147	
Dd	63	IIWGF---GPSQWDATFLVQLNQRIEIEFNARQAISRLEGLSNLYQIVAESFRWEA	119	
Ov	148	NRNNTRARSVVRSOYTAEMLMFVKPLSPSFAYSGSEEVPLLPIYAQAAHLHLLLRDAIFG	207	

Db 120 DPTNPALREEMRIQFNDMNSALTATPLFAVQNTQVPLLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDRTLM 267
Db 180 QRWGFDAAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDRWIRYNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTTAQLTREVYTDAGTVHPPHPSFTSTTWYNNNAPS- S 323
Db 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYNPV- - - - -LENFDCSFRGSAQ 285
Qy 324 AIEAAVVRNPHLLDFEQVTIYSLSR- - - - -WSNTQYMM- - - - -WGGHKLFRITGTLNI 376
Db 286 GIEGS-IRSPHLMILNSITITDAHRGEYWSGHQIMASPVGSGPEFTFPLYGTWNA 344
Qy 377 STQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPRVDFHMKFVTHPIASDN 436
Db 345 APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN- - - - -NQQLSVLDGTEFAYG- - - - -TSSN 395
Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHGLI- - - - -SASHVKALVY 489
Db 396 LPSAVYRKSGT- - - - -VDSLDEIPQNNVPPRQGFHSHLSHVSMPRSGFSNVSIIRAPMF 453
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTCTFGDIRV 549
Db 454 SWHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSPQISTLRV 513
Qy 550 NINPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTRTGVGTT 609
Db 514 NITAPLSQRVYRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGTT 573
Qy 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVTALFTSTNP 669
Db 574 PNFNSGSSVFTLSAHVFNSEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633
Qy 670 RGLKTDVKYHIDQVSNLVESLSEDEFYLDKRELFEIVKYANLHIERNM 719
Db 634 IGLKTDVTDYHIDQVSNLVESLSEDEFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 12
A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.4%; Score 1443; DB 2; Length 1156;
Best Local Similarity 44.2%; Pred. No. 3.1e-93;
Matches 314; Conservative 109; Mismatches 231; Indels 56; Gaps 13;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG- - - - -IGIAGKILGTGVFPAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKGLDALAVYHDSLESVWG 147
Db 63 IIWGI- - -GPSQWDAFLVQIEQLINRIEFAFNQAIISRLGSLNLYQIYAESFREWEA 119
Qy 148 NRNNTARSVRSQYIALELMFVQKLPSPFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTATPLFAVQNTQVPLLSVYVQAANLHLSVLDRDVSFG 179

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDRTLM 267
Db 180 QRWGFDAAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDRWIRYNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTTAQLTREVYTDAGTVHPPHPSFTSTTWYNNNAPS- S 323
Db 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYNPV- - - - -LENFDCSFRGSAQ 285
Qy 324 AIEAAVVRNPHLLDFEQVTIYSLSR- - - - -WSNTQYMM- - - - -WGGHKLFRITGTLNI 376
Db 286 GIEGS-IRSPHLMILNSITITDAHRGEYWSGHQIMASPVGSGPEFTFPLYGTWNA 344
Qy 377 STQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPRVDFHMKFVTHPIASDN 436
Db 345 APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN- - - - -NQQLSVLDGTEFAYG- - - - -TSSN 395
Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHGLI- - - - -SASHVKALVY 489
Db 396 LPSAVYRKSGT- - - - -VDSLDEIPQNNVPPRQGFHSHLSHVSMPRSGFSNVSIIRAPMF 453
Qy 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTCTFGDIRV 549
Db 454 SWHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSPQISTLRV 513
Qy 550 NINPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTRTGVGTT 609
Db 514 NITAPLSQRVYRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGTT 573
Qy 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVTALFTSTNP 669
Db 574 PNFNSGSSVFTLSAHVFNSEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633
Qy 670 RGLKTDVKYHIDQVSNLVESLSEDEFYLDKRELFEIVKYANLHIERNM 719
Db 634 IGLKTDVTDYHIDQVSNLVESLSEDEFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 13
I39838
parasporal crystal protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39838
R:Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
J. Biotechnol. 6, 307-322, 1987
A:Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki
A:Reference number: I39838
A:Accession: I39838
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1155 <RES>
A:Cross-references: UNIPROT:P06578; GB:M37263; NID:gi42885; PIDN:AAA22420.1; PID:gl42886
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.1%; Score 1434; DB 2; Length 1155;
Best Local Similarity 44.1%; Pred. No. 1.3e-92;
Matches 313; Conservative 109; Mismatches 232; Indels 56; Gaps 13;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG- - - - -IGIAGKILGTGVFPAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKGLDALAVYHDSLESVWG 147
Db 63 IIWGI- - -GPSQWDAFLVQIEQLINRIEFAFNQAIISRLGSLNLYQIYAESFREWEA 119
Qy 148 NRNNTARSVRSQYIALELMFVQKLPSPFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTATPLFAVQNTQVPLLSVYVQAANLHLSVLDRDVSFG 179
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDRTLM 267

Db 180 QRWGDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDRWIRYNQFRRELTLT 239
QY 268 VLDLVALFSDYDQMPYIKTKTAQLTREYVTDAGTVHPHPSFTSTTWYNNAPSPF---S 323
Db 240 VLDIVLSPFNYSRTYPIRTVSQTLREIYNTPV-----LENFDGSRGSAQ 285
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR---WSNTQYMM---WGCHKLEFRFTGGTLNI 376
Db 286 GIEGS-IRSPHLMIDLNSITITDAHGEYVWSGHQIMASVFGSPFPTFLYGTMGNA 344
QY 377 STQSGTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHMKFVTHPIASDN 436
Db 345 APOQRIVAGLGGVYRTLSSTLYRRPNIGIN---NQQLSVLDGTEFAYG-----TSSN 395
QY 437 FYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIRAPMF 453
QY 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGDIRV 549
Db 454 SWIHRSAFNENIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTPSGQISTLRV 513
QY 550 NINPPFAQRYRIRYASTTDLPHTSINGKAINQGNFSATMNRGSDLDYKTRFTVGF 609
Db 514 NITAPLSQRYRIRYASTTNLQFHTSIHGRFINQGNFSATMSSSGLNSLQSGSRHLGFTT 573
QY 610 PFSFLDVQSTFTIGAWNSSGNEVYIDRIEFVPEVVEYAEYDPEAKQKVTAFTSTNP 669
Db 574 PFNFSNGSSVFTLSAHVFNSEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633
QY 670 RGLKTDVKDHYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719
Db 634 IGLKTDVTDHYHIDQVSNLVESLSEDFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 14
A22798
parasporal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Accession: A22798
R;Shibano, Y.; Yanagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A;Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuringiensis parasporal crystal protein
A;Reference number: A22798
A;Accession: A22798
A;Molecule type: DNA
A;Residues: 1-934 <SHI>
A;Cross-references: UNIPROT:Q9SSV8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:G551713
C;Comment: The authors translated the codon ACA for residue 264 as Ser.
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1430.5; DB 2; Length 934;
Best Local Similarity 43.3%; Pred. No. 1.7e-92;
Matches 308; Conservative 116; Mismatches 227; Indels 61; Gaps 12;
QY 36 NINHEDCLKMSEVENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPAGQVSLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKGDLGALAVYHDSLESVWG 147
Db 63 IIWGI---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFWEA 119
QY 148 NNNTRARSVRSQYIAELMFVQKLPFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDMLTM 267
Db 180 QRWGDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDRWIRYNQFRRELTLT 239

QY 268 VLDLVALFSPVDQMPYIKTKTAQLTREYVTDAGTVHPHPSFTSTTWYNNAPSPFSAIEA 327
Db 240 VLDIVLSPFNYSRTYPIRTVSQTLREIYNTPV-----LENFDGSRGMAQ 285
QY 328 AV---VRNPHLLDFLEQVTIYSLLSRWSNTQYMMNMGHKLFEFTIGT---LNISTOGS 381
Db 286 RIEQNIHQPHLMDILNRITITDVRHG-----FNYWSGHQITASPVGSGPFAFPLPGN 340
QY 382 TWTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHMKFVTHPI 432
Db 341 AGNAAPPVLSLTGLGIFRFTLSPLRYRIILGSGPN---NQELFVLDGTEFSASLTNL 397
QY 433 ASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGTGTV-----DSLVDVIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGDI 547
Db 451 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTPSGQISTL 510
QY 548 RVNINPPFAQRYRIRYASTTDLPHTSINGKAINQGNFSATMNRGSDLDYKTRFTVGF 607
Db 511 RVNITAPLSQRYRIRYASTTNLQFHTSIHGRFINQGNFSATMSSSGLNSLQSGSRFTVGF 570
QY 608 TTPFSFLDVQSTFTIGAWNSSGNEVYIDRIEFVPEVVEYAEYDPEAKQKVTAFTST 667
Db 571 TTPFNFSNGSSVFTLSAHVFNSEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSS 630
QY 668 NFRGLKTDVKDHYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719
Db 631 NQIGLKTDVTDHYHIDQVSNLVESLSEDFCLDEKSELSEKVKHAKRLSDERNL 682

RESULT 15
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N;Alternate names: 135K insecticidal protein
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JT0241
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
Agric. Biol. Chem. 52, 1565-1573, 1988
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A;Reference number: JT0241
A;Accession: JT0241
A;Molecule type: DNA
A;Residues: 1-1176 <SHI>
A;Cross-references: UNIPROT:P02965
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1429.5; DB 2; Length 1176;
Best Local Similarity 43.3%; Pred. No. 2.8e-92;
Matches 308; Conservative 115; Mismatches 228; Indels 61; Gaps 12;
QY 36 NINHEDCLKMSEVENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPAGQVSLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKGDLGALAVYHDSLESVWG 147
Db 63 IIWGI---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFWEA 119
QY 148 NNNTRARSVRSQYIAELMFVQKLPFAVSGEEVPLPIYQAANLHLLLRDASIFG 207
Db 120 DPTPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDMLTM 267
Db 180 QRWGDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMGPDSDRWIRYNQFRRELTLT 239

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds
(without alignments)
3909.384 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761

Sequence: 1 MKLKNDKHQSFSSNAKVDK.....KRELFEIVKYANLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3724	99.0	719	16	US-10-782-020-10
2	3724	99.0	719	16	US-10-782-141-8
3	3442.5	91.5	710	15	US-10-428-961-42
4	2250.5	59.8	1228	16	US-10-809-953-10
5	2236.5	59.5	1207	10	US-09-988-462-7
6	2157.5	57.4	1227	15	US-10-428-961-63
7	2142.5	57.0	1186	9	US-09-826-660-23
8	2087	55.5	1228	15	US-10-428-961-38
9	2087	55.5	1228	15	US-10-614-524-2
10	1909.5	50.8	643	9	US-09-826-660-25
11	1694.5	45.1	1167	14	US-10-089-678-1
12	1658.5	44.1	653	15	US-10-428-961-6
13	1643.5	43.7	1157	16	US-10-782-141-16

14	1485	39.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1485	39.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1485	39.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1469	39.1	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1469	39.1	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1469	39.1	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1459.5	38.8	1156	14	US-10-099-285-72	Sequence 72, Appl
21	1459.5	38.8	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1443	38.4	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1443	38.4	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1443	38.4	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1443	38.4	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1443	38.4	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1443	38.4	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1443	38.4	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1443	38.4	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1443	38.4	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1443	38.4	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1443	38.4	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1443	38.4	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1443	38.4	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1438	38.2	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1436	38.2	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1435	38.2	1177	14	US-10-102-469-24	Sequence 24, Appl
38	1419.5	37.7	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1407.5	37.4	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1407.5	37.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1376	36.6	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1355	36.0	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1355	36.0	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1355	36.0	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1355	36.0	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 99.0%; Score 3724; DB 16; Length 719;
Best Local Similarity 99.3%; Pred. No. 1.9e-306;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

Qy	1	MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVFVSASTI	60
Db	1	MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVFVSASTI	60
Qy	61	QTGIGIAGKILGTGLGVPPAGQVASYLSFTLGMWPKGNQWEILFMEHVEE-INQKISTY	119
Db	61	QTGIGIAGKILGTGLGVPPAGQVASYLSFTLGMWPKGNQWEILFMEHVEE-INQKISTY	119

QY	120	ARNKALTDLKGGLDALAVYHDSLESWVGNRNTRARSVRSQYIALELMFVQKLPSPAVS	179
Db	120	ARNKALTDLKGGLDALAVYHDSLESWVGNRNTRARSVRSQYIALELMFVQKLPSPAVS	179
QY	180	GEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKMY	239
Db	180	GEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKMY	239
QY	240	STGLNLRGTNAESWVRVYNOFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVYTDA	299
Db	240	STGLNLRGTNAESWVRVYNOFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVYTDA	299
QY	300	IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN	359
Db	300	IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN	359
QY	360	WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP	419
Db	360	WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP	419
QY	420	RVDPHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI	479
Db	420	RVDPHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI	479
QY	480	SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
Db	480	SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
QY	540	NTGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY	599
Db	540	NTGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY	599
QY	600	KTFRTVGTTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK	659
Db	600	KTFRTVGTTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSEDFYLDKEKRELFEIVKYAKQLHIERNM	719
Db	660	VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSEDFYLDKEKRELFEIVKYAKQLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Kozziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.0%; Score 3724; DB 16; Length 719;			
Best Local Similarity 99.3%; Pred. No. 1.9e-306;			
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLMKSEYENVEPFFVSASTI	60

NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match
Best Local Similarity 91.5%; Score 3442.5; DB 15; Length 710;
Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;

Qy 1 MKLKNQKHQSFSNAKVDKISTDLKNETDIELQNIHEDCLKMWSEYENVEPVFVSASTI 60
Db 1 MFSKNQKHQSFSNAKVDKISTDLKNETDIELQNIHEDCLKMWSEYENVEPVFVSASTI 51

Qy 61 QTGIGIAGKILGTLGVPFAGQVASYLFIILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 52 QTGIGIAGKILGTLGVPFAGQVASYLFIILGELWPKGNQWEILFMEHVEE-INQKISTY 110

Qy 120 ARNKALTDKLGDLALAVHDSLESWVGNNRNTARSVVRQYIALELMFVQKLPSPAVS 179
Db 111 ARNKALTDKLGDLALAVHDSLESWVGNNRNTARSVVRQYIALELMFVQKLPSPAVS 170

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDSDHCVKMY 239
Db 171 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDSDHCVKMY 230

Qy 240 STGLNLRGNTAESWVRYNQFRDMTLMVLDLVALFPSYDTQYPIKTAQLTREVYTD 299
Db 231 STGLNLRGNTAESWVRYNQFRDMTLMVLDLVALFPSYDTQYPIKTAQLTREVYTD 290

Qy 300 IGTVHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNM 359
Db 291 IGTVHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNM 350

Qy 360 WGGHKLFEFRTIGTGLNISTQSTNTSINPVTLPTSTRDYRTESLAGNLFQPVNGVP 419
Db 351 WGGHKLFEFRTIGTGLNISTQSTNTSINPVTLPTSTRDYRTESLAGNLFQPVNGVP 410

Qy 420 RVDEHKKFVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLI 479
Db 411 RVDEHKKFVTHPIASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLI 470

Qy 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRR 539
Db 471 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRR 530

Qy 540 NTGTFGDIRVNINPPFAQRVRIYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 531 NTGTFGDIRVNINPPFAQRVRIYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 590

Qy 600 KTFRTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659
Db 591 KTFRTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 650

Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 651 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Van Mellaert, Herman
APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match
Best Local Similarity 59.8%; Score 2250.5; DB 16; Length 1228;
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

Qy 23 TDSLKNETDIELQNIHEDCLKMWSEYENVEPVFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVVSASTVQTGINIAGRI 61

Qy 71 LGTLGVPFAGQVASYLFIILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
Db 62 LGTLGVPFAGQVASYLFIILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 120

Qy 130 GLGDALAVHDSLESWVGNNRNTARSVVRQYIALELMFVQKLPSPAVSGEEVPLPIY 189
Db 121 GLGDALAVHDSLESWVGNNRNTARSVVRQYIALELMFVQKLPSPAVSGEEVPLPIY 180

Qy 190 AQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDSDHCVKMYSTGLNLRGT 249
Db 181 AQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDSDHCVKMYSTGLNLRGT 240

Qy 250 NAESWVRYNQFRDMTLMVLDLVALFPSYDTQYPIKTAQLTREVYTDAGTGVHPHPSF 309
Db 241 NAESWVRYNQFRDMTLMVLDLVALFPSYDTQYPIKTAQLTREVYTDAGTGVHPHPSF 309

Qy 310 TSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMVGCHKEPRT 369
Db 299 ASMNWNNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMVGCHKEPRT 358

Qy 370 IGGTGLNISTQSTNTSINPVTLPTSTRDYRTESLAGNLF--LTPQVNGVPRVDFHWKF 427
Db 359 IGGTGLNISTQSTNTSINPVTLPTSTRDYRTESLAGNLF--LTPQVNGVPRVDFHWKF 416

Qy 428 VTHP-----IASDNFYPGYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLI 482
Db 417 -TNPNISDRGTANYQSP-YESPGLQKDSSETLPPETTERPNYESYSHRLSHIGLI 474

Qy 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
Db 475 RVNVPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 534

Qy 543 TFGDIRVNINPPFAQRVRIYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTF 602
Db 535 TFGDIRVNINPPFAQRVRIYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTF 594

Qy 603 RTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKVTA 662
Db 595 VRAFTTPFTFTQIIRTSIQGLSGNEVYIDRIEFVPEVTEAEYDPEKAQEKVTA 654

Qy 663 LFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 655 LFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 59.5%; Score 2236.5; DB 10; Length 1207;
Best Local Similarity 64.1%; Pred. No. 5.8e-180;
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;

Qy 40 EDCLKMSYENVEPVASVSTQIGTIGIAGKILGTLPVAGQVAVSLYFSLGELWPKGN 99
Db 10 EDSLCTAEGNNIDPFVASTVGTGINIAGRIILGVLPVAGQVAVSLYFSLGELWPKGRD 69
Qy 100 QWEILFMEHVEE-INQKISTYARNKALTDKGLGDALAVYHDSLESWSVGNRNTRARSVV 158
Db 70 QWEI-FLEHVEQLINQOITENARNTALRQLGDSFRAYQOSLEDWLENRDDARTSVL 128
Qy 159 RSQYIALELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIS 218
Db 129 YTOYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSBEGLTSQEIQ 188
Qy 219 TFYNRQVERAGDYSCHVKYVSTGLNLRGTNAESWVRYNQFRDWTLMVLDLVALPPSY 278
Db 189 RYVERQVERTRDYSYCVENYNTGLNLRGTNAASWVRYNQFRDWTLMVLDLVALPPSY 248
Qy 279 DTQMPYPIKTTAQLTREYVYDAIGTGVHPHPSFTSTTWYNNAPSFSAEAAVVRNPHLLDF 338

Db 249 DTRTPINTSAQLTREYVYDAIGAT--GVNMASMNWNNNAPSFSALAEAAIRSPHLLDF 306
Qy 339 LEQVTIYSLSRWSNTQYNNMWGKHLBERTIGTGLNISTQGSTNTSINPVTLPFTSRDV 398
Db 307 LEQLTIFSASSRWSNTRHMTYWRGHTIOSRPIGGGLNTSTHGATNTSINPVTLPFTSRDV 366
Qy 399 YRTESLAGLNLF--LTQPVNGVPRVDFHKKFVTHP-----IASDNFYYPGYAGIGTQLOD 451
Db 367 YRTESYAGVLLWGIYLEPIHGVPTVRNF--TNPQNISDRGTANYSQP-YESPGQLQKD 422
Qy 452 SENELPPEATQPNYESYSHRLSHIGLSASHVKALVYSWTHRSADRTNTEPNSITQIP 511
Db 423 SETELPPETTERPNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTEPNSITQIP 482
Qy 512 LVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPFAQRYRVRIRYASTTDL 571
Db 483 MVKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNNINPFAQRYRVRIRYASTTDL 542
Qy 572 QFHTSINGKAINQGNFSATMNRGDDLYKTFRTVGTTPESFLDVQSTFTIGAWNFSSGN 631
Db 543 DFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRATFTPTFTQIQDIIRTSIQGLSGNG 602
Qy 632 EYVIDRIEFVEVYEAEDYFEKAQKVTALFTSTNPRGLKTDVKYHIDQVSNLVESL 591
Db 603 EYVIDKIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 662
Qy 692 SDEFYLDKRELFEIVKYANLHIERNM 719
Db 663 SDEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6

US-10-428-961-63
; Sequence 63, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 63
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-63

Query Match 57.4%; Score 2157.5; DB 15; Length 1227;
Best Local Similarity 59.0%; Pred. No. 3e-173;
Matches 422; Conservative 103; Mismatches 175; Indels 15; Gaps 5;

Qy 13 SSNAKVDKISTDSLKN-----ETDIELQINIHEDCLKMSYENVEPVASVSTQIGTIG 65
Db 7 NENEIINALSIPAVSNHSAQMLSTDARI-----EDSLCIAEGNNIDPFVASTVQGTGIN 61
Qy 66 IAGKILGTLPVAGQVAVSLYFSLGELWPKGNQWEILFMEHVEE-INQKISTYARNKA 124
Db 62 IAGRIILGVLPVAGQVAVSLYFSLGELWPKGRDPWEI-FLEHVEHLIRQVTTENTRTDA 120
Qy 125 LTDILKGLGDALAVYHDSLESWSVGNRNTRARSVRSQYIALELMFVQKLPSFAVSGEEVP 184

Query Match 55.5%; Score 2087; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.8e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;
US-10-614-524-2

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECKMSEYENVEPFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
DB 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEI-FLEHVEQLINQITENARNTALARLQ 125

QY 130 GLGDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVKQLPSFAVSGEEVPLPIY 189
DB 126 GLGDSFRAYQOSLEDWLENRDDARTSVLYTQYIALELDFLNAMPFLFAIRNQEVPLLMVY 185

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYSTGLNNLRGT 249
DB 186 AQANLHLLLRDASLFGSEFGLTSQEIQRYRQVEQTRDYSDYCVWYNTGLNSLRGT 245

QY 250 NAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTREVTYDAIGT--GVNM 303
DB 246 NAASWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTREVTYDAIGT--GVNM 303

QY 310 TSTTWNNNAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMWGGHKLERT 369
DB 304 ASMWYNNNAPSIAETAIVIRSPHLLDFLEQVTIYSLLSRWSTQYMMWGGHKLERT 363

QY 370 IGGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNF--LTQPVNGVPRVDFHWKF 427
DB 364 IGGGLNTSTHGSTNTSINPVLSPFSDRDYVWTSYAGVLLWGIYLEPIHGVPVTFNFRN 423

QY 428 V--THPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 485
DB 424 PONTFERGTANYSQP--YESPGLQKDSYELPPTETTERPNYESYSHRLSHIGLISASHVK 482

QY 486 ALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTFTG 605
DB 543 SMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRPA 602

QY 606 GFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTAFT 665
DB 603 EFPVGISASGSQ--TAGISISNNAGRTQTHFDKIEFIPITATFEAEYDLERAQEAVALFT 661

QY 666 STNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDKRELFEIVKYANELHIERNM 719
DB 662 NTNPRRLKTDVTDYHIDQVSNLVACLSDFFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 9
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from *Bacillus thuringiensis*.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: *Bacillus thuringiensis*
US-10-614-524-2

Query Match 55.5%; Score 2087; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.8e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;
US-10-614-524-2

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECKMSEYENVEPFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
DB 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEI-FLEHVEQLINQITENARNTALARLQ 125

QY 130 GLGDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVKQLPSFAVSGEEVPLPIY 189
DB 126 GLGDSFRAYQOSLEDWLENRDDARTSVLYTQYIALELDFLNAMPFLFAIRNQEVPLLMVY 185

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYSTGLNNLRGT 249
DB 186 AQANLHLLLRDASLFGSEFGLTSQEIQRYRQVEQTRDYSDYCVWYNTGLNSLRGT 245

QY 250 NAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTREVTYDAIGT--GVNM 303
DB 246 NAASWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTREVTYDAIGT--GVNM 303

QY 310 TSTTWNNNAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMWGGHKLERT 369
DB 304 ASMWYNNNAPSIAETAIVIRSPHLLDFLEQVTIYSLLSRWSTQYMMWGGHKLERT 363

QY 370 IGGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNF--LTQPVNGVPRVDFHWKF 427
DB 364 IGGGLNTSTHGSTNTSINPVLSPFSDRDYVWTSYAGVLLWGIYLEPIHGVPVTFNFRN 423

QY 428 V--THPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 485
DB 424 PONTFERGTANYSQP--YESPGLQKDSYELPPTETTERPNYESYSHRLSHIGLISASHVK 482

QY 486 ALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTFTG 545
DB 483 VPVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTFTG 542

QY 546 DIRVINPFPQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRPA 605
DB 543 SMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRPA 602

QY 606 GFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTAFT 665
DB 603 EFPVGISASGSQ--TAGISISNNAGRTQTHFDKIEFIPITATFEAEYDLERAQEAVALFT 661

QY 666 STNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDKRELFEIVKYANELHIERNM 719
DB 662 NTNPRRLKTDVTDYHIDQVSNLVACLSDFFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 10
US-09-826-660-25
; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05


```
Db 521 IYSDKITQIPAVKGMVLYLGGSVVQPGFTGGDILKRTNPSILGTFAVTVNGSLSQRYRV 580
Qy 562 RIRYASTTDLOPHTSINGKAINQGNFSATMNRGDLDTYKTRFTVGVFTTTPFSLDVQSFT 621
Db 581 RIRYASTTDFEF-TLYLGDITKRNFKNTMDNGASLTETFKFASFTDFQFRETQDKIL 639
Qy 622 IGAWNFSGNEVYIDRIEFVVEVYEAEDFEKAQKVTAFTSTNPRGLKTDVVDKHYI 681
Db 640 LSGMDFSSGQVEYIDRIEFVDETYEAQDLEAAKAVNALFTNTKD-GLRPGVTDEV 698
Qy 682 DQVSNLVESLDEFYLDKRELFEIVKYANELHIERNM 719
Db 699 NQAANLVECLSDLLYPNEKRLLLFDVAREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 39.5%; Score 1485; DB 13; Length 1206;
Best Local Similarity 44.3%; Pred. No. 3e-116;
Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQINHEDECLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRYPPANEPTNALQNDYKDYLKMSAGNASEYPS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNQWEILFMEH 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGKESQWEI-FMEQ 118
Qy 109 VEE-INQKISTYARNKALTDLKLGLDALAVYHDSLESWGNRNNTNRARSVVRQYIALEL 167
Db 119 VEELINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNGRALRDVRNFEILDS 178
Qy 168 MFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVER 227
Db 179 LFTQYMPFSFRVTNFEVFLTVYAMAANLHLLLRDASIFGEEWGSTTTTNNYDRQMKL 238
Qy 228 AGDYSCHVKVYSTGLNLRGTNAESWVRVYQFRDMLVLDLVALFPSYDTQMPYIKT 287
Db 239 TABYSDHCVKMYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTFTYPMET 298
Qy 288 TAQLTREYVYTDAGTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSL 347
Db 299 KAQLTREYVYTDPLGAVNVS---SIGSWY-DKAPSGVIESVIRPPHVFYDIYGLTVVTO 354
Qy 348 LSRWSNTQYMNWGGHKLKLEFRITIGTLNISTQGSTNTSINPV-TLPFTSRDVRVYTESLAG 406
Db 355 SRSISSARYIRHWAGHQISYHVRSGSNLQOMYGTGNQLHSTSTPFDFTNYDIYKTLSDKA 414
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Qy 407 LNLFLTQP-----VNGVPRVDVHMKFVTHPIASDN---FYYPGYAGIGTQLOQDSENELPP 458
Db 415 VLLDIVPGVYTIIFGMEVEF---FMVNLNTRKTLKYNPVSKDIIASTRDSLELEPP 471
Qy 459 EATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKA 515
Db 472 ETSQPNYESYSHRLCHITSIPATGNTTGLVPFVSWTHRSADLNNNTIYSDKITQIPAVKC 531
Qy 516 FNLSSGAAVRGPFGTGDILR-RTNTGTFGDI---RVNPPFAQRYRVRIRIYASTTDL 571
Db 532 WDNLPFVPVVGKPGHGTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKRVRLRYATDADI 591
Qy 572 QFHTSINGKAINQGNFSATMNRGDLDTYKTR-----TVGFTTTPFSEL-----DVQS 618
Db 592 VLH--VNDQAI---QMPKTMNPGEDLTSTKFKVADAITTLNLTATDSSLAKHNLGDEPNS 646
Qy 619 TFTIGAWNFSGNEVYIDRIEFVVEVYEAEDFEKAQKVTAFTSTNPRGLKTDVVDK 678
Db 647 TLS-----GIVVVDRIEFIPVDETYEAQDLEAAKAVNALFTNTKD-GLRPGVTD 696
Qy 679 YHIDQVSNLVESLDEFYLDKRELFEIVKYANELHIERNM 719
Db 697 YEVNQAANLVECLSDLLYPNEKRLLLFDVAREAKRLSEARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 39.5%; Score 1485; DB 14; Length 1206;
Best Local Similarity 44.3%; Pred. No. 3e-116;
Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQINHEDECLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRYPPANEPTNALQNDYKDYLKMSAGNASEYPS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNQWEILFMEH 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGKESQWEI-FMEQ 118
Qy 109 VEE-INQKISTYARNKALTDLKLGLDALAVYHDSLESWGNRNNTNRARSVVRQYIALEL 167
Db 119 VEELINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNGRALRDVRNFEILDS 178
Qy 168 MFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVER 227
Db 179 LFTQYMPFSFRVTNFEVFLTVYAMAANLHLLLRDASIFGEEWGSTTTTNNYDRQMKL 238
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds
(without alignments)
2403.590 Million cell updates/sec

Title: US-10-019-823B-58
Perfect score: 3761
Sequence: 1 MKLNQDKHQSPSSNAKVDK.....KRELPEIVKYANELHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3720	98.9	719	3	US-08-286-870A-8
2	3442.5	91.5	710	4	US-09-661-322A-42
3	3370	89.6	648	3	US-08-286-870A-4
4	3341	88.8	719	2	US-09-003-217-2
5	3336	88.7	719	3	US-09-218-942-2
6	2776	73.8	535	3	US-08-286-870A-6
7	2417.5	64.3	1229	1	US-08-100-709-4
8	2417.5	64.3	1229	1	US-08-176-865-4
9	2417.5	64.3	1229	1	US-08-474-038-4
10	2417.5	64.3	1229	2	US-08-779-046-4
11	2417.5	64.3	1229	2	US-08-881-340-4
12	2318.5	61.6	488	1	US-08-448-170-10
13	2318.5	61.6	488	3	US-08-961-803-10
14	2236.5	59.5	1207	1	US-07-951-715A-7
15	2236.5	59.5	1207	2	US-08-459-448A-7
16	2236.5	59.5	1207	3	US-08-459-595A-7
17	2236.5	59.5	1207	3	US-08-459-504B-7
18	2236.5	59.5	1207	3	US-08-459-444-7
19	2236.5	59.5	1207	3	US-09-053-549-8
20	2236.5	59.5	1207	3	US-09-547-422-7
21	2236.5	59.5	1207	4	US-09-988-462-7
22	2236.5	59.5	1207	3	US-09-053-549-2
23	2166.5	57.6	1227	1	US-08-448-170-8
24	2166.5	57.6	1227	3	US-08-961-803-9
25	2157.5	57.4	1227	4	US-09-661-322A-63
26	2142.5	57.0	1186	3	US-09-178-252-23
27	2142.5	57.0	1186	4	US-09-826-660-23

28	2087	55.5	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1909.5	50.8	643	3	US-09-178-252-25	Sequence 25, Appl
30	1909.5	50.8	643	4	US-09-826-660-25	Sequence 25, Appl
31	1872	49.8	380	5	PCT-US91-02560-4	Sequence 4, Appli
32	1658.5	44.1	653	4	US-09-661-322A-6	Sequence 6, Appli
33	1643.5	43.7	1157	1	US-07-876-280-30	Sequence 30, Appli
34	1643.5	43.7	1157	1	US-07-812-180A-2	Sequence 2, Appli
35	1643.5	43.7	1157	1	US-08-315-468-2	Sequence 2, Appli
36	1643.5	43.7	1157	3	US-07-941-650A-2	Sequence 2, Appli
37	1481.5	39.4	1176	1	US-08-257-999-2	Sequence 2, Appli
38	1466	39.0	1157	2	US-08-532-547-5	Sequence 5, Appli
39	1466	39.0	1157	2	US-08-379-656B-5	Sequence 5, Appli
40	1466	39.0	1157	3	US-08-455-838-5	Sequence 5, Appli
41	1466	39.0	1157	3	US-09-019-809-5	Sequence 5, Appli
42	1466	39.0	1157	4	US-09-471-177-5	Sequence 5, Appli
43	1466	39.0	1157	4	US-09-220-806-5	Sequence 5, Appli
44	1461	38.8	1168	1	US-08-291-368-4	Sequence 4, Appli
45	1461	38.8	1168	2	US-08-962-190-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Tue Feb 15 10:07:55 2005

Query Match 98.9%; Score 3720; DB 3; Length 719;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 714; Conservative 3; Mismatches 1; Indels 2; Gaps 2;
1 MCLKNODKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFSASTI 60
1 MCLKNODKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFSASTI 60
61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
120 ARNKALTDLKGDLALAVYHDSLESWVGNRNTRARSVVSQYIALELMFVQKLPSPAVS 179
120 ARNKALTDLKGDLALAVYHDSLESWVGNRNTRARSVVSQYIALELMFVQKLPSPAVS 179
180 GEEVPLLPITYAQAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
180 GEEVPLLPITYAQAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
240 STGLNLRGTNAESWVRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREVIYDA 299
240 STGLNLRGTNAESWVRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREVIYDA 299
300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMN 359
300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMN 359
360 WGGHKLFEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLLTOPVNGVP 419
360 WGGHKLFEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLLTOPVNGVP 419
420 RVDHFWKVFTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
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600 KTFRTVGFTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAEYDFEKAQEK 659
660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFELVVKYAKQLHIERNM 719
660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFELVVKYAKQLHIERNM 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Wei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 91.5%; Score 3442.5; DB 4; Length 710;
Best Local Similarity 91.9%; Pred. No. 3.5e-304;
Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;
1 MCLKNODKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPFSASTI 60
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61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
52 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 110
120 ARNKALTDLKGDLALAVYHDSLESWVGNRNTRARSVVSQYIALELMFVQKLPSPAVS 179
120 ARNKALTDLKGDLALAVYHDSLESWVGNRNTRARSVVSQYIALELMFVQKLPSPAVS 179
111 ARNKALADLKGDLALAVYHDSLESWVGNRNTRARSVVSQYIALELMFVQKLPSPAVS 170
180 GEEVPLLPITYAQAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
171 GEEVPLLPITYAQAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 230
240 STGLNLRGTNAESWVRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREVIYDA 299
231 NTGLNRLMGNNAESWVRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREVIYDA 290
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291 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTTIYSLSRWSNTQYMN 350
360 WGGHKLFEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLLTOPVNGVP 419
351 WGGHKLFEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLLTOPVNGVP 410
420 RVDHFWKVFTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
411 RVDHFWKVFTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 470
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471 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 530
540 NTGTFGDIRVNINPPFAQRYVRIRYASITDLOFHTSINGKAINQGNFSATMNRGDLDY 599
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600 KTFRTVGFTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAEYDFEKAQEK 659
591 KTFRTVGFTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAEYDFEKAQEK 650
660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFELVVKYAKQLHIERNM 719
651 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFELVVKYAKQLHIERNM 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 89.6%; Score 3370; DB 3; Length 648;
Best Local Similarity 99.5%; Pred. No. 1.2e-297;
Matches 646; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEFPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEFPVSASTI 60

Qy 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

Qy 120 ARNKALTDKGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALTDKGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPSFAVS 179

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239

Qy 240 STGLNLRGTHNAESWRYNQPRRDMTLMVLDLVALFPSPYDTQMPYIKTTAQLTREVYDA 299
Db 240 STGLNLRGTHNAESWRYNQPRRDMTLMVLDLVALFPSPYDTQMPYIKTTAQLTREVYDA 299

Qy 300 IGTVHPHPSFTSTTWYNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
Db 300 IGTVHPHPSFTSTTWYNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359

Qy 360 WGGHKLFRITGCTLNISTQSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419
Db 360 WGGHKLFRITGCTLNISTQSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419

Qy 420 RYDFHKKFVTHPIASDNFYYPGAGTGTQDSENELPPEATGPNYBSYSHRLSHIGLI 479
Db 420 RYDFHKKFVTHPIASDNFYYPGAGTGTQDSENELPPEATGPNYBSYSHRLSHIGLI 479

Qy 480 SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAENLSSGAAVVRGFGTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAENLSSGAAVVRGFGTGGDILRRT 539

Qy 540 NTGTFGDIRVNINPPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599

Qy 600 KTFRTVGTFTTFFSLDVQSTFTTIGAWNFGSGNEVYIDRIEFVPEVTVE 648
Db 600 KTFRTVGTFTTFFSLDVQSTFTTIGAWNFGSGNEVYIDRIEFVPEVTVE 648

RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 881 3175
TELEFAX: 919 420 2202
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 88.8%; Score 3341; DB 2; Length 719;
Best Local Similarity 89.2%; Pred. No. 6.1e-295;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEFPVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVEFPVSASTI 60

Qy 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

Qy 120 ARNKALTDKGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALTDKGLDALAVYHDSLESWVGNNRNRARSVVRVRSQYIALELMFVQKLPSFAVS 179

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239

Db 180 GEEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVERTRDYSHCVKWN 239
Qy 240 STGLNLRGTNAESWRYNQRRDMTLMVLDLVALFPSYDTOMYPIKTAQLTRREYVYDA 299
Db 240 NTGLNLRATNGOSWRYNQRRDKIDELMVLDRVFPSTYDTLVYPIKTSQLTREYVYDA 299
Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVYIYSLSRWSNTQYMMN 359
Db 300 IGTVDPNQALRSTWYNNNAPSFAIEAAVVRNPHLLDLEQVYIYSLSRWSNTQYMMN 359
Qy 360 WGGHKLFRPTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGVP 419
Db 360 WGGHRLSRPIGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGVP 419
Qy 420 RVDPHWKFTVTHPIASDNFYYPGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDPHWKFTVTHPIASDNFYYPGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 KSGTFGHIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRTVGFTTFFSFDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
Db 600 KTFRTVGFTTFFSFDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSELYLDEKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSELYLDEKRELFEIVKYANELHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osmann, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: Cry11
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2
Query Match 88.7%; Score 3336; DB 3; Length 719;
Best Local Similarity 89.2%; Pred. No. 1.7e-294;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;
Qy 1 MLLKNQDQKHSFSSNAKVDKISTDSLNKNETDIELQINHBDCMKSEVENVEPVFSASTI 60
Db 1 MLLKNPDKHQTLSSNAKVDKIATDSLNKNETDIELKNMNNEDYLRSEHESIDPFVSASTI 60
Qy 61 QTGIGIAGKILGTGVPPAGVAVSLYFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTGVPPAGVAVSLYFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Qy 120 ARNKALTDLKLGLDALAVYHDSLESVGNVNRNTRARSVRSQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALTDLKLGLDALAVYHDSLESVGNVNRNTRARSVRSQYIALELMFVQKLPSFAVS 179

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKMY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVERTRDYSHCVKWN 239
Qy 240 STGLNLRGTNAESWRYNQRRDMTLMVLDLVALFPSYDTOMYPIKTAQLTRREYVYDA 299
Db 240 NTGLNLRATNGOSWRYNQRRDKIDELMVLDRVFPSTYDTLVYPIKTSQLTREYVYDA 299
Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVYIYSLSRWSNTQYMMN 359
Db 300 IGTVDPNQALRSTWYNNNAPSFAIEAAVVRNPHLLDLEQVYIYSLSRWSNTQYMMN 359
Qy 360 WGGHKLFRPTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGVP 419
Db 360 WGGHRLSRPIGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGVP 419
Qy 420 RVDPHWKFTVTHPIASDNFYYPGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDPHWKFTVTHPIASDNFYYPGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 KSGTFGHIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRTVGFTTFFSFDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
Db 600 KTFRTVGFTTFFSFDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSELYLDEKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSELYLDEKRELFEIVKYANELHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 73.8%; Score 2776; DB 3; Length 535;
Best Local Similarity 99.4%; Pred. No. 1e-243; 0; Indels 2; Gaps 2;
Matches 533; Conservative 1; Mismatches 0;

QY 1 MKLKNQKHQSPSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFVSASTI 60
DB 1 MKLKNQKHQSPSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTLPVFPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTLPVFPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTY 119

QY 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPSPAVS 179
DB 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPSPAVS 179

QY 180 GEEVPLPIYAQAANLHLLRDASIFGKEWGLSSEISTFYNNQVERAGDYSCHCKWY 239
DB 180 GEEVPLPIYAQAANLHLLRDASIFGKEWGLSSEISTFYNNQVERAGDYSCHCKWY 239

QY 240 STGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQYPIKTTAQLTREVYTD 299
DB 240 STGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQYPIKTTAQLTREVYTD 299

QY 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNM 359
DB 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNM 359

QY 360 WGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVTSIAGLNFLTPQVNGVP 419
DB 360 WGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVTSIAGLNFLTPQVNGVP 419

QY 420 RVDHFHFKVTHPIASDNFYFGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RVDHFHFKVTHPIASDNFYFGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECKMSEYENVEPFVSASTIQTGIGIAGKI 70
DB 7 NENEINALSITPTVSNPSTQNLSPDARIEDSLCVAEANNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 129
DB 67 LGVLGVFPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 125

QY 130 GLGDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPSPAVSGEEVPLPIY 189
DB 126 GLGRGVRSYQQALETWLDNDRDARSIIILERYVALELDITTAIPLFRINEEVPLLMVY 185

QY 190 AQANLHLLRDASIFGKEWGLSSEISTFYNNQVERAGDYSCHCKWYSTGLNLRGT 249
DB 186 AQANLHLLRDASIFGKEWGLSSEISTFYNNQVERAGDYSCHCKWYSTGLNLRGT 245

QY 250 NAESWRYNQFRDMTLMVLDLVALFPSYDTQYPIKTTAQLTREVYTDAGTVHPHPSF 309
DB 246 NAESWRYNQFRDMTLMVLDLVALFPSYDTQYPIKTTAQLTREVYTDAGTVHPHPSF 305

QY 310 TSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMGHKLERT 369
DB 306 ASTNWFNNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMGHKLERT 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVTSIAGLNFLTPQVNGVPRVDFHFKV 428
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVTSIAGLNFLTPQVNGVPRVDFHFKV 422

QY 429 THPIASDNFYFGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 481
DB 423 ---INPQNIYERGATTYSQPYQGVIGLFDSEITELPPTTERPNYESYSHRLSHIGLI 479

QY 482 SHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541
DB 480 NTLRAPVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 539

QY 542 GTFGDIRVNNPFPQAQRYRVRVASTTDLQFHTSINGKAINQGNFSATMNRGSDLDYKT 601
DB 540 GTFGDIRVNNPFPQAQRYRVRVASTTDLQFHTSINGKAINQGNFSATMNRGSDLDYKT 599

QY 602 FRTVGTFTTSPSFLDQSTFTIGAMNFSGNEVYIDRIEFVFPVEVITYAEYDFEKAQKVT 661
DB 600 FRTAGFTSTPFLNAQSTFTIGAMNFSGNEVYIDRIEFVFPVEVITYAEYDFEKAQKVT 658

QY	662	ALFTSTNPRGLKTDVYHIDQVSNLVESLDEFYLDKRELFEIVKYANELHIERNM	719
Db	659	ALFTSTNPRRLKTDVTDYHIDQVSNVACLSEFCLDEKRELFEKVKYAKRLSDERNL	716
RESULT 8			
US-08-176-865-4			
; Sequence 4, Application US/08176865			
; Patent No. 5616319			
; GENERAL INFORMATION:			
; APPLICANT: Donovan, William P.			
; APPLICANT: Tan, Yuping			
; APPLICANT: Jany, Christine S.			
; APPLICANT: Gonzalez Jr., Jose M.			
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5			
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.			
; ADDRESSEE: Nadel			
; STREET: 1601 Market Street, 36th Floor			
; CITY: Philadelphia			
; STATE: Pennsylvania			
; COUNTRY: U.S.A.			
; ZIP: 19103			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/176,865			
; FILING DATE: 30-DEC-1993			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/100,709			
; FILING DATE: 29-JUL-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Egolf, Christopher			
; REGISTRATION NUMBER: 27633			
; REFERENCE/DOCKET NUMBER: 7205-49			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 215-757-1590			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1229 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-176-865-4			
Query Match 64.3%; Score 2417.5; DB 1; Length 1229;			
Best Local Similarity 65.3%; Pred. No. 1.7e-210;			
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;			
QY	13	SSNAKVDKISTSLKN-ETDIELQ-NINHEDCLKMSEYENVEPVSASTIQTGIGIAGKI	70
Db	7	NENEIINALSIPTVSNFSTOMLSPDARIEDSLCAVANNIDPFVSAVQTGINIAGRI	66
QY	71	LGTLPVPAGVAVSLYSFILGELWPKGKNQWEILFMEHVEE-INQKISTYARNKALTDLK	129
Db	67	LGLVGVFAGQLASFYFLVGLWPSGRDPWEI-FLEHVEQLIRQQVTNTRNTAIARLE	125
QY	130	GLGDALAVYHDSLESVGNRNTRNSVRSQYIALELMFVQKLPFAVSGEVPPLPIY	189
Db	126	GLGGRYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVY	185
QY	190	AQAANHLILLRLDASIFGKEWGLSSBSISTFVNRQVAGDYSDHCVKWYSTGLNNLRGT	249
Db	186	AQAANHLILLRLDASLFCGSEWGMASSDVNYQQEIRYTRYEYSNHCQVNTYGLNNLRGT	245
QY	250	NAESWVRNQFRDMLVLDLVALPFSYDITQWYPIKTTAQLTREVYTDATGTVHPHPSF	309

Db	246	NAESWLRNQFRDLTLGVLDLVALPSPYDTRTYPINTSQAQLTRTYITDPIGRINAPSGF	305
QY	310	TSTWYNNAPSPSAIEAAVVRNPHLLDELEQVITYSLSRWSNTQYMMWGGHKLFRPT	369
Db	306	ASTWNFNAPSPSAIEAAIFRPPHLLDFPEQLTIYSSASRWSSTQHMMNVVGHRLNFRP	365
QY	370	IGGTINISTQGST-NTSINPVTLPFTSRDVTYRTESLAGLNLFLTQPVNGVPRVDFHWKEV	428
Db	366	IGGTINTSTQGLTNNTSINPVTLPFTSRDVTYRTESNAGTNILFTTPVNGVFWARFNF---	422
QY	429	THPIASDNFYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA	481
Db	423	---INPQNIYERGATTYQPYQGVIGIQLFDSSETLPETTERPNYESYSHRLSHIGLIIG	479
QY	482	SHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT	541
Db	480	NTLRAPVYSWTHRSADRTNTEIPNSITQIPLVKALNLSHGVTVVGGPGFTGGDILRRNT	539
QY	542	GTFGDIRVAINPPEAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKT	601
Db	540	GTFGDIRLNLINVPISQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLNLEYS	599
QY	602	FRTVGFTTSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVT	661
Db	600	FRTAGFSTPFNLNAQSTFTGLAQFSN-QEVYIDRVEFVPAEVTPEAEYDLERAQAVN	658
QY	662	ALFTSTNPRGLKTDVYHIDQVSNLVESLSEFCLDEKRELFEIVKYANELHIERNM	719
Db	659	ALFTSTNPRRLKTDVTDYHIDQVSNVACLSEFCLDEKRELFEKVKYAKRLSDERNL	716
RESULT 9			
US-08-474-038-4			
; Sequence 4, Application US/08474038			
; Patent No. 5679343			
; GENERAL INFORMATION:			
; APPLICANT: Donovan, William P.			
; APPLICANT: Tan, Yuping			
; APPLICANT: Jany, Christine S.			
; APPLICANT: Gonzalez Jr., Jose M.			
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5			
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.			
; ADDRESSEE: Nadel			
; STREET: 1601 Market Street, 36th Floor			
; CITY: Philadelphia			
; STATE: Pennsylvania			
; COUNTRY: U.S.A.			
; ZIP: 19103			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/474,038			
; FILING DATE: 07-JUN-1995			
; CLASSIFICATION: 514			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/176,865			
; FILING DATE: 30-DEC-1993			
; APPLICATION NUMBER: US 08/100,709			
; FILING DATE: 29-JUL-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Egolf, Christopher			
; REGISTRATION NUMBER: 27633			
; REFERENCE/DOCKET NUMBER: 7205-49			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 215-757-1590			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1229 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-176-865-4			
Query Match 64.3%; Score 2417.5; DB 1; Length 1229;			
Best Local Similarity 65.3%; Pred. No. 1.7e-210;			
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;			
QY	13	SSNAKVDKISTSLKN-ETDIELQ-NINHEDCLKMSEYENVEPVSASTIQTGIGIAGKI	70
Db	7	NENEIINALSIPTVSNFSTOMLSPDARIEDSLCAVANNIDPFVSAVQTGINIAGRI	66
QY	71	LGTLPVPAGVAVSLYSFILGELWPKGKNQWEILFMEHVEE-INQKISTYARNKALTDLK	129
Db	67	LGLVGVFAGQLASFYFLVGLWPSGRDPWEI-FLEHVEQLIRQQVTNTRNTAIARLE	125
QY	130	GLGDALAVYHDSLESVGNRNTRNSVRSQYIALELMFVQKLPFAVSGEVPPLPIY	189
Db	126	GLGGRYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVY	185
QY	190	AQAANHLILLRLDASIFGKEWGLSSBSISTFVNRQVAGDYSDHCVKWYSTGLNNLRGT	249
Db	186	AQAANHLILLRLDASLFCGSEWGMASSDVNYQQEIRYTRYEYSNHCQVNTYGLNNLRGT	245
QY	250	NAESWVRNQFRDMLVLDLVALPFSYDITQWYPIKTTAQLTREVYTDATGTVHPHPSF	309


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SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-038-4

Query Match      64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEVENVEPVFVASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVASTVQTGINIAGRI 66

Qy 71 LGTLGVPPFAGQVASYLFIKELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 129
Db 67 LGVLGVPPFAGQLASFYSLFVGLWPSGRDPWEI-FLEHVEQLIRQQVTENTRTAARLE 125

Qy 130 GIGDALAVYHDSLESVGNVGNNTRRARSVRSQYIALELMFVQKLPSFAVSGSEVPLPIY 189
Db 126 GLGRGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVPLLMVY 185

Qy 190 AQANLHLLLRDASIFGKELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 249
Db 186 AQANLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEEYSHNCHVQWYNTGLNLRGT 245

Qy 250 NAESWRYNQFRDRTMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVTDAGTVHPHPSF 309
Db 246 NAESWRYNQFRDRTMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVTDAGTVHPHPSF 305

Qy 310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWSTQYNNMGGHKLFRFT 369
Db 306 ASTNWFNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWSTQYNNMGGHKLFRFT 365

Qy 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPRVDFHKNFV 428
Db 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPRVDFHKNFV 422

Qy 429 THPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQYQGVGIQDFSETELPPETERPNYESYSHRLSHIGLIIG 479

Qy 482 SHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541
Db 480 NTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRNT 539

Qy 542 GTFGDIRVNIPLPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKT 601
Db 540 GTFGDIRVNIPLPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKT 599

Qy 602 FRTVGTTPFSLDQSTFTIGAMNFSNGNEVYIDRIEFVPPVEVTEYAEYDFEKAQSKVT 661
Db 600 FRTAGSTPFNLAQSTFTILGAQFSN-QEYVYIDRVEFVPAEVTFFAEYDLERAKAVN 658

Qy 662 ALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFVLDEKRELPEIKVYANELHIERNM 719
Db 659 ALFTSTNPRRLKTDVYDHYIDQVSNMVACLSDDEFCLDEKRELPEIKVYAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYBET4 AND CYBET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-046-4

Query Match      64.3%; Score 2417.5; DB 2; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEVENVEPVFVASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEYNNIDPFVASTVQTGINIAGRI 66

Qy 71 LGTLGVPPFAGQVASYLFIKELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 129
Db 67 LGVLGVPPFAGQLASFYSLFVGLWPSGRDPWEI-FLEHVEQLIRQQVTENTRTAARLE 125

Qy 130 GIGDALAVYHDSLESVGNVGNNTRRARSVRSQYIALELMFVQKLPSFAVSGSEVPLPIY 189
Db 126 GLGRGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVPLLMVY 185

Qy 190 AQANLHLLLRDASIFGKELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 249
Db 186 AQANLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEEYSHNCHVQWYNTGLNLRGT 245

Qy 250 NAESWRYNQFRDRTMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVTDAGTVHPHPSF 309
Db 246 NAESWRYNQFRDRTMLVLDLVALFPPSYDTQMPYIKTTAQLTREYVTDAGTVHPHPSF 305

Qy 310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWSTQYNNMGGHKLFRFT 369
Db 306 ASTNWFNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWSTQYNNMGGHKLFRFT 365

Qy 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPRVDFHKNFV 428
Db 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPRVDFHKNFV 422

Qy 429 THPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQYQGVGIQDFSETELPPETERPNYESYSHRLSHIGLIIG 479

Qy 482 SHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541
Db 480 NTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRNT 539
```



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 61.6%; Score 2318.5; DB 1; Length 488;
Best Local Similarity 89.4%; Pred. No. 3.8e-202;
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

Qy 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MFSKNQNMHQSLNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFVSASTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGQWEI-FMEHVEELINQKISTY 110

Qy 120 ARNKALTDLKGDLALAVYHDSLESVWGNRNTRRSVRSQYIALELMFVQKLPSPFAVS 179
Db 111 ARNKALADLKGDLALAVYHESLESWIENRNTRRSVVKVQYITLMLFVQSLPSPFAVS 170

Qy 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239
Db 171 GEEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWY 230

Qy 240 STGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 299
Db 231 NTGLNRLMGNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 290

Qy 300 IGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 359
Db 291 IGTVHPHPSFTSTTWNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 350

Query Match 61.6%; Score 2318.5; DB 3; Length 488;
Best Local Similarity 89.4%; Pred. No. 3.8e-202;
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

Qy 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MFSKNQNMHQSLNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFVSASTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGQWEI-FMEHVEELINQKISTY 110

Qy 120 ARNKALTDLKGDLALAVYHDSLESVWGNRNTRRSVRSQYIALELMFVQKLPSPFAVS 179
Db 111 ARNKALADLKGDLALAVYHESLESWIENRNTRRSVVKVQYITLMLFVQSLPSPFAVS 170

Qy 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239
Db 171 GEEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWY 230

Qy 240 STGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 299
Db 231 NTGLNRLMGNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 290

Qy 300 IGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 359
Db 291 IGTVHPHPSFTSTTWNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 350

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 61.6%; Score 2318.5; DB 3; Length 488;
Best Local Similarity 89.4%; Pred. No. 3.8e-202;
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

Qy 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MFSKNQNMHQSLNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFVSASTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGQWEI-FMEHVEELINQKISTY 110

Qy 120 ARNKALTDLKGDLALAVYHDSLESVWGNRNTRRSVRSQYIALELMFVQKLPSPFAVS 179
Db 111 ARNKALADLKGDLALAVYHESLESWIENRNTRRSVVKVQYITLMLFVQSLPSPFAVS 170

Qy 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239
Db 171 GEEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWY 230

Qy 240 STGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 299
Db 231 NTGLNRLMGNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 290

Qy 300 IGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 359
Db 291 IGTVHPHPSFTSTTWNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 350
```

RESULT 13
US-08-961-803-10
Sequence 10, Application US/08961803
Patent No. 6150589
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

Tue Feb 15 10:07:55 2005

QY 360 WGGHKLERTIGTGLNLTSTQSTNTSINPVTLPFTSRDYRTSLAGLNFLTQPVNGVP 419
DB 351 WGGHKLERTIGTGLNLTSTQSTNTSINPVTLPFTSRDYRTSLAGLNFLTQPVNGVP 410
QY 420 RVDPHWKFTVTHPTASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 411 RVDPHWKFTVTHPTASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 470
QY 480 SASHVKALVYSWTHRSAD 497
DB 471 SASHVKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-951-715A-7

Query Match 59.5%; Score 2236.5; DB 1; Length 1207;

Best Local Similarity 64.1%; Pred. No. 5e-194;
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;
QY 40 EDCUKMSYENVEPFPVSASTTGTGIGIAGKLTGTPVPPAGOVASLYSIFILGELWPKGN 99
DB 10 EDSLCIAEGNNIDPFVSASTVGTGINIAGILGVLGVPFAGQLASFYSFLVGLWPRGRD 69
QY 100 QWEILFMEHVEE-INQKISTYARNKALTDLKGLDALAVVHDSLESVGNRNNTARSVV 158
DB 70 QWEI-FLEHVEQLINQITENARNTALARLOGLGDSFRAQQOSLEDWLENRDDARTSVL 128
QY 159 RSQYIALELMFVOKLPSPFVSGEEVPLPIYAQAANLHLLLRDASIFGKEMGLSSSEIS 218
DB 129 YTOYIALELDFLNA MPLFAIRNOQEVPLMLVTAQAANLHLLLRDASLFGSEFGLTSQEIQ 188
QY 219 TFPNROVERAGDYSCHCVKWSYSTGLNLRGTNAESWVRYNQFRFRDMLVLDLVALFPYS 278
DB 189 RYERQVERTRDYSYCVWEYNTGLNLRGTNAESWVRYNQFRFRDMLVLDLVALFPYS 248
QY 279 DTQYPIKTTAQLTREVYTDAGTGVHHPSPFTSTWYNNNAPSFAIAAAVVRNPHLLDF 338
DB 249 DTRTPINTSAQLTREVYTDAGT--GVNMAAMNWNNAAPSFAIAAAVVRNPHLLDF 306
QY 339 LEQVTIYSLSRWNTQYNNMGHKLERTIGTGLNLTSTQSTNTSINPVTLPFTSRDV 398
DB 307 LEQVTIYSLSRWNTQYNNMGHKLERTIGTGLNLTSTQSTNTSINPVTLPFTSRDV 366
QY 399 YRTESLAGLNLF--LTQPVNGVPRVDFHWKFTVTHP-----IASDNFYYPGAGIGTQLOD 451
DB 367 YRTESLAGLNLF--LTQPVNGVPRVDFHWKFTVTHP-----IASDNFYYPGAGIGTQLOD 422
QY 452 SENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSTQIP 511
DB 423 SETELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSTQIP 482
QY 512 LVKAFNLSGGAUVGPGFTGGDILRRNTGTGDIRVNNPFPFAQRYRVRIRYASTDL 571
DB 483 MVKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNNPFPFAQRYRVRIRYASTDL 542
QY 572 QFHTSINGKAINQGNFSAATNRGDELDTYKTRFTVGTFTTFFSFLDVQSTFTIGAMNFSGN 631
DB 543 DFFVSRGTTVNNFRRLTNWSGDELKYNFVRRAFTTFTTQIIDIIRTSIQGLSGNG 602
QY 632 EYVIDRIEFVPEVVEAYEYDFEKAQKVTALFTSTNPRGLKTDVYHIDQVSNLVESL 691
DB 603 EYVIDKIEIIPVTATFEAYEDLERAQEAVALFTNTNPRRLKTDVYHIDQVSNLVACL 662
692 SDEFYLDKRELFEIVKYANLHIERNM 719
663 SDEFYLDKRELFEIVKYANLHIERNM 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds
(without alignments)
2827.419 Million cell updates/sec

Title: US-10-019-823B-58
Perfect score: 3761
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3736	99.3	719	4	AAB66911 Insectici
2	3736	99.3	719	6	AAB66911 Insectici
3	3724	99.0	719	4	AAB66908 Insectici
4	3724	99.0	719	4	AAB66909 Insectici
5	3724	99.0	719	6	AAB66909 Insectici
6	3724	99.0	719	6	AAB66909 Insectici
7	3724	99.0	719	6	AAB66909 Insectici
8	3720	98.9	719	4	AAB66910 Insectici
9	3720	98.9	719	6	AAB66910 Insectici
10	3715	98.8	719	4	AAB66910 Insectici
11	3703	98.5	719	2	AAR08041 81 kD end
12	3692.5	98.2	718	6	AAB66911 Insectici
13	3686.5	98.0	718	4	AAB66907 Insectici
14	3517	93.5	719	7	Adm74717 B. thurin
15	3484	92.6	719	4	AAB66912 Insectici
16	3484	92.6	719	6	AAB66912 Insectici
17	3442.5	91.5	710	4	AAB66912 Insectici
18	3363	89.4	719	3	AB07073 Bacillus
19	3341	88.8	719	2	AAB66907 Insectici
20	3257	86.6	1217	4	AAB66907 Insectici
21	2705	71.9	1208	4	AAB66907 Insectici
22	2419	64.3	1230	8	AdK98484 B thuring
23	2419	64.3	1230	8	AdK98489 B thuring
24	2419	64.3	1230	8	AdK98481 B thuring
25	2419	64.3	1230	8	AdK98491 B thuring

26	2419	64.3	1230	8	ADK98487
27	2417.5	64.3	1229	2	AAR54074
28	2417.5	64.3	1229	2	AAR54074
29	2417.5	64.3	1229	2	AAW35259
30	2417.5	64.3	1229	2	AAW35259
31	2417.5	64.3	1229	2	AAW35259
32	2417.5	64.3	1229	2	AAW35259
33	2417.5	64.3	1229	2	AAW35259
34	2417.5	64.3	1229	2	AAW35259
35	2417.5	64.3	1229	2	AAW35259
36	2417.5	64.3	1229	2	AAW35259
37	2417.5	64.3	1229	2	AAW35259
38	2417.5	64.3	1229	2	AAW35259
39	2417.5	64.3	1229	2	AAW35259
40	2417.5	64.3	1229	2	AAW35259
41	2417.5	64.3	1229	2	AAW35259
42	2417.5	64.3	1229	2	AAW35259
43	2417.5	64.3	1229	2	AAW35259
44	2087	55.5	1228	4	AAB84628
45	2087	55.5	1228	4	AAB84628

ALIGNMENTS

RESULT 1
AAB66911
ID AAB66911 standard; protein; 719 AA.

XX AAB66911;
AC
XX 12-APR-2001 (first entry)
DT
XX Insecticidal protein cryIIa5.
DE
XX Insecticide; transgenic plant; insect-resistance.
KW
XX Paecilomyces sp.
OS
XX
XX WO200100841-A1.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 23-JUN-2000; 2000WO-GB002457.
PF
XX
XX 29-JUN-1999; 99GB-00015215.
PR
XX 23-DEC-1999; 99GB-00030536.
PR
XX (ZENE) ZENECA LTD.
PA
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
PI
XX WPI; 2001-123015/13.
DR
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
PT
XX Claim 14; Page 62-64; 72pp; English.
PS
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66911 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;
SQ

Query Match 99.3%; Score 3736; DB 4; Length 719;
Best Local Similarity 99.7%; Pred. No. 1.2e-291;
Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Tue Feb 15 10:07:55 2005

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQIKISTY 119
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQIKISTY 119
QY 120 ARNKALTDLKGDLAVYHDSLESVGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179
DB 120 ARNKALTDLKGDLAVYHDSLESVGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKWY 239
QY 240 STGLNNLRGTNAESVRYNQFRDMLVLDLVALFPSTYDQYPIKTTAQLTREVTDA 299
DB 240 STGLNNLRGTNAESVRYNQFRDMLVLDLVALFPSTYDQYPIKTTAQLTREVTDA 299
QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
DB 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 360 WGGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLLTOPVNGVP 419
DB 360 WGGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLLTOPVNGVP 419
QY 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPPAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
DB 540 NTGTFGDIRVNIINPPPAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
DB 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2

AAE36275
ID AAE36275 standard; protein; 719 AA.

AC AAE36275;

XX 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN) SYNGENTA LTD.

XX

Vincent JL, Viner R;

WPI; 2003-175137/17.

New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

Claim 12; Page 53-56; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Sequence 719 AA;

Query Match 99.3%; Score 3736; DB 6; Length 719;
Best Local Similarity 99.7%; Pred. No. 1.2e-291;
Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECKMSEYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQIKISTY 119
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQIKISTY 119
QY 120 ARNKALTDLKGDLAVYHDSLESVGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179
DB 120 ARNKALTDLKGDLAVYHDSLESVGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKWY 239
QY 240 STGLNNLRGTNAESVRYNQFRDMLVLDLVALFPSTYDQYPIKTTAQLTREVTDA 299
DB 240 STGLNNLRGTNAESVRYNQFRDMLVLDLVALFPSTYDQYPIKTTAQLTREVTDA 299
QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
DB 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 360 WGGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLLTOPVNGVP 419
DB 360 WGGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLLTOPVNGVP 419
QY 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPPAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
DB 540 NTGTFGDIRVNIINPPPAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
DB 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3	
ID	AAB66908
XX	AAB66908 standard; protein; 719 AA.
AC	AAB66908;
DT	12-APR-2001 (first entry)
DB	Insecticidal protein cryIIa2.
XX	Insecticide; transgenic plant; insect-resistance.
OS	Paecilomyces sp.
XX	WO200100841-A1.
PD	04-JAN-2001.
PF	23-JUN-2000; 2000WO-GB002457.
XX	29-JUN-1999; 99GB-00015215.
PR	23-DEC-1999; 99GB-00030536.
XX	(ZENE) ZENECA LTD.
PI	Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI	Vincent JL, Lee MD;
XX	WPI; 2001-123015/13.
DR	Novel insecticidal protein obtained from species of Paecilomyces for
PT	controlling insects, and for insect-resistant transgenic plant
PT	production.
XX	Claim 14; Page 55-57; 72pp; English.
XX	The present invention relates to novel insecticidal proteins obtained
CC	from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC	insecticidal proteins can be used to produce transgenic plants, which are
CC	insect-resistant. Also, the insecticidal proteins are useful for
CC	controlling insects by providing them at a locus where insects feed
XX	Sequence 719 AA;
SQ	
Query Match	
Best Local Similarity 99.0%; Score 3724; DB 4; Length 719;	
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;	
Qy	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Qy	61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db	61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWEI-FMEHVEEINQKISTY 119
Qy	120 ARNKALTDLKGGLDALAVYHDSLESVWGNRNTRARSVVRSQYIALELMFVQKLPSFAVS 179
Db	120 ARNKALTDLKGGLDALAVYHDSLESVWGNRNTRARSVVRSQYIALELMFVQKLPSFAVS 179
Qy	180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239
Db	180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239
Qy	240 STGLNLRGNTAESWRYNQPRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTD 299
Db	240 STGLNLRGNTAESWRYNQPRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTD 299
Qy	300 ICTVHPHPSFTSTTWNNAFSAIAEAAVVRNPHLLDFLEQVTIYSLLRWSNTQYNNM 359
Db	300 ICTVHPHPSFTSTTWNNAFSAIAEAAVVRNPHLLDFLEQVTIYSLLRWSNTQYNNM 359

Qy	360 WGGHKLERTIGGTINISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNFLTQPVNGVP 419
Db	360 WGGHKLERTIGGTINISTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNFLTQPVNGVP 419
Qy	420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479
Db	420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479
Qy	480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILART 539
Db	480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILART 539
Qy	540 NTGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Db	540 NTGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Qy	600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Db	600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Qy	660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db	660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 4

AAB66909

ID AAB66909 standard; protein; 719 AA.

XX AAB66909;

DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa3.

XX Insecticide; transgenic plant; insect-resistance.

OS Paecilomyces sp.

XX WO200100841-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

PI Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

DR Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

PT production.

XX Claim 14; Page 55-57; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained

CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The

CC insecticidal proteins can be used to produce transgenic plants, which are

CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

SQ

Query Match

Best Local Similarity 99.4%; Score 3724; DB 4; Length 719;

Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

Qy 99.0%; Score 3724; DB 4; Length 719;

Best Local Similarity 99.4%; Pred. No. 1.1e-290;

Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

Tue Feb 15 10:07:55 2005

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I L F M E H V E E - I N Q K I S T Y 119
D b 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I I N Q K I S T Y 119
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V R S Q Y I A L E M F V Q K L P S F A V S 179
D b 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V R S Q Y I A L E M F V Q K L P S F A V S 179
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239
D b 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S H C V K W Y 239
QY 240 S T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299
D b 240 S T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299
QY 300 I G T V H P H P S T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359
D b 300 I G T V H P H P S T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359
QY 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419
D b 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419
QY 420 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479
D b 420 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479
QY 480 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539
D b 480 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539
QY 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599
D b 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599
QY 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659
D b 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659
QY 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
D b 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 5
AAE36273
ID AAE36273 standard; protein; 719 AA.
AC AAE36273;
XX 26-JUN-2003 (first entry)
DT
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.
XX
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
OS Bacillus thuringiensis.
XX
XX WO200298911-A2.
PD 12-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-GB002666.
PF
XX 07-JUN-2001; 2001GB-00013900.
PR
XX (SYGN) SYNGENTA LTD.
PA
XX

PI Vincent JL, Viner R;
XX WPI; 2003-175137/17.
D b New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
XX Claim 12; Page 47-50; 67pp; English.
PS
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 719 AA;

Query Match 99.0%; Score 3724; DB 6; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.1e-290;
Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I I N Q K I S T Y 119
D b 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I I N Q K I S T Y 119
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V R S Q Y I A L E M F V Q K L P S F A V S 179
D b 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V R S Q Y I A L E M F V Q K L P S F A V S 179
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239
D b 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S H C V K W Y 239
QY 240 S T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299
D b 240 S T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299
QY 300 I G T V H P H P S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359
D b 300 I G T V H P H P S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359
QY 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419
D b 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419
QY 420 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479
D b 420 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479
QY 480 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539
D b 480 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539
QY 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599
D b 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599
QY 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659
D b 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659
QY 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
D b 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 6					
ID	AAE36272	standard; protein; 719 AA.			
XX	AC				
XX	AAE36272;				
XX	AC				
DT	26-JUN-2003	(first entry)			
XX					
DE	B. thuringiensis	insecticidal crystal endotoxin (CRY) protein, cryIIa2.			
XX	KW	Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.			
XX	OS	Bacillus thuringiensis.			
PX	WO200298911-A2.				
XX					
PD	12-DEC-2002.				
XX					
PF	30-MAY-2002; 2002WO-GB002666.				
XX					
PR	07-JUN-2001; 2001GB-00013900.				
XX					
PA	(SYGN) SYNGENTA LTD.				
XX					
PI	Vincent JL, Viner R;				
XX					
DR	WPI; 2003-175137/17.				
XX					
PT	New insecticidal protein comprising an X-glycine motif at the amino-				
PT	terminus, useful as an active ingredient of a pesticide.				
XX					
PS	Claim 12; Page 44-47; 67pp; English.				
XX					
CC	The invention relates to insecticidal protein comprising an X-glycine				
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the				
CC	invention are useful for producing plants or plant parts that are				
CC	resistant to insects. The protein or synergistic combination is useful as				
CC	an active ingredient of a pesticide or for controlling insects.				
CC	Antibodies raised to the insecticidal proteins can be used to identify				
CC	other proteins with insecticidal activity. The present sequence is				
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This				
CC	sequence is used in the invention				
XX					
SQ	Sequence 719 AA;				
	Query Match	99.0%; Score 3724; DB 6; Length 719;			
	Best Local Similarity	99.3%; Pred. No. 1.1e-290;			
	Matches 715; Conservative	2; Mismatches 1; Indels 2; Gaps 2;			
Qy	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNINHEDECLMSEYENVEPFFVASTI	60		
Dd	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNINHEDECLMSEYENVEPFFVASTI	60		
Qy	61	QTGIGIAGKILGTGLGVPPFAGQVASLYSFILGELWPKGKNOEILFMHVTEE-INOKISTY	119		
Dd	61	QTGIGIAGKILGTGLGVPPFAGQVASLYSFILGELWPKGKNOEI-FMEHVSEIINOIKISTY	119		
Qy	120	ARNKALTDLKGDLAVYHDLSLESVWGVRNTRARSVVPSOYIALELMFVKLPSPFAVS	179		
Dd	120	ARNKALTDLKGDLAVYHDLSLESVWGVRNTRARSVVKSQYIALELMFVKLPSPFAVS	179		
Qy	180	GEEVPLLPPIYAQAANHLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSDHCVKWY	239		
Dd	180	GEEVPLLPPIYAQAANHLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSDHCVKWY	239		
Qy	240	STGLNNLRGTNAESWVRYNQFRDMTLMVLDDLVALFPSPYDTQMYPICKTTAQLTREYITDA	299		
Dd	240	STGLNNLRGTNAESWVRYNQFRDMTLMVLDDLVALFPSPYDTQMYPICKTTAQLTREYITDA	299		
Qy	300	IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHELLDFLEQVTIYSLLSRWSNTQYMMN	359		
Dd	300	IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHELLDFLEQVTIYSLLSRWSNTQYMMN	359		

QY	360	WGGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTQPVNGVP	419
DB	360	WGGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTQPVNGVP	419
QY	420	RVDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSSENLPEATGQPNYESYSHRLSHIGLI	479
DB	420	RVDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSSENLPEATGQPNYESYSHRLSHIGLI	479
QY	480	SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
DB	480	SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
QY	540	NTGTFGDIRVINPFPFAQRYRVRIRYASTDQLQHTSINGKAINQGNFSATMNRGDLDDY	599
DB	540	NTGTFGDIRVINPFPFAQRYRVRIRYASTDQLQHTSINGKAINQGNFSATMNRGDLDDY	599
QY	600	KTRFTVGFTTFFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPVEVTEAEYDFEKAQEK	659
DB	600	KTRFTVGFTTFFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPVEVTEAEYDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719
DB	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 7			
ADR89421			
ID	ADR89421 standard; protein; 719 AA.		
XX			
AC	ADR89421;		
XX			
DT	18-NOV-2004 (first entry)		
XX			
DE	cryIIa.		
XX			
KW	delta-endotoxin; delta-endotoxin associate polypeptide;		
KW	expression cassette; transformation; transgenic; plant; bacteria;		
KW	lepidoptera; coleoptera; pest; pesticide; resistance;		
KW	pesticidal activity.		
XX			
OS	Bacillus thuringiensis.		
XX			
PN	WO2004074462-A2.		
XX			
PD	02-SEP-2004.		
XX			
PF	20-FEB-2004; 2004WO-US005829.		
XX			
PR	20-FEB-2003; 2003US-0448632P.		
PR	20-FEB-2003; 2003US-0448633P.		
PR	20-FEB-2003; 2003US-0448797P.		
PR	20-FEB-2003; 2003US-0448806P.		
PR	20-FEB-2003; 2003US-0448810P.		
PR	20-FEB-2003; 2003US-0448812P.		
PR	19-FEB-2004; 2004US-00781979.		
PR	19-FEB-2004; 2004US-00782020.		
PR	19-FEB-2004; 2004US-00782096.		
PR	19-FEB-2004; 2004US-00782141.		
PR	19-FEB-2004; 2004US-00782570.		
PR	19-FEB-2004; 2004US-00783417.		

XX This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

XX Sequence 719 AA;

Query Match 99.0%; Score 3724; DB 8; Length 719;
Best Local Similarity 99.3%; Pred. No. 1.1e-290;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

QY 120 ARNKALTDLKGDLAVYHDSLESWVGNNRNRARSVRSQVYALFVQKLPSPFAYS 179
DB 120 ARNKALTDLKGDLAVYHDSLESWVGNNRNRARSVRSQVYALFVQKLPSPFAYS 179

QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWY 239

QY 240 STGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREYVYTD 299
DB 240 STGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREYVYTD 299

QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359
DB 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359

QY 360 WGGHKLFEFTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVNGVP 419
DB 360 WGGHKLFEFTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVNGVP 419

QY 420 RVDPHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RVDPHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILERT 539
DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILERT 539

QY 540 NTGFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMRGDLDY 599
DB 540 NTGFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMRGDLDY 599

QY 600 KTFRTVGTTFPESFLDVOSTFTIGAMNPSGNEVYIDRIEFPVPEVYEAEDFEKAQEK 659
DB 600 KTFRTVGTTFPESFLDVOSTFTIGAMNPSGNEVYIDRIEFPVPEVYEAEDFEKAQEK 659

QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 8

AAB66910
ID AAB66910 standard; protein; 719 AA.
XX
AC AAB66910;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa4.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE) ZENECA LTD.
XX
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
XX WPI; 2001-123015/13.
XX
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
XX Claim 14; Page 60-62; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66910 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
XX Sequence 719 AA;

Query Match 98.9%; Score 3720; DB 4; Length 719;
Best Local Similarity 99.2%; Pred. No. 2.3e-290;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

QY 120 ARNKALTDLKGDLAVYHDSLESWVGNNRNRARSVRSQVYALFVQKLPSPFAYS 179
DB 120 ARNKALTDLKGDLAVYHDSLESWVGNNRNRARSVRSQVYALFVQKLPSPFAYS 179

QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWY 239

QY 240 STGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREYVYTD 299
DB 240 STGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDQMPYIKTTAQLTREYVYTD 299

QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359
DB 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359

QY 360 WGGHKLFEFTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVNGVP 419

Db 360 WGGHKLFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVTSLAGLNLFLTQPVNGVP 419
Qy 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNINPPPAQRVVRIRYASTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPPAQRVVRIRYASTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEK 659
Db 600 KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 9
AAE36274
ID AAE36274 standard; protein; 719 AA.

AC AAE36274;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX

OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT
PS Claim 12; Page 50-53; 67pp; English.
PS

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
CC

SQ Sequence 719 AA;

Query Match 98.9%; Score 3720; DB 6; Length 719;
Best Local Similarity 99.2%; Pred. No. 2.3e-290;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60
Qy 61 QTGIGTAGKILGTGVPFAGQVASYLSFTLGELWPKGKNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGTAGKILGTGVPFAGQVASYLSFTLGELWPKGKNQWEI-FMEHVEEINQKISTY 119
Qy 120 ARNKALTDLKGLDALAVYHDSLESVGNRNNTARSVVRYSQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALTDLKGLDALAVYHDSLESVGNRNNTARSVVRYSQYIALELMFVQKLPSFAVS 179
Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCVKMY 239
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCVKMY 239
Qy 240 STGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFSPYDTOMYPIKTTAQLTREVYTDA 299
Db 240 STGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFSPYDTOMYPIKTTAQLTREVYTDA 299
Qy 300 IGTVHPHPSTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
Db 300 IGTVHPHPSTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNM 359
Qy 360 WGGHKLFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVTSLAGLNLFLTQPVNGVP 419
Db 360 WGGHKLFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVTSLAGLNLFLTQPVNGVP 419
Qy 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNINPPPAQRVVRIRYASTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPPAQRVVRIRYASTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEK 659
Db 600 KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 10
AAU02095
ID AAU02095 standard; protein; 719 AA.

XX AC AAU02095;
XX
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.

XX Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle; mutant; mutein.
XX
OS Bacillus thuringiensis.

XX Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..719
FT /label= Mature_CryIIa

XX EP1099760-A1.
XX
PD 16-MAY-2001.

XX	09-NOV-1999;	99EP-00203723.	600	KTFTVGTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEK	659
PF			600	KTFTVGTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEK	659
XX	09-NOV-1999;	99EP-00203723.	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM	719
PR			660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM	719
XX	(CPRO-) CPRO-DLO CENT PLANTENVERDEBELINGS REPROD.				
PA	De Maagd RA, Bosch HJ;				
XX					
XX	WPI; 2001-337141/36.				
DR	N-PSDB; AAS04855.				
XX	New hybrid Bacillus thuringiensis hybrid toxins comprising structural				
PT	domains derived from at least 2 different crystal proteins, such as				
PT	CryIIa and CryIIb, and having insecticidal activity, useful for combating				
PT	insects.				
XX					
PS	Example; Page 30-32; 43pp; English.				
XX					
CC	The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA				
CC	encoding which was mutated to allow cloning of domain III or domains I				
CC	and II, to make the hybrid protoxins of the invention. The hybrid toxins				
CC	of the invention, having structural domains I, II and III in this order				
CC	starting from the N-terminal derived from at least 2 different crystal				
CC	proteins, are useful for protecting plants against pest insects, e.g.				
CC	moths, butterflies and Colorado potato beetle or for combating insects				
XX					
SQ	Sequence 719 AA;				
	Query Match 98.8%; Score 3715; DB 4; Length 719;				
	Best Local Similarity 99.2%; Pred. No. 5.7e-290;				
	Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;				
QY	1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHEDCLKMEYENVEPVSASTI	60			
DB	1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHEDCLKMEYENVEPVSASTI	60			
QY	61 QTGIGIAGKILGTLPVFPAGQVASYSLFELGELWPKGNQWELFMEHVEE-INQKISTY	119			
DB	61 QTGIGIAGKILGTLPVFPAGQVASYSLFELGELWPKGNQWELFMEHVEE-INQKISTY	119			
QY	120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVRVRSQYIALLELMFVKLPSPFAVS	179			
DB	120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVRVRSQYIALLELMFVKLPSPFAVS	179			
QY	180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNRQVERAGDYSHCVKWY	239			
DB	180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNRQVERAGDYSHCVKWY	239			
QY	240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTQAQLTREYVYTD	299			
DB	240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTQAQLTREYVYTD	299			
QY	300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDPLEQVITYLSLLSRWSNTQYMMN	359			
DB	300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDPLEQVITYLSLLSRWSNTQYMMN	359			
QY	360 WGGHKLFRITIGTTLNISTQSTNTSINPVLPTFTSRDVRTSLAGNLFLTQPVNGVP	419			
DB	360 WGGHKLFRITIGTTLNISTQSTNTSINPVLPTFTSRDVRTSLAGNLFLTQPVNGVP	419			
QY	420 RVDPHWKFVTHPIASDNFYYPGAGIGTQLQDSENELPPEATGQPNYSYSHRLSHGLI	479			
DB	420 RVDPHWKFVTHPIASDNFYYPGAGIGTQLQDSENELPPEATGQPNYSYSHRLSHGLI	479			
QY	480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539			
DB	480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539			
QY	540 NTGTFGDIRVNNPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY	599			
DB	540 NTGTFGDIRVNNPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY	599			

QY	600	KTFTVGTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEK	659
DB	600	KTFTVGTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM	719
DB	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM	719
	RESULT 11		
ID	AAR08041		
XX	AAR08041 standard; protein; 719 AA.		
AC	AAR08041;		
XX			
DT	24-OCT-2003 (revised)		
DT	25-MAR-2003 (revised)		
DT	27-FEB-1991 (first entry)		
XX			
DE	81 kD endotoxin deduced from DNA carried on pJH12.		
XX			
KW	Crystal; insecticide; toxin; delta endotoxin.		
XX			
OS	Bacillus thuringiensis; JHCC 4353 and 4835.		
XX			
PN	WO9013651-A.		
XX			
PD	15-NOV-1990.		
XX			
PF	09-MAY-1989; 89GB-00010624.		
XX			
PR	09-MAY-1989; 89GB-00010624.		
XX			
PA	(ICIL) IMPERIAL CHEM IND PLC.		
XX			
PI	Blenk RG, Ely S, Tailor RH, Tippet JM;		
XX			
DR	WPI; 1990-361486/48.		
DR	N-PSDB; AAQ06636.		
XX			
PT	Bacillus thuringiensis strains - used for producing an endotoxin for		
PT	protecting plants against insects, partic. Lepidoptera and Coleoptera.		
XX			
PS	Claim 5; Fig 5-10; 66pp; English.		
XX			
CC	The sequence carried on pJH12 which was isolated from B. thuringiensis		
CC	strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can		
CC	be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,		
CC	or bacteriophage EMBl4 vector (NCIB 40279) or E.coli strain Bl21/pJH11		
CC	(NCIB 40275). The delta-endotoxin produced by the transformants can be		
CC	used in formulations for combatting Lepidoptera and Coleoptera pests.		
CC	(Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to		
CC	standardise OS field)		
XX			
SQ	Sequence 719 AA;		
	Query Match 98.5%; Score 3703; DB 2; Length 719;		
	Best Local Similarity 98.9%; Pred. No. 5.3e-289;		
	Matches 712; Conservative 2; Mismatches 4; Indels 2; Gaps 2;		
QY	1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHEDCLKMEYENVEPVSASTI	60	
DB	1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEHEDCLKMEYENVEPVSASTI	60	
QY	61 QTGIGIAGKILGTLPVFPAGQVASYSLFELGELWPKGNQWELFMEHVEE-INQKISTY	119	
DB	61 QTGIGIAGKILGTLPVFPAGQVASYSLFELGELWPKGNQWELFMEHVEE-INQKISTY	119	
QY	120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVRVRSQYIALLELMFVKLPSPFAVS	179	
DB	120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVVRVRSQYIALLELMFVKLPSPFAVS	179	
QY	180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNRQVERAGDYSHCVKWY	239	

Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWY 239
Qy 240 STGLNLRGTNAESWRYNQFRDRMTLMVLDLVALFPPSYDTOMYPIKTTAQLTREVTDA 299
Db 240 STGLNLRGTNAESWRYNQFRDRMTLMVLDLVALFPPSYDTOMYPIKTTAQLTREVTDA 299
Qy 300 IGTVHPHPSFTSTTWNNAPSAIEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNM 359
Db 300 IGTVHPHPSFTSTTWNNAPSAIEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNM 359
Qy 360 WGGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419
Db 360 WGGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419
Qy 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRTNTEIENSIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEIENSIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNINPPFAQRYRIRYASTDQLQHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPFAQRYRIRYASTDQLQHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRTVGTTPFPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
Db 600 KTFRTVGTTPFPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12

AAB66907
ID AAB66907 standard; protein; 718 AA.
XX
AC AAB66907;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIaI.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
DR
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
PT
PS Claim 12; Page 42-44; 67pp; English.
XX

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as

CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 718 AA;

Query Match 98.2%; Score 3692.5; DB 6; Length 718;
Best Local Similarity 98.9%; Pred. No. 3.7e-288;
Matches 712; Conservative 2; Mismatches 3; Indels 3; Gaps 3;

Qy 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNKTDIELQNIHEDCLKMSEYENVEPVSASTI 60
Db 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNKTDIELQNIHEDCLKMSEYENVEPVSASTI 60
Qy 61 QTGIGTAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEILFMEHVEE-INQIKISTY 119
Db 61 QTGIGTAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEI-FMEHVEEIIINQIKISTY 119
Qy 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVVRQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVVRQYIALELMFVQKLPSFAVS 179
Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWY 239
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWY 239
Qy 240 STGLNLRGTNAESWRYNQFRDRMTLMVLDLVALFPPSYDTOMYPIKTTAQLTREVTDA 299
Db 240 STGLNLRGTNAESWRYNQFRDRMTLMVLDLVALFPPSYDTOMYPIKTTAQLTREVTDA 299
Qy 300 IGTVHPHPSFTSTTWNNAPSAIEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNM 359
Db 300 IGTVHPHPSFTSTTWNNAPSAIEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNM 359
Qy 360 WGGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419
Db 360 WGGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVP 419
Qy 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRTNTEIENSIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEIENSIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNINPPFAQRYRIRYASTDQLQHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPFAQRYRIRYASTDQLQHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRTVGTTPFPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
Db 600 KTFRTVGTTPFPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 13

AAB66907
ID AAB66907 standard; protein; 718 AA.
XX
AC AAB66907;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIaI.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX

Db 120 ARNIALADLKGGLDALAVYHESLESWIKRNNARATSVKSYQIALELLFVQKLPSFAVS 179
Qy 180 GBEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVRAGDYSDDHCVKMY 239
Db 180 GBEVPLLPPIYAQAANLHLLLRDASVFGKEWGLSNSQISTFYNNRQVERTSDYSDHCVKMY 239
Qy 240 STGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVYTDA 299
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Qy 300 IGTVHPHPSFTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 359
Db 300 IGTVHPNASFASTTWNNNAPSFSAIESAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 359
Qy 360 WGGHKLFRITGGTLNISTQSTNTSINPVTLPTSTRDYRTESLAGLNLFLTQPVNGVP 419
Db 360 WGGHRLFRITGGVLTSTQSTNTSINPVTLPTSTRDYRTESLAGLNLFLTQPVNGVP 419
Qy 420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLI 479
Db 420 RVDFHWKFATLPIASDNFYYPGYAGVGTQLODSENELPPEATTGPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNIINPPPAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 NTGTFGDIRVNIINPPPAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRTVGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659
Db 600 KTFRTVGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKIHERNM 719
Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKIHERNM 719

RESULT 15

AAB66912 standard; protein; 719 AA.

XX AAB66912;

AC 12-APR-2001 (first entry)

XX Insecticidal protein cryIIb1.

DE Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

PN 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

PI Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.

XX

PS Claim 14; Page 64-66; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;

Query Match 92.6%; Score 3484; DB 4; Length 719;
Best Local Similarity 92.2%; Pred. No. 2.3e-271;
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDLSLKNKTDIELQNIHEDCLMKSEYENVEPVFSASTI 60

Db 1 MKLKNPDKHQSLSSNAKVDKIATDLSLKNKTDIELKNMNEDEYLRMSEHESIDPFVSASTI 60

Qy 61 QTGIGTAGKILGTGVPFAGQVASYLSYFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

Db 61 QTGIGTAGKILGTGVPFAGQIASLYSIFILGELWPKGKSQWEI-FMEHVEEIIINQKILTY 119

Qy 120 ARNKALTDLKGGLDALAVYHDSLESWGNRNNTRARSVVRYSQYIALELMFVQKLPSFAVS 179

Db 120 ARNKALSDLKGGLDALAVYHESLESWVRNNTARSVVNQYIALELMFVQKLPSFAVS 179

Qy 180 GBEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVRAGDYSDDHCVKMY 239

Db 180 GBEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVRTRDYSDDHCVKMY 239

Qy 240 STGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVYTDA 299

Db 240 NTGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVYTDA 299

Qy 300 IGTVHPHPSFTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYNNM 359

Db 300 IGTVHPNQAFSTTWNNNAPSFSAIEAAVIRSPLLDFLEQVTIYSLLSRWSTNTQYNNM 359

Qy 360 WGGHKLFRITGGTLNISTQSTNTSINPVTLPTSTRDYRTESLAGLNLFLTQPVNGVP 419

Db 360 WGGHRLFRITGGVLTSTQSTNTSINPVTLPTSTRDYRTESLAGLNLFLTQPVNGVP 419

Qy 420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLI 479

Db 420 RVDFHWKFPTLPIASDNFYYPGYAGVGTQLODSENELPPEATTGPNYESYSHRLSHIGLI 479

Qy 480 SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539

Db 480 SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539

Qy 540 NTGTFGDIRVNIINPPPAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599

Db 540 NTGTFGDIRVNIINPPPAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599

Qy 600 KTFRTVGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659

Db 600 KTFRTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659

Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKIHERNM 719

Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKIHERNM 719

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Job time : 101.351 secs

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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.6029 Seconds
(without alignments)
3350.901 Million cell updates/sec

Title: US-10-019-823B-58
Perfect score: 3761
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3724	99.0	719	16	US-10-782-141-8
3	3442.5	91.5	710	15	US-10-428-961-42
4	2250.5	59.8	1228	16	US-10-809-953-10
5	2236.5	59.5	1207	10	US-09-988-462-7
6	2157.5	57.4	1227	15	US-10-428-961-63
7	2142.5	57.0	1186	9	US-09-826-660-23
8	2087	55.5	1228	15	US-10-428-961-38
9	2087	55.5	1228	15	US-10-614-524-2
10	1909.5	50.8	643	9	US-09-826-660-25
11	1694.5	45.1	1167	14	US-10-089-678-1
12	1658.5	44.1	653	15	US-10-428-961-6
13	1643.5	43.7	1157	16	US-10-782-141-16

14	1485	39.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1485	39.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1485	39.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1469	39.1	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1469	39.1	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1469	39.1	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1459.5	38.8	1156	14	US-10-099-285-72	Sequence 72, Appl
21	1459.5	38.8	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1443	38.4	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1443	38.4	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1443	38.4	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1443	38.4	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1443	38.4	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1443	38.4	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1443	38.4	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1443	38.4	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1443	38.4	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1443	38.4	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1443	38.4	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1443	38.4	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1443	38.4	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1438	38.2	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1436	38.2	1177	14	US-10-102-469-24	Sequence 24, Appl
37	1435	38.2	1177	14	US-10-782-141-6	Sequence 6, Appli
38	1419.5	37.7	1176	16	US-09-837-961-2	Sequence 2, Appli
39	1407.5	37.4	1176	11	US-10-825-751-2	Sequence 2, Appli
40	1407.5	37.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1376	36.6	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1355	36.0	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1355	36.0	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1355	36.0	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1355	36.0	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 99.0%; Score 3724; DB 16; Length 719;
Best Local Similarity 99.3%; Pred. No. 1.6e-306;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

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DB	1	MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI	60
QY	61	QTGIGIAGKILGTGLGVPAGQVASFILGELWPKGNQWEILFMEHVEE-INOIKISTY	119
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360 WGGHKLFRFTIGGTINISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP 419
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540 NTGTFGDIRVNNPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDLDY 599
600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYEAEDFEKAQEK 659
600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYEAEDFEKAQEK 659
660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3

US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rugar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
; FEATURE:

120 ARNKALTDLKGGLDALAVYHDSLESVWGNRNTRARSVVRSSQYIALELMFVQKLPSFAVS 179
120 ARNKALTDLKGGLDALAVYHDSLESVWGNRNTRARSVVRSSQYIALELMFVQKLPSFAVS 179
180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNNROVERAGDYSCHCVKWY 239
180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNNROVERAGDYSCHCVKWY 239
240 STGLNLRGTNAESWVRYNQFRDMLMVLVALPSPSYDTOMYPIKTTAQLTREVTDA 299
240 STGLNLRGTNAESWVRYNQFRDMLMVLVALPSPSYDTOMYPIKTTAQLTREVTDA 299
300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNM 359
300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNM 359
360 WGGHKLFRFTIGGTINISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP 419
360 WGGHKLFRFTIGGTINISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP 419
420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDLRRT 539
480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDLRRT 539
540 NTGTFGDIRVNNPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDLDY 599
540 NTGTFGDIRVNNPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDLDY 599
600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYEAEDFEKAQEK 659
600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYEAEDFEKAQEK 659
660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2

US-10-782-141-8
; Sequence 8, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 719
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
US-10-782-141-8

Query Match 99.0%; Score 3724; DB 16; Length 719;
Best Local Similarity 99.3%; Pred. No. 1.6e-306;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;
QY 1 MKLNQDKHQSFSSNAKVDKISTDLSKNETDIELQNIHEDCLQMSYEYENVEPFFVSASTI 60

NAME/KEY: misc feature
LOCATION: (2007)..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 91.5%; Score 3442.5; DB 15; Length 710;
Best Local Similarity 91.9%; Pred. No. 1.2e-282;
Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;

QY 1 MRLKQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60
DB 1 MKSKQNMHQSLNNATVDKNTFGSLENNNTLQNFH-----EGIEPFFVSASTI 51
QY 61 QTGIGIAGKILGTGVPAGQVASYLSPILGELWPKGNQWELFMEHVEE-INOKISTY 119
DB 52 QTGIGIAGKILGNLGVFPAGQVASYLSPILGELWPKGNQWELFMEHVEE-INOKISTY 110
QY 120 ARNKALTDKGLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPSPFVS 179
DB 111 ARNKALADLKLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPSPFVS 170
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNNQVERAGDYSDHCVKWY 239
DB 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNNQVERAGDYSDHCVKWY 230
QY 240 STGLNNLRGTNAESWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVTD 299
DB 231 NTGLNRLMGNNAESWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVTD 290
QY 300 IGVHPPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYLLSWSNTQYMMN 359
DB 291 IGVHPPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYLLSWSNTQYMMN 350
QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLFVTPVNGVP 419
DB 351 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLFVTPVNGVP 410
QY 420 RVDFHFWKFTHTPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLI 479
DB 411 RVDFHFWKFTHTPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLI 470
QY 480 SASHVKALVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRR 539
DB 471 SASHVKALVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRR 530
QY 540 NTGTFGDIRVNIWPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATNRGDL 599
DB 531 NTGTFGDIRVNIWPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATNRGDL 590
QY 600 KTFRTVGTFTTFFSFDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEE 659
DB 591 KTFRTVGTFTTFFSFDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEE 650
QY 660 VTALFTSTNPRGLTKDVXHYHIDQVSNLVESLSDKFLYDEKRELFEIVKYANELHIERNM 719
DB 651 VTALFTSTNPRGLTKDVXHYHIDQVSNLVESLSDKFLYDEKRELFEIVKYANELHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US2004018125A1
GENERAL INFORMATION:
APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809, 953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 59.8%; Score 2250.5; DB 16; Length 1228;
Best Local Similarity 62.5%; Pred. No. 3.4e-181;
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

QY 23 TDSLKNETDIELQNH-----EDCLKMEYENVEPFFVSASTIQTGIGIAGKI 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVGTGINIAGRI 61
QY 71 LGTLGVFPAGQVASYLSPILGELWPKGNQWELFMEHVEE-INOKISTYARNKALTDLK 129
DB 62 LGVLGVFPAGQVASYLSPILGELWPKGNQWELFMEHVEE-INOKISTYARNKALTDLK 120
QY 130 GLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPSPFVSAGEVPLLPY 189
DB 121 GLGDSFRAYQQSLEDWLENRDDARTSRVLTQYIALELDLFLNAMPFAIRNQEVPLLMVY 180
QY 190 AQAANLHLLLRDASIFGKEMGLSSSEISTFYNNQVERAGDYSDHCVKWYSTGLNLRGT 249
DB 181 AQAANLHLLLRDASIFGSEFGTQSEIQRYYERQVTRDYSDYCVIEWYNTGLNLRGT 240
QY 250 NAESWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVTDALGTGTHPHPSF 309
DB 241 NAASWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVTDALGTGTHPHPSF 298
QY 310 TSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYLLSWSNTQYMMNMGCHLEFRT 369
DB 299 ASMNWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYLLSWSNTQYMMNMGCHLEFRT 358
QY 370 IGGTILNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLF--LTQPVNGVPRVDHFWK 427
DB 359 IGGTILNISTQGSTNTSINPVTLPFTSRDVRYSYTESLAGNLF--LTQPVNGVPRVDHFWK 416
QY 428 VTHP-----IASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLISAS 482
DB 417 -TNQNISDRGTANYSQP-YESPGLQKDSLELPPETTERNYESYSHRLSHIGLISAS 474
QY 483 HVKALVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542
DB 475 RVNVPVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 534
QY 543 TFGDIRVNIWPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATNRGDLKYTF 602
DB 535 GFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTAVNFRFLRTMNSGDELKYNF 594
QY 603 RTVGFTTFFSFDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662
DB 595 VRRFTTFTTFTQIQTIDRTSIQGLSGNGEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 654
QY 663 LFTSTNPRGLTKDVXHYHIDQVSNLVESLSDKFLYDEKRELFEIVKYANELHIERNM 719
DB 655 LFTSTNPRGLTKDVXHYHIDQVSNLVESLSDKFLYDEKRELFEIVKYANELHIERNM 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 7:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7
Query Match 59.5%; Score 2236.5; DB 10; Length 1207;
Best Local Similarity 64.1%; Pred. No. 5.1e-180;
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;

QY 40 EDCLMKSEYENVPFVSASTIQTGIGTAGKILGTGVFPAGQVASYLSFILGELWPKGN 99
DB 10 EDSLCAEAGNNIDPFVSASTVQTGINAGRLGLVGLVFPAGQVASYLSFILGELWPKGRD 69
QY 100 QWEILFMEHVEE-INQKISTYARNKALTDLKLGLDALAVYHDSLSWVGNRNTRARSVV 158
DB 70 QWEI-FLEHVEQLNQITENARTALRQGLGDSFRAVQOSLEDWLENRDARTSVL 128
QY 159 RSQYIALELMFVQKLPSFAVSGREVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIS 218
DB 129 YQYIALELDLFLNAMPFAIRNQEVPLMVAQAANLHLLLRDASLFGSEFGLTSQEIQ 198
QY 219 TFYNRQVAGADYSDHCVKWYSTGLNLRGTNAESWRYNQRFRDMLVLDLVALFPSY 278
DB 189 RYERQVTRDYSYDCVWYNTGLNLRGTNAESWRYNQRFRDMLVLDLVALFPSY 248
QY 279 DTQMPYIKTAQLTRREVYDAIGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDF 338

DB 249 DTRTYPINTSAQUTREVYDAIGAT--GVNWSMWNNAAPSFAIEAAVVRNPHLLDF 306
QY 339 LEQVTIYLLSRWSNTQYMMWGGHKLFRITGIGTLNISTQGSTNTSINPVTLPFTSRDV 398
DB 307 LEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFASRDV 366
QY 399 YRTESLAGLNLF--LTQPVNGVPRVDVFWKFWTHP-----IASDNFYYPGVAGIGTQLOD 451
DB 367 YRTESYAGVLLWGIYLEPIHGVPTVRNF---TNPQNISDRGTANYSQP-YESPGLQLKD 422
QY 452 SENELPPEATQPNYESYSHRLSHIGLSASHVYKALVYSWTHRSADRTNTEPNSTIQTIP 511
DB 423 SETELPPETTERPNYESYSHRLSHIGILQSRVNVVYVSWTHRSADRTNTEPNSTIQTIP 482
QY 512 LVKAFNLSSGAAVVRGPGFTGGDILRRNTNTGFGDIRVNIINPPFAQRYRVRIYASTTDL 571
DB 483 MVKASELPQGTTVVRGPGFTGGDILRRNTNTGFGDIRVNIINPPFAQRYRVRIYASTTDL 542
QY 572 QPHTSINGKAINQGNFSAATMNRGDLVDYKTRFTVGFPTTFFSFLDVQSTFTTIGAMNFSGN 631
DB 543 DFFVSRGGTTVNNFRFLRTMNSGDELKYGNVRRAFITPFTTQIQDIIRTSIQGLSGNG 602
QY 632 EYIDRIEFVPEVTVYEAEDFEKAQKVTALTSTNPRGLKTDVVDYHIDQVSNLVESL 691
DB 603 EYIDKIEIIPVATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 662
QY 692 SDFYLDKRELFEIVKYANELHIERNM 719
DB 663 SDFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6

US-10-428-961-63
Sequence 63, Application US/10428961
Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupa, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201--1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent in version 3.2
SEQ ID NO 63
LENGTH: 1227
TYPE: PRT
ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 57.4%; Score 2157.5; DB 15; Length 1227;
Best Local Similarity 59.0%; Pred. No. 2.6e-173;
Matches 422; Conservative 103; Mismatches 175; Indels 15; Gaps 5;

QY 13 SSSNAKVDKISTDSLKN-----ETDIELQNIHEDCLKMSYENVEPVFSASTIQTGIG 65
DB 7 NENEIINALSIPAVSNHSAQMLSTDARI-----EDSLCAEAGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTLGVFPAGQVASYLSFILGELWPKGNQWELFMEHVEE-INQKISTYARNKA 124
DB 62 IAGRILGLVGLVFPAGQVASYLSFILGELWPKGRDPWEI-FLEHVEHLIRQOVNTTRDTA 120
QY 125 LTDLKGLGDALAVYHDSLSWVGNRNTRARSVVRSQYIALELMFVQKLPSFAVSGEEVP 184

Query Match 55.5%; Score 2087; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.5e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLMKSEYENVEPFSASTIQTGIGIAGKI 70
7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
67 LGVLGVPPAGQIASFYSLFVGLWPRGRDQWEI-FLEHVEQLINQOITENARNALTALRLQ 125
130 GLGDALAVYHDSLESWGNRNTRARSVRSOYIALELMFVQKLPSPAVSGEEVPLLPY 189
126 GLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPFLFAIRNQEVPLLMVY 185
190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKXWYSTGLNNLRGT 249
186 AQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEYNTGLNSLRGT 245
250 NAESWVRYNQFRDMLMVLVALFPSTQYPIKTTAQLTREYVYDAIGTGVHPHPSF 309
246 NAASWVRYNQFRDLTLGVLDLVALFPSTQYPIKTTAQLTREYVYDAIGT--GVNM 303
310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 369
304 ASMNWNNNAPSFSAIETAVIRSPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 363
370 IGGTLNISTQGSTNTSINPVLPTSRDVRTESLAGLNLF--LTQPVNGVPRVDFHWKF 427
364 IGGGLNTSTHGSTNTSINPVLSPFRSDVYWTESYAGVLLWGIYLEPIHGVTPTVRFRFN 423
428 V--THPIASDNFYPGYAGIGTQLODSENLPEATGPQPNYESYSHRLSHIGLISASHVK 485
424 PONTFERGTANYSQP-YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISQSRVH 482
486 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTG 545
483 VPVYSWTHRSADRTNTISSDITQIPLVKSFLNLSGTSVSGPGFTGGDIIRTNVNGSVL 542
546 DIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYKTRTV 605
543 SMGLNFNNTSLQRYRVRVRYAASQTMVLRTVVGSGSTTFDQGFPTMSANESLTSQSFRA 602
606 GFTTPPSFLDVQSTFTIGANWSSGNEVYIDRIEFVPVEVYEAAYDFEKAQEKVTAFT 665
603 EFPVGISASGSQ-TAGISISNNAGRTFHFDPKIEFIPITATFEAYDLERAQAVNALFT 661
666 STNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
662 NTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 715

Query Match 55.5%; Score 2087; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.5e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLMKSEYENVEPFSASTIQTGIGIAGKI 70
7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
67 LGVLGVPPAGQIASFYSLFVGLWPRGRDQWEI-FLEHVEQLINQOITENARNALTALRLQ 125
130 GLGDALAVYHDSLESWGNRNTRARSVRSOYIALELMFVQKLPSPAVSGEEVPLLPY 189
126 GLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPFLFAIRNQEVPLLMVY 185
190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKXWYSTGLNNLRGT 249
186 AQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEYNTGLNSLRGT 245
250 NAESWVRYNQFRDMLMVLVALFPSTQYPIKTTAQLTREYVYDAIGTGVHPHPSF 309
246 NAASWVRYNQFRDLTLGVLDLVALFPSTQYPIKTTAQLTREYVYDAIGT--GVNM 303
310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 369
304 ASMNWNNNAPSFSAIETAVIRSPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 363
370 IGGTLNISTQGSTNTSINPVLPTSRDVRTESLAGLNLF--LTQPVNGVPRVDFHWKF 427
364 IGGGLNTSTHGSTNTSINPVLSPFRSDVYWTESYAGVLLWGIYLEPIHGVTPTVRFRFN 423
428 V--THPIASDNFYPGYAGIGTQLODSENLPEATGPQPNYESYSHRLSHIGLISASHVK 485
424 PONTFERGTANYSQP-YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISQSRVH 482
486 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTG 545
483 VPVYSWTHRSADRTNTISSDITQIPLVKSFLNLSGTSVSGPGFTGGDIIRTNVNGSVL 542
546 DIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYKTRTV 605
543 SMGLNFNNTSLQRYRVRVRYAASQTMVLRTVVGSGSTTFDQGFPTMSANESLTSQSFRA 602
606 GFTTPPSFLDVQSTFTIGANWSSGNEVYIDRIEFVPVEVYEAAYDFEKAQEKVTAFT 665
603 EFPVGISASGSQ-TAGISISNNAGRTFHFDPKIEFIPITATFEAYDLERAQAVNALFT 661
666 STNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
662 NTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 10
US-09-826-660-25
; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05

Query Match 55.5%; Score 2087; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.5e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLMKSEYENVEPFSASTIQTGIGIAGKI 70
7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
67 LGVLGVPPAGQIASFYSLFVGLWPRGRDQWEI-FLEHVEQLINQOITENARNALTALRLQ 125
130 GLGDALAVYHDSLESWGNRNTRARSVRSOYIALELMFVQKLPSPAVSGEEVPLLPY 189
126 GLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPFLFAIRNQEVPLLMVY 185
190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKXWYSTGLNNLRGT 249
186 AQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEYNTGLNSLRGT 245
250 NAESWVRYNQFRDMLMVLVALFPSTQYPIKTTAQLTREYVYDAIGTGVHPHPSF 309
246 NAASWVRYNQFRDLTLGVLDLVALFPSTQYPIKTTAQLTREYVYDAIGT--GVNM 303
310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 369
304 ASMNWNNNAPSFSAIETAVIRSPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 363
370 IGGTLNISTQGSTNTSINPVLPTSRDVRTESLAGLNLF--LTQPVNGVPRVDFHWKF 427
364 IGGGLNTSTHGSTNTSINPVLSPFRSDVYWTESYAGVLLWGIYLEPIHGVTPTVRFRFN 423
428 V--THPIASDNFYPGYAGIGTQLODSENLPEATGPQPNYESYSHRLSHIGLISASHVK 485
424 PONTFERGTANYSQP-YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISQSRVH 482
486 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTG 545
483 VPVYSWTHRSADRTNTISSDITQIPLVKSFLNLSGTSVSGPGFTGGDIIRTNVNGSVL 542
546 DIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYKTRTV 605
543 SMGLNFNNTSLQRYRVRVRYAASQTMVLRTVVGSGSTTFDQGFPTMSANESLTSQSFRA 602
606 GFTTPPSFLDVQSTFTIGANWSSGNEVYIDRIEFVPVEVYEAAYDFEKAQEKVTAFT 665
603 EFPVGISASGSQ-TAGISISNNAGRTFHFDPKIEFIPITATFEAYDLERAQAVNALFT 661
666 STNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
662 NTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 715

Query Match 55.5%; Score 2087; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.5e-167;
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLMKSEYENVEPFSASTIQTGIGIAGKI 70
7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
67 LGVLGVPPAGQIASFYSLFVGLWPRGRDQWEI-FLEHVEQLINQOITENARNALTALRLQ 125
130 GLGDALAVYHDSLESWGNRNTRARSVRSOYIALELMFVQKLPSPAVSGEEVPLLPY 189
126 GLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPFLFAIRNQEVPLLMVY 185
190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKXWYSTGLNNLRGT 249
186 AQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEYNTGLNSLRGT 245
250 NAESWVRYNQFRDMLMVLVALFPSTQYPIKTTAQLTREYVYDAIGTGVHPHPSF 309
246 NAASWVRYNQFRDLTLGVLDLVALFPSTQYPIKTTAQLTREYVYDAIGT--GVNM 303
310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 369
304 ASMNWNNNAPSFSAIETAVIRSPHLLDFLEQVITYLSLRWSNTQYMMWGGHKLFRPT 363
370 IGGTLNISTQGSTNTSINPVLPTSRDVRTESLAGLNLF--LTQPVNGVPRVDFHWKF 427
364 IGGGLNTSTHGSTNTSINPVLSPFRSDVYWTESYAGVLLWGIYLEPIHGVTPTVRFRFN 423
428 V--THPIASDNFYPGYAGIGTQLODSENLPEATGPQPNYESYSHRLSHIGLISASHVK 485
424 PONTFERGTANYSQP-YESPGLQKDSLETLPETTERPNYESYSHRLSHIGLISQSRVH 482
486 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTG 545
483 VPVYSWTHRSADRTNTISSDITQIPLVKSFLNLSGTSVSGPGFTGGDIIRTNVNGSVL 542
546 DIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYKTRTV 605
543 SMGLNFNNTSLQRYRVRVRYAASQTMVLRTVVGSGSTTFDQGFPTMSANESLTSQSFRA 602
606 GFTTPPSFLDVQSTFTIGANWSSGNEVYIDRIEFVPVEVYEAAYDFEKAQEKVTAFT 665
603 EFPVGISASGSQ-TAGISISNNAGRTFHFDPKIEFIPITATFEAYDLERAQAVNALFT 661
666 STNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
662 NTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 9
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28


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; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match      50.8%; Score 1909.5; DB 9; Length 643;
Best Local Similarity 57.6%; Pred. No. 1e-152;
Matches 371; Conservative 99; Mismatches 159; Indels 15; Gaps 5;

QY 13 SSNAKVDTKSTDSLKN-----ETDIELQNHEDCLKMSYENVEPFVSASTIQTGIG 65
DB 7 NENEIINALSIPAVSNHSAQMNLSLDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTGVPFAGQVASLYSFLGELMPKGNQWELFMEHVEE-INQKISTYARNKA 124
DB 62 IAGRILGVLGVPFAGQIASFYSLVGLWMPGRDPEWEI-FLEHVEQLIRQVTTENTRTDA 120

QY 125 LTDLKGLGDALAVYHDSLSWGNRNTRARSVVRVSQVIALELMFVQKLPSFAVSGEEVP 184
DB 121 LARLQGLGNSFRAYQQSLDWNLRDARTRSVLYQTYQIALELDLFLNAMPLFAIRNQEVP 180

QY 185 LLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERBAGDYSDHCVKWYSTGLN 244
DB 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRVERQVEKTRREYSDYCARWYNTGLN 240

QY 245 NLRGTNAESWVRNQFRDMLMVLDLVALFSDYDTQWPIKTTAQLTREYVYTDAGTVH 304
DB 241 NLRGTNAESWVRNQFRDMLMVLDLVALFSDYDTQWPIKTTAQLTREYVYTDAGTVH 300

QY 305 PHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTVISLLSRWSNTQYMMWGGHK 364
DB 301 APSGFASWNNNAPSFAIAEAAVVRNPHLLDLEQVTVISLLSRWSNTQYMMWGGHK 360

QY 365 LEFRITGGLNISTQSTNTSINPVLTPFTSRDVRVTESLAGNLFLTPQVNGVPRVDFH 424
DB 361 LESRTIRGLSTSTHGNTSINPVLTPFTSRDVRVTESLAGNLFLTPQVNGVPRVDFH 420

QY 425 WKFTVPIASDNFYYPGAGIGTQLQDSENEPPEATGQPNYESYSHRLSHIGLSASHV 484
DB 421 WRNPLNSLRGSLTYTIGYGVGTQLFDSFTELEPPETTERPNYESYSHRLSNIRLISGNTL 480

QY 485 KALVYSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTG 544
DB 481 RAPVYSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTG 540

QY 545 GDIRVNIINPPFAQRYRVRIRYASTDLQFHTSINGKAINQGNFSAATNRGDLDTYKFT 604
DB 541 LSMGLNFNTSLQRYRVRIRYASTDLQFHTSINGKAINQGNFSAATNRGDLDTYKFT 600

QY 605 VGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYE 648
DB 601 AEFPVGISAGSQ-TAGISISNAGRQTFHFDEKIEFIPITALE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

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; FILE REFERENCE: Q68921
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; OTHER INFORMATION: US-10-089-678-1

Query Match      45.1%; Score 1694.5; DB 14; Length 1167;
Best Local Similarity 47.7%; Pred. No. 4.6e-134;
Matches 360; Conservative 125; Mismatches 219; Indels 51; Gaps 14;

QY 1 MCLKNQDKHQ---SFSSNAKVDTKSTDSLKNETDIELQNHEDCLKMSYEB-----NV 51
DB 1 MSPNNQNEYEILDASSSTVSVDNSVRYPLANDQTTTLQNNMNYKDYLRMSEGENPELFGNP 60

QY 52 EPPFVSASTIQTGIGIAGKILGTGVPFAGQVASLYSFLGELMPKGNK-NQWELFMEHVE 110
DB 61 ETFISSTVQTGIGIVGVLGALGVPFAGQIASFYSLVGLWMPSSVSVVWEMI-MKQVE 119

QY 111 E-INQKISTYARNKALTDLKGGLDALAVYHDSLSWGNRNTRARSVVRVSQVIALELMF 169
DB 120 DLIDQKITDSVRKTALAGLQGLDGLDVYQKSLKNWLENRNDTRARSVVVTVQYIALELDF 179

QY 170 VQKLPSFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAG 229
DB 180 VAKIPSPFAISGQEVPLLPYIAQAANLHLLLRDASIFGAEWFTPGEISTFYDRQVTRTA 239

QY 230 DYSCHCVKWSYSTGLNNGTNAESWVRNQFRDMLMVLDLVALFSDYDTQWPIKTTA 289
DB 240 QYSDYCVKWSYSTGLNNGTNAESWVRNQFRDMLMVLDLVALFSDYDTQWPIKTTA 299

QY 290 QLTREYVYTDAGTVHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTVISLLS 349
DB 300 QLTREYVYTDAGTVHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTVISLLS 359

QY 350 --RWSNTQYMMWGGHKLEFRITGGLNISTQSTNTSINPVLTPFTSRDVRVTESL-AG 406
DB 360 GLPLNNTLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYDLANCKDIFQVRSGLAD 419

QY 407 LNLFLTQPVNGVPRVDFHVKFTHPIASDNFYYPGAGIG-----TQLQDS 452
DB 420 LANYAQ-VYGVPIYASF-----TLDDKN---TGSGSVGGFTYSKPHTTMQVCTQNYNT 468

QY 453 ENELPPEATGQPNYESYSHRLSHIGLS-----ASHVKALVYSWTHRSADRTNITIEP 504
DB 469 IDEIPPE--NEPLSRGYSHRLSHITSYFSKNASSPARYGNLPVFAWTHRSADVTNTVYS 526

QY 505 NSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNIINPPFAQRYRVRIR 564
DB 527 DKITQIPVVKAHVLTGVTVIKPGFTGGNLLKRTSSGPLAYTSVSKSPLSQRYRARI 586

QY 565 YASTTDLQFHTSINGKAINQGNFSAATNRGDLDTYKFTFRTVGTTPSPFLDVQSTFTIGA 624
DB 587 YASTTNLRFLVTISGTRIYSINVKNTWKNGDDLTFTNTFDLATIGTATFTSNYSDSLTVGA 646

QY 625 WNFSSGNEVYIDRIEFVPEVTEYEAEVDFEKAQEKVTAFTTNPRLKTDVQYHIDQV 684
DB 647 DSFASGGEVYVDKFEIIPVNAFEEAEEDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNOA 705

685 SNLVESLSDFEYLDKRELFEIVKYANELHIERNM 719
706 ANLVECLSDLEYPNKRMMLWDAVKEAKRLVQARNL 740

RESULT 12

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QY	646	TYEAEYDFEKAQE 658 : : :
Db	640	TFEYVDLERAQK 652 : : :
RESULT 13		
US-10-782-141-16		
; Sequence 16, Application US/10782141		
; Publication No. US20040197917A1		
; GENERAL INFORMATION:		
; APPLICANT: Carozzi, Nadine		
; APPLICANT: Hargies, Tracy		
; APPLICANT: Koziel, Michael G.		
; APPLICANT: Duck, Nicholas B.		
; APPLICANT: Carr, Brian		
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and		
; TITLE OF INVENTION: Methods for Its Use		
; FILE REFERENCE: 045600/274143		
; CURRENT APPLICATION NUMBER: US/10/782,141		
; CURRENT FILING DATE: 2004-02-20		
; PRIOR APPLICATION NUMBER: 60/448,632		
; PRIOR FILING DATE: 2003-02-20		
; NUMBER OF SEQ ID NOS: 23		
; SOFTWARE: Fast-SEQ for Windows Version 4.0		
; SEQ ID NO 16		
; LENGTH: 1157		
; TYPE: PRT		
; ORGANISM: Bacillus thuringiensis		
US-10-782-141-16		
QY		Query Match 43.7%; Score 1643.5; DB 16; Length 1157;
Db		Best Local Similarity 49.1%; Pred. No. 9.5e-130;
		Matches 372; Conservative 96; Mismatches 229; Indels 61; Gaps 21;
QY	1	MKLKNODKHQSFSSNAKVDKI STDS-----LKNETDIELQNINHDCLCKMSEYE-----N 50
Db	1	MSPNNQNEYEIIDATPST-SVSSDSNRYPFANEPTDALQNMNYKYVKMGSGENPELFGN 59
QY	51	VEPVFASTIQTGIGIAGKI LGLTGVFPAGOVASLYSFI LGELWP-KGKNOW-EILFMEH 108
Db	60	PETISSSTIQTGIGIVGRILGALGVFPASQIASFYSFIVQLWPSKSVDIWGEEI--MER 117
QY	109	VEE-INQKISTYARKNALTDLKGLDALAVYHDSLESWVGHNTRNSRVSQYIALEL 167
Db	118	VEELVDQKEKYVKDKALAEKLG LNALDVYQQSLEDWLERNRDARTSRVSNQFI ALDL 177
QY	168	MFVQKLPSFAVSGBEVPLPIPYAQAAHLHLLLRDASIFGKEWGLSSSEISFTFYNQVER 227
Db	178	NFVSSIPSAVSGHEVLLLA VYAQAUNHLLLRDASIFGEWEFTTPEGISRFYNRVQL 237
QY	228	AGDYSDHCWKMYSTGLNLRLGTNAESWVRYNQPRRRMTLMVL DLVALFPSTQMYPIT 287
Db	238	TAEYSDCVKWKYKTGLDKLKGTTSKSLWNHYHQFRREMTLLVLDLVALFPNYDTHMYPIET 297
QY	288	TAQLTREVTDAICTVHPHPSFIST----TWYNNAPSAIEAAVVNRNPHLLDLEQVT 343
Db	298	TAQLTRDVTDPDIA----FNIVTSTGFCNPWSTHGILFYEVENNVIRPPHFLDILSSVE 353
QY	344	IYSLLSR-----WSNTQYMNMGGHKLEPR-----TIGGTLNISTQGSINTSINPVTLPPT 394
Db	354	INT--SRGGITLNNDAYINWSGHTLKYRRTADSTVTVTYANYGRITSEKNS-----FALE 406
QY	395	SRDVVRTESLAGNLFLTQPNGVPRVDPHWKFVTHPTASDNFY-----YPGVAGIGTOL 449
Db	407	DRDIFFINSTVANLANYYQKAYVPGSWFH--MVKRGTSSTTAYLSKTH TALQGC-TQV 463
QY	450	QDSENELPPEATGPQNYESYSHRLSHI-----GLTSASHVKALVYSWTHRSADRNT 501
Db	464	YESSDEIPLDRT-VPAVESYSHRLSHITSHSFSKNG--SAYYGSFPVFVWTHTSADLNT 520
QY	502	IEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTTGTFGDIRVNINPPFAQRV 561

Db 521 IYSDKITQIPAVKGMVYLGSSVQGPFGTGGDILKRTNPSILGTFAVTNGSLSQRYR 580

Qy 562 RIRYASTTDQFHTSINGKAINQGNFSATMNRGDDLYKTFRTVGTTPFPFLDVQSTFT 621

Db 581 RIRYASTTDFEF-TLYLGDITKRNFKMTDNGASLTETFKFASFTDFQFRETQDKIL 639

Qy 622 IGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTAFTSTNPRGLKTDVYDI 681

Db 640 LSGMGFSSGQEVYIDRIEFIPVDEYAEQDLEAKKAVNALFTNTKD-GLRPGVTDYEV 698

Qy 682 DQVSNLVESSDEFYLDKRELFELVKYANELHIERNM 719

Db 699 NQAAANLVECLSDLLYPNEKRLFLDAVREAKRLSGARNL 736

RESULT 14

US-10-032-717-2

; Sequence 2, Application US/10032717

; Publication No. US20020151709A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Nicholas B. Duck

; APPLICANT: Xiang Feng

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Theodore W. Kahn

; APPLICANT: Lynn E. Sims

; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With

; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

; FILE REFERENCE: 35718/237005

; CURRENT APPLICATION NUMBER: US/10/032,717

; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: 60/242,838

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1206

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-032-717-2

Query Match 39.5%; Score 1485; DB 13; Length 1206;

Best Local Similarity 44.3%; Pred. No. 2.8e-116;

Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

Qy 1 MCLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKM-----SEYE-N 50

Db 1 MSPNNQNEVEIIDATPST-SVNSDSNRPFFANEPTNALQNDYKDYKMSAGNASSEYPGS 59

Qy 51 VEPFVSA-STIQTGIGIAGKILGTGVPPAGQVAVSLYSFILGELWPKG-KNOWEILFMEH 108

Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLVGPFVGPVIVSLYTLQIDILWPSGKESQWEI-FMEQ 118

Qy 109 VEE-INQKISTYARNKALTDLKGLGDALAVYHDSLESVGNRNTRRSVVRVRSQYIALEL 167

Db 119 VEELINQKIAEYARNKALSELEGNNYQLYLTALAEENENPNSGRALDRVNRFEILDS 178

Qy 168 MFVQKLPSPAVSGEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVER 227

Db 179 LFTQYMPSPRVTFEVPFLTVYAMAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVER 238

Qy 228 AGDYSCHCKWYSTGLNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSSYDTOMYPIKT 287

Db 239 TAEYSDHCWKWYETGLAKLGTSAKQWVDYNOQFRREMTLAVLDVVALFPNYDTRTYPMET 298

Qy 288 TAQLTREVTYDAIGTVHPHPSFTSTTWNNAEYAEYDFEKAQEKVTAFTSTNPRGLKTDVYDI 347

Db 299 KAQLTREVTYDPLGAVNVS---SIGSWY-DKAPSGVIESSVIRPPHVFVITGLTVYITQ 354

Qy 348 LSRWSNTQYNNMGGHKLBEFRITGTLNISTQSTNTSINPV-TLPFTSRDVRVYTESLAG 406

Db 355 SRSISSARYIRHWAGHQISYHRVSRGSLNQMYGTQNLHLSISTFDTNYYIKTISKDA 414

Qy 407 LNLFLTQP-----VNGVPRVDFHMKFVTHPIASDN---FYYPGVAGIGTQLODSENELPP 458

Db 415 VLLDIVPGYTYIFFGMPEVEF---FMVNQLNTRKTLKYNPVSKDIIASTRDSLELPP 471

Qy 459 EATGQPNYESYSHRSLHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKA 515

Db 472 ETSQDPNYESYSHRSLCHITSIPATGNTTGLVPVFSWTHRSADLNNNTIYSDKITQIPAVKC 531

Qy 516 FNLSSGAAVRGPFGTGGDILR-RTNTGTFGDI---RVNINPFAQRYRVRIYASTTDL 571

Db 532 WDNLPFVPVVKGPFGHTGGDLYQNRSTGVTFLARVGLALEKAGKYRVLRYATDADI 591

Qy 572 QFHTSINGKAINQGNFSATMNRGDDLYKTFR-----TVGFTTTPFSFL-----DVQS 618

Db 592 VLH--VNDQAI---QMPKTMNPGEDLTSKTFKVADAITTLNLTADSSLALKHNLGDPNS 646

Qy 619 TFTIGAWNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTAFTSTNPRGLKTDVVKD 678

Db 647 TLS-----GIVYVDRIEFIPVDEYAEQDLEAKKAVNALFTNTKD-GLRPGVTD 696

Qy 679 YHIDQVSNLVESSDEFYLDKRELFELVKYANELHIERNM 719

Db 697 YEVAQAANLVECLSDLLYPNEKRLFLDAVREAKRLSEARNL 737

RESULT 15

US-10-414-637-2

; Sequence 2, Application US/10414637

; Publication No. US20030177528A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Nicholas B. Duck

; APPLICANT: Xiang Feng

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Theodore W. Kahn

; APPLICANT: Lynn E. Sims

; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With

; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

; FILE REFERENCE: 35718/237005

; CURRENT APPLICATION NUMBER: US/10/414,637

; CURRENT FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: US/10/032,717

; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: 60/242,838

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1206

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-414-637-2

Query Match 39.5%; Score 1485; DB 14; Length 1206;

Best Local Similarity 44.3%; Pred. No. 2.8e-116;

Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

Qy 1 MCLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKM-----SEYE-N 50

Db 1 MSPNNQNEVEIIDATPST-SVNSDSNRPFFANEPTNALQNDYKDYKMSAGNASSEYPGS 59

Qy 51 VEPFVSA-STIQTGIGIAGKILGTGVPPAGQVAVSLYSFILGELWPKG-KNOWEILFMEH 108

Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLVGPFVGPVIVSLYTLQIDILWPSGKESQWEI-FMEQ 118

Qy 109 VEE-INQKISTYARNKALTDLKGLGDALAVYHDSLESVGNRNTRRSVVRVRSQYIALEL 167

Db 119 VEELINQKIAEYARNKALSELEGNNYQLYLTALAEENENPNSGRALDRVNRFEILDS 178

Qy 168 MFVQKLPSPAVSGEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVER 227

Db 179 LFTQYMPSPRVTFEVPFLTVYAMAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVER 238

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds
(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-58
Perfect score: 3761
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANLHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3720	98.9	719	3	US-08-286-870A-8
2	3442.5	91.5	710	4	US-09-661-322A-42
3	3370	89.6	648	3	US-08-286-870A-4
4	3341	88.8	719	2	US-09-003-217-2
5	3336	88.7	719	3	US-09-218-942-2
6	2776	73.8	535	3	US-08-286-870A-6
7	2417.5	64.3	1229	1	US-08-100-709-4
8	2417.5	64.3	1229	1	US-08-176-865-4
9	2417.5	64.3	1229	1	US-08-474-038-4
10	2417.5	64.3	1229	2	US-08-779-046-4
11	2417.5	64.3	1229	2	US-08-881-340-4
12	2318.5	61.6	488	1	US-08-448-170-10
13	2318.5	61.6	488	3	US-08-961-803-10
14	2236.5	59.5	1207	1	US-07-951-715A-7
15	2236.5	59.5	1207	2	US-08-459-448A-7
16	2236.5	59.5	1207	3	US-08-459-595A-7
17	2236.5	59.5	1207	3	US-08-459-504B-7
18	2236.5	59.5	1207	3	US-08-459-444-7
19	2236.5	59.5	1207	3	US-09-053-549-8
20	2236.5	59.5	1207	3	US-09-547-422-7
21	2236.5	59.5	1207	4	US-09-988-462-7
22	2235.5	59.4	1227	3	US-09-053-549-2
23	2166.5	57.6	1227	1	US-08-448-170-8
24	2166.5	57.6	1227	3	US-08-961-803-9
25	2157.5	57.4	1227	4	US-09-661-322A-63
26	2142.5	57.0	1186	3	US-09-178-252-23
27	2142.5	57.0	1186	4	US-09-826-660-23

28	2087	55.5	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1909.5	50.8	643	3	US-09-178-252-25	Sequence 25, Appl
30	1909.5	50.8	643	4	US-09-826-660-25	Sequence 25, Appl
31	1872	49.8	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1658.5	44.1	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1643.5	43.7	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1643.5	43.7	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1643.5	43.7	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1643.5	43.7	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1481.5	39.4	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1466	39.0	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1466	39.0	1157	2	US-08-379-658B-5	Sequence 5, Appl
40	1466	39.0	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1466	39.0	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1466	39.0	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1466	39.0	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1461	38.8	1168	1	US-08-291-368-4	Sequence 4, Appl
45	1461	38.8	1168	2	US-08-962-190-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Query Match 98.9%; Score 3720; DB 3; Length 719;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 714; Conservative 3; Mismatches 1; Indels 2; Gaps 2;
1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I L F M E H V E E - I N Q K I S T Y 119
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I - F M E H V E E I I N Q K I S T Y 119
120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q Y I A L E L M F V Q K L P S F A V S 179
120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q Y I A L E L M F V Q K L P S F A V S 179
180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239
180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239
240 S T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299
240 S T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299
300 I G T V H P H P S F T S T T W Y N N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359
300 I G T V H P H P S F T S T T W Y N N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359
360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419
360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419
420 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T O L Q D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479
420 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T O L Q D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479
480 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539
480 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539
540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599
540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599
600 K T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659
600 K T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659
660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661.322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PR

ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
Query Match 91.5%; Score 3442.5; DB 4; Length 710;
Best Local Similarity 91.9%; Pred. No. 3.5e-304;
Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;
1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
1 M K S K N Q N M H O S L S N N A T V D K N F T G S L E N T N T E L Q N F N H - - - - - E G I E P F V S V S T I 51
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I L F M E H V E E - I N Q K I S T Y 119
52 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G S Q W E I - F M E H V E E L I N Q K I S T Y 110
120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q Y I A L E L M F V Q K L P S F A V S 179
111 A R N K A L A D L K G L G D A L A V Y H E S L E S W I E N R N N T R T R S V V K S O Y I T L E L M F V O S L P S F A V S 170
180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239
171 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S G K S K E Y S D H C V K W Y 230
240 S T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299
231 N T G L N R L M G N N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 290
300 I G T V H P H P S F T S T T W Y N N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359
291 I G T V H P H P S F T S T T W Y N N N A P S F S T E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 350
360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419
351 W G G H K L E F R T I G G T L N T S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 410
420 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T O L Q D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479
411 R V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T O L Q D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 470
480 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539
471 S A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R K 530
540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599
531 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 590
600 K T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659
591 K T F R T V G F T T P F S F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E E 650
660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
651 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K O L H I E R N M 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286.870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 89.6%; Score 3370; DB 3; Length 648;
Best Local Similarity 99.5%; Pred. No. 1.2e-297;
Matches 646; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

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DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTGLVPPFAGQVASYLSTFGLWPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGLVPPFAGQVASYLSTFGLWPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKLGLDALAVYHDSLESWGNRNNTRARSVVRVSVYALFELMFVQKLPFAVS 179
DB 120 ARNKALTDLKLGLDALAVYHDSLESWGNRNNTRARSVVRVSVYALFELMFVQKLPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWY 239
QY 240 STGLNLRGTNAESWVRVYQFRRDMLVLDLVALFPSTYDTQMPYIKTAQLTREVYTD 299
DB 240 STGLNLRGTNAESWVRVYQFRRDMLVLDLVALFPSTYDTQMPYIKTAQLTREVYTD 299
QY 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
DB 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 360 WGGHKLFRFTIGTILNISTQSTNTSINPVTLPFTSRDVRVYTESLAGNLFITQPVNGVP 419
DB 360 WGGHKLFRFTIGTILNISTQSTNTSINPVTLPFTSRDVRVYTESLAGNLFITQPVNGVP 419
QY 420 RVDFHFKFVTHPIASDNFYPGYAGIGTQLQDSENELPPEATQCPNYESYSHRLSHIGLI 479
DB 420 RVDFHFKFVTHPIASDNFYPGYAGIGTQLQDSENELPPEATQCPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVYSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599
DB 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY 599
QY 600 KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYE 648
DB 600 KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYE 648
RESULT 4
US-09-003-217-2
Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-217-2

Query Match 88.8%; Score 3341; DB 2; Length 719;
Best Local Similarity 89.2%; Pred. No. 6.1e-295;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTGLVPPFAGQVASYLSTFGLWPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGLVPPFAGQVASYLSTFGLWPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKLGLDALAVYHDSLESWGNRNNTRARSVVRVSVYALFELMFVQKLPFAVS 179
DB 120 ARNKALTDLKLGLDALAVYHDSLESWGNRNNTRARSVVRVSVYALFELMFVQKLPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWY 239
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWY 239

Db 180 GEEVLLPIYAQAANLHLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWN 239
Qy 240 STGLNNLRGTNAESWVRNQFRDMTLMVLDLVALPSPDYDTOMYPIKTTAQLTREVYTDA 299
Db 240 NTGLNNLRATNGQSWVRNQFRKDIEMVLDLVRVPSPDYDTLVYPIKTTSQLTREVYTDA 299
Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359
Db 300 IGTVDPNQALRSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359
Qy 360 WGGHKLFRFTIGTINISTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVNGVP 419
Db 360 WGGHRLSRPIGGALNTSTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVNGVP 419
Qy 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLI 479
Db 420 RVDHFKFPTLPASDNFYVLGYAGVGTQLODSENELPPEATGPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRT 539
Db 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRT 539
Qy 540 NTGTFGDIRVNIINPPFAQRYVRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
Db 540 KSGTFGHIRVNIINPPFAQRYVRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
Qy 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Db 600 KTFRTVGTTPPSFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEYAEYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELFLYLDKRELFEIVKYAKQIHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Oman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; TITLE OF INVENTION: Activity
; FILE REFERENCE: CryII
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

Query Match 88.7%; Score 3336; DB 3; Length 719;
Best Local Similarity 89.2%; Pred. No. 1.7e-294;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;
Qy 1 MCLKNQDQKHSFSSNAKVDKISTDLKQVETDIELQINHEDCLKMXEYENVEPVSASTI 60
Db 1 MCLKNPKHQTLSSNAKVDIATDSLKNETDIELKNMNNEDYLRMSHEHSIDPFVSASTI 60
Qy 61 QTGIGIAGKILGTLPVFPAGVASYLSFILGELWPKGKNQWELPMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTLPVFPAGVASYLSFILGELWPKGKSQWEI-FMEHVEAIINRKISTY 119
Qy 120 ARNKALTDLKLGLDALAVYHDSLESWGNNRNNTRSVRSQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALTDLKLGLDALAVYHDSLESWGNNRNNTRSVRSQYIALELMFVQKLPSFAVS 179

Qy 180 GEEVLLPIYAQAANLHLLLRDASIFEKNGGLSASEISTFYNRQVERAGDYSDHCVKMY 239
Db 180 GEEVLLPIYAQAANLHLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWN 239
Qy 240 STGLNNLRGTNAESWVRNQFRDMTLMVLDLVALPSPDYDTOMYPIKTTAQLTREVYTDA 299
Db 240 NTGLNNLRATNGQSWVRNQFRKDIEMVLDLVRVPSPDYDTLVYPIKTTSQLTREVYTDA 299
Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359
Db 300 IGTVDPNQALRSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359
Qy 360 WGGHKLFRFTIGTINISTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVNGVP 419
Db 360 WGGHRLSRPIGGALNTSTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVNGVP 419
Qy 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLI 479
Db 420 RVDHFKFPTLPASDNFYVLGYAGVGTQLODSENELPPEATGPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRT 539
Db 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRT 539
Qy 540 NTGTFGDIRVNIINPPFAQRYVRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
Db 540 KSGTFGHIRVNIINPPFAQRYVRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599
Qy 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Db 600 KTFRTVGTTPPSFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEYAEYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELFLYLDKRELFEIVKYAKQIHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: ELENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: FILLISBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286, 870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 73.8%; Score 2776; DB 3; Length 535;
Best Local Similarity 99.4%; Pred. No. 1e-243;
Matches 533; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKMEYENVEPFSASTI 60
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKMEYENVEPFSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSIFLGELWPKGNQWEILFMEHVEE-INOKISTY 119
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSIFLGELWPKGNQWEILFMEHVEE-INOKISTY 119

QY 120 ARNKALTDLKGDLAVVHDSLESWGNRNTRARSVVRQYIALELMFVQKLPFAVS 179
DB 120 ARNKALTDLKGDLAVVHDSLESWGNRNTRARSVVRQYIALELMFVQKLPFAVS 179

QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239

QY 240 STGLNNLRGTNAESWVRNQFRDMLVLDLVALPFSYDTQMPYPIKTTAQLTREYVTD 299
DB 240 STGLNNLRGTNAESWVRNQFRDMLVLDLVALPFSYDTQMPYPIKTTAQLTREYVTD 299

QY 300 IGTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMN 359
DB 300 IGTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMN 359

QY 360 WGGHKLFRPTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419
DB 360 WGGHKLFRPTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419

QY 420 RVDPHKFWTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479
DB 420 RVDPHKFWTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDI 535
DB 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLKMEYENVEPFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPVSNFSTQMLSPDARIEDSLCVAEVNNDPFSVASTVQTGINIAGRI 66

QY 71 LGTIGVPFAGQVASYLSIFLGELWPKGNQWEILFMEHVEE-INOKISTVARNKALTDLK 129
DB 67 LGVLGVPFAGQVASYLSIFLGELWPKGNQWEILFMEHVEE-INOKISTVARNKALTDLK 125

QY 130 GLGDALAVHDSLESWGNRNTRARSVVRQYIALELMFVQKLPFAVSFAVSGEVEVLLPIY 189
DB 126 GLGRGYRYSQALETWLDNRDARSIIILERYVALELDITTAIPLFIIRNEEVPLLMVY 185

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWYSTGLNNLRGT 249
DB 186 AQANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWYSTGLNNLRGT 245

QY 250 NAESWVRNQFRDMLVLDLVALPFSYDTQMPYPIKTTAQLTREYVTDITGTVHPHPSF 309
DB 246 NAESWVRNQFRDMLVLDLVALPFSYDTQMPYPIKTTAQLTREYVTDITGTVHPHPSF 305

QY 310 TSITWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMNMGHKLFEFT 369
DB 306 ASTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMNMGHKLFEFT 365

QY 370 IGTGLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHVKFV 428
DB 366 IGTGLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHVKFV 422

QY 429 THPIASDNFYYPG-----YAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 481
DB 423 ---INPQNIYERAGTATYQYQGVIGIQLFDSSETLPETTERPNYESYSHRLSHIGLI 479

QY 482 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDIILRTNT 541
DB 480 NTLRAPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDIILRTNT 539

QY 542 GTFGDIRVNNPPFAQRVRIYASTTDLQFHTSINGKAINQGNFSATNWRGDLDYKT 601
DB 540 GTFGDIRVNNPPFAQRVRIYASTTDLQFHTSINGKAINQGNFSATNWRGDLDYKT 599

QY 602 FRTVGTTPFSLDVQSTFTIGAWNPFSSGNEVYIDRIEFVPEVTEAEVDFEKAQKVT 661
DB 600 FRTAGFSTPFNFLNAQSTFTLGAQSFNS-QEYVYIDRIEFVPEVTEAEVDFEKAQKVT 658

QY 662 ALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELVKYANELHIERNM 719
Db 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDKRELFELVKYAKRLSDERNL 716

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-865-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLMSEVENVEPVSVASTIQTGIGIAGKI 70
Db 7 NENEINALSPTVSPSTQNLSPDARIEDSLCAEVNNDPFSVASTVQIGINIAGRI 66

QY 71 LGTLGVFPAGVAVSLYFILGELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 129
Db 67 LGVLGVFPAGVAVSLYFILGELWPKGNQWEILFMEHVEE-INQKISTYARKNALTDLK 125

QY 130 GLGDALAVYHDSLESVGNRNTRRSVRSQYIALELMFVQKLPSPFVSGEVPPLPIY 189
Db 126 GLGRGYSYQQALETWLDNRNDARSISILERYVALELDITTAIPLFRIRNEEVPPLMVY 185

QY 190 AQANLHLLLRDASIFGKWLGSLSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGT 249
Db 166 AQANLHLLLRDASIFGSEWGMASSDVNOYYQEQIRYTBESYHNCHVQWYNTGLNLRGT 245

QY 250 NAEWSVRYNQFRDRLTMDLVLPVPSYDTQMYPIKTTAQLTREVTDAIGTVHPHPSF 309


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEVENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEINALSIPTVSNPSTQMNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
Db 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEI-FLEHVEQLIRQVVTENTRTAARLE 125

QY 130 GLGDALAVYHDSLSWGNRNNTARSVRSQVIALELMFVQKLPSFAVSGEEVPLPIY 189
Db 126 GLGRGYRSYQQALETWLDNRNDARSILERYVALELDITTAIPLFRIRNEEVPLLMVY 185

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYSTGLNNLRGT 249
Db 186 AQANLHLLLRDASLFGSEWGMASDVNQYQEIYRTEYSNHCYQWYNTGLNNLRGT 245

QY 250 NAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTAQLTREYVTDATGTVHPHPSF 309
Db 246 NAESWLRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQLTREIYTDPIGRTNAPSGF 305

QY 310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMGHKLFRFT 369
Db 306 ASTNWFNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSSASSRWSSTQHMNYVWGHRLNFRP 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDYYRTESLAGNLFLLTPQVNGVPRVDFHWKFV 428
Db 366 IGGTLNISTQGLTNNTSINPVTLPFTSRDYYRTESLAGNLFLLTPQVNGVPRVDFHWKFV 422

QY 429 THPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQPYQGVGIQLFDSSETLPETTERPNYESYSHRLSHIGLIIG 479

QY 482 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRNT 541
Db 480 NTLRAPVSWTHRSADRTNTIGPNRIITQIPLVKALNLHSGVTVVGGPGFTGCDILRRNT 539

QY 542 GTFGDIRVINPPAQRVRIYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYKT 601
Db 540 GTFGDIRLINVPISQRYRIRYASTTDLQFPTRINGTIVNIGNFSRTMNRGDNLEYS 599

QY 602 FRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDFEKAQKVT 661
Db 600 FRTAGFSTPFNLAQSTFTLGAQSFN-QEVYIDRVEFVPAEVTFAEYDLERAQKAVN 658

QY 662 ALFTSTNPRGLKTPDKVDYHIDQVSNLVESLSEDFYDLDEKRELFEIVKYANELHIERNM 719
Db 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSEDFCLDEKRELFEIVKYAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      64.3%; Score 2417.5; DB 2; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEVENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEINALSIPTVSNPSTQMNLSPDARIEDSLCVAEYNNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
Db 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEI-FLEHVEQLIRQVVTENTRTAARLE 125

QY 130 GLGDALAVYHDSLSWGNRNNTARSVRSQVIALELMFVQKLPSFAVSGEEVPLPIY 189
Db 126 GLGRGYRSYQQALETWLDNRNDARSILERYVALELDITTAIPLFRIRNEEVPLLMVY 185

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYSTGLNNLRGT 249
Db 186 AQANLHLLLRDASLFGSEWGMASDVNQYQEIYRTEYSNHCYQWYNTGLNNLRGT 245

QY 250 NAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTAQLTREYVTDATGTVHPHPSF 309
Db 246 NAESWLRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQLTREIYTDPIGRTNAPSGF 305

QY 310 TSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMGHKLFRFT 369
Db 306 ASTNWFNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSSASSRWSSTQHMNYVWGHRLNFRP 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDYYRTESLAGNLFLLTPQVNGVPRVDFHWKFV 428
Db 366 IGGTLNISTQGLTNNTSINPVTLPFTSRDYYRTESLAGNLFLLTPQVNGVPRVDFHWKFV 422

QY 429 THPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQPYQGVGIQLFDSSETLPETTERPNYESYSHRLSHIGLIIG 479

QY 482 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRNT 541
Db 480 NTLRAPVSWTHRSADRTNTIGPNRIITQIPLVKALNLHSGVTVVGGPGFTGCDILRRNT 539
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QY      542 GTFGDIRVNNPPFAQRXVRIRVASTTDLQFHTSINGKAINOQNFSATMNRGDDLKYKT   601
Db      540 GTFGDRLNINVPISQRYRVRIRVASTTDLQFFTRNGITTVNIGNFSRTMNRGDNLEYS    599

QY      602 FRTVGFTTPSFELDVQSSTETIGAWNFSSGNEVIIDRIEFVPEVTYEAEYDFEKAQEKV     661
Db      600 FRTAGFTFPNFLNAQAOSTFTLGAOSFSN-QEVYIDRVFEVPAEVTFEAYEDLERAKAVN    658

QY      662 ALFTSTNPRLKTDVKDYHDOVSNLVESLSDEFYLDEKRELFIKKVANELLHIERNM       719
Db      659 ALFTSTNPRLKTDVDYHDQVSNMVACLSEDFCLDEKRELFKKVKARLSDERNL        716


RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryETS
; DATE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-881-340-4


Query Match          64.3%; Score 2417.5; DB 2; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e+210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

Qy      13 SSNAKVDKISTDSLKN-ETDIQLQ-NINHEDCLKMEYENVEPFFVASSTIQTGIGIAGKI    70
Db      7 NENEIIINALSIPTSPNSPTQMNLSPDAIEDSLCAVEVNNDIPFVSASTVQTGINIAGRI    66

Qy      71 LGTLGVFPAGVASLYSYFILGLBWPCKGNQWIELFWEHVEE-INOKISTYAARNKALTDLK     129
Db      67 LGVLGVFPAGQASFYFLVGLWPSGRDPWEI-FLEHV EOLIRQQVNTENTRTALEARLE     125

Qy      130 GLGDALAVYHDSLESWGVRNRRNTRARSQVIALDELMTFKQLPSFAVSGEEVPLPIY         189
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QY 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVP 419
Db 351 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVP 410
QY 420 RVDPHMKFVTHPIASDNFYPGVAGICTQLODSSENLPPREATQPNYESYSHRLSHIGLI 479
Db 411 RVDPHMKFVTHPIASDNFYPGVAGICTQLODSSENLPPREATQPNYESYSHRLSHIGLI 470
QY 480 SASHVKALVYSWTHRSAD 497
Db 471 SASHVKALVYSWTHRSAD 488

RESULT 14
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

Query Match 59.5%; Score 2236.5; DB 1; Length 1207;

Best Local Similarity 64.1%; Pred. No. 5e-194;
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;
QY 40 EDCMKSEYENVEPPFYSASTIQTGTIGIAGKILGTLPVGPAGQVASYLSFILGELWPKGN 99
Db 10 EDSLCTAEGNNIDPFYSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGLWPRGRD 69
QY 100 QWEILFMEHVER-INOKISTYARNKALTDLKGLGDALAVYHDSLESWVGNNRNTARSVV 158
Db 70 QWEI-FLEHVEQLINQOITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTSVL 128
QY 159 RSQYIALELMFVKQLPFSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIS 218
Db 129 YTOYIALELDFLNAMPLFAIRNOQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQ 188
QY 219 TFYNRQVERAGDYSCHCVKWTSTGLNNLRGTNAESVVRVYNQFRRDMLVLDLVALFPSY 278
Db 189 RYVERQVERTRDYSYCVQVWYNTGLNSLRGTNAASVVRVYNQFRRDMLVLDLVALFPSY 248
QY 279 DTOMYPIKTTAQLTRVYVTDAGTVVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLOF 338
Db 249 DTRTPINTSAQLTRVYVTDAGT--GVNMMASMNWNNNAPSFAIEAAAIRSPHLLDF 306
QY 339 LEQVTIYSLLSRWSNTQYMMNMWGGHKLFRITGGTINISTQGSTNTSINPVTLPFTSRDV 398
Db 307 LEQVTIYSLLSRWSNTQYMMNMWGGHKLFRITGGTINISTQGSTNTSINPVTLPFTSRDV 366
QY 399 YRTESLAGLNLF--LTQPVNGVPRVDFHMKFVTHP-----IASDNFYPGVAGICTQLOD 451
Db 367 YRTESYAGVLLWGIYLEPIHGVTPTVRNF---TNPONISDRGTANYSQP-YESPGLQLKD 422
QY 452 SENELPPREATQPNYESYSHRLSHIGLI SASHVKALVYSWTHRSADRTNTEPNISITQIP 511
Db 423 SETELPPETTERPNYESYSHRLSHIGLI LQSRVNVVYSWTHRSADRTNTEPNISITQIP 482
QY 512 LVKAFNLSSGAADVVRGPGFTGGDILRRTNTGTFGDIRVNIINPPFAQRYRVRIRYASTTDL 571
Db 483 MVKASELPQGTTVVRGPGFTGGDILRRTNTGTFGDIRVNIINPPFAQRYRVRIRYASTTDL 542
QY 572 QFHTSINGKAINQGNFSATMRGEDLDYKTFRTVGTTPFTSFLDVQSTFTTIGANWPFSSGN 631
Db 543 DFFVSRGTTVNNFRFLRTMSGDELKYGNEVRRATFTPTFTTQIQQDIIRTSIQGLSGNG 602
QY 632 EVYIDRIEFVPEVTVYEAEDFEKAQKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESL 691
Db 603 EVYIDKIEIIPVTATFEABYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACL 662
QY 692 SDEFYLDKRELEFEIVKYANLHIERNM 719
Db 663 SDEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds
(without alignments)
4171.616 Million cell updates/sec

Title: US-10-019-823B-59
Perfect score: 3742
Sequence: 1 MKLKNPKHQSLSNAKVDK.....KRELPEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3742	100.0	719	2	I40590
2	3520	94.1	719	2	I39815
3	3511	93.8	719	2	S25383
4	3503	93.6	719	2	I39814
5	2321.5	62.0	1228	2	S00873
6	1813	48.5	380	2	B42459
7	1507	40.3	1157	1	S49247
8	1503.5	40.2	1166	2	S32645
9	1491.5	39.9	1174	2	S32649
10	1487.5	39.8	1155	2	A26513
11	1480.5	39.6	1155	2	J00002
12	1480.5	39.6	1156	2	A29125
13	1463.5	39.1	1155	2	S02134
14	1463.5	39.1	1181	2	A41052
15	1461.5	39.1	1155	2	I39838
16	1459	39.0	934	2	A22798
17	1457	38.9	1176	2	J02041
18	1451	38.8	1176	2	J02219
19	1447	38.7	1176	2	A22617
20	1447	38.7	1176	2	S02215
21	1367	36.5	1174	2	A42459
22	1348	36.0	1156	2	A29838
23	1343	35.9	1138	2	A48944
24	1340.5	35.8	823	2	S04181
25	1331.5	35.6	1189	2	S00944
26	1326	35.4	1154	2	S39536
27	1292	34.5	1171	2	I40572
28	1292	34.5	1171	2	A37829
29	1286	34.4	1176	2	A48970

30	1232	32.9	1160	2	S32647	parasporal crystal
31	1230.5	32.9	1165	2	S11446	parasporal crystal
32	1220.5	32.6	655	2	J07140	protoxin - Bacilli
33	1196.5	32.0	1172	2	S32689	parasporal crystal
34	1179	31.5	1160	2	I40589	parasporal crystal
35	1178	31.5	652	2	A27323	parasporal crystal
36	1165	31.1	1178	1	USBSXH	parasporal crystal
37	1164.5	31.1	1177	2	A49785	parasporal crystal
38	1159	31.0	659	2	S10228	parasporal crystal
39	1124.5	30.1	652	2	I39811	parasporal crystal
40	995	26.6	649	1	JH0261	parasporal crystal
41	938.5	25.1	618	2	S11445	parasporal crystal
42	896	23.9	1156	2	S19306	parasporal crystal
43	845	22.6	1136	1	USBS8I	parasporal crystal
44	662.5	17.7	934	2	B29838	parasporal crystal
45	637	17.0	1180	2	I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I40590
cryV465 protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40590
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I40590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g467234
C;Genetics:
A;Gene: cryV465
C;Superfamily: parasporal crystal protein

Query Match	100.0%	Score	3742;	DB 2;	Length	719;			
Best Local Similarity	100.0%	Pred. No.	3.1e-258;						
Matches	719;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MKLKNPKKHOSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI	60						
Db	1	MKLKNPKKHOSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI	60						
Qy	61	QTGIGTAGKILGTGLGVPPFAGQIASLYSFIILGELWPKGKSQWEIFMEHVEEIIINQILTYA	120						
Db	61	QTGIGTAGKILGTGLGVPPFAGQIASLYSFIILGELWPKGKSQWEIFMEHVEEIIINQILTYA	120						
Qy	121	RNKALSDLRLGDLALAVYHESLESWVENRNNTARSVVKNQYIALELMFVQKLPSPFVSG	180						
Db	121	RNKALSDLRLGDLALAVYHESLESWVENRNNTARSVVKNQYIALELMFVQKLPSPFVSG	180						
Qy	181	BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVTRDRYSDHCHIKWYN	240						
Db	181	BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVTRDRYSDHCHIKWYN	240						
Qy	241	TGLNNLRGTNAKSWRYNQPRKMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI	300						
Db	241	TGLNNLRGTNAKSWRYNQPRKMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI	300						
Qy	301	GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYISLLSRWSNTQYMNW	360						
Db	301	GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYISLLSRWSNTQYMNW	360						
Qy	361	GGHRLSRPIGCALANTSTQGSTNTSINPVTLQFTSRDVRVTTESLAGNLFLOTPVNGVPR	420						
Db	361	GGHRLSRPIGCALANTSTQGSTNTSINPVTLQFTSRDVRVTTESLAGNLFLOTPVNGVPR	420						

QY 421 VDFHWKFPPTLPASDNFYILGYAGVGTQLODSENELPPETTQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFPPTLPASDNFYILGYAGVGTQLODSENELPPETTQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAWMNRGDLDYK 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAWMNRGDLDYK 600
QY 601 TFRITGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
DB 601 TFRITGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
RESULT 2
I39815
insecticidal protein cryv - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39815
R:Gleave, A.P.; Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1993
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for
iensis subsp. kurstaki
A:Reference number: I39815; MUID:93298009; PMID:8517758
A:Accession: I39815
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768
C:Genetics: cryv
C:Superfamily: parasporal crystal protein

Query Match 94.1%; Score 3520; DB 2; Length 719;
Best Local Similarity 92.9%; Pred. No. 2e-242;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;
QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQIASLYSFILGELWPKGKSOWEIMFHEHVEEIIINOKILTYA 120
DB 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALSDLRGLGDALAVYHESLESWENNRNTRARSVVKQVIALELMFVQKLPSPFVSG 180
DB 121 RNKALTDKGLGDALAVHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPSPFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSCHCIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRAGDYSCHCVKWS 240
QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPIKTTSQLTREYVYTDI 300
DB 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQTREYVYTDI 300
QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRNSNTQYMMNW 360
DB 301 GTVHPNPSFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMMNW 360
QY 361 GGHRLSPRTGGALNTSTQGSTNTSINPVTLOFTSRDVRVTSAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVTSAGLNFLTQPVNGVPR 420

QY 421 VDFHWKFPPTLPASDNFYILGYAGVGTQLODSENELPPETTQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFPPTLPASDNFYILGYAGVGTQLODSENELPPETTQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAWMNRGDLDYK 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAWMNRGDLDYK 600
QY 601 TFRITGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
DB 601 TFRITGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
RESULT 3
S25383
parasporal crystal protein cryIIa1 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin; parasporal crystal protein cryv
C:Species: Bacillus thuringiensis
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S25383
R:Taylor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A:Reference number: S25383; MUID:92269582; PMID:1588820
A:Accession: S25383
A:Molecule type: DNA
A:Residues: 1-719 <TAI>
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290
C:Genetics: cryv
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 93.8%; Score 3511; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 8.6e-242;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;
QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQIASLYSFILGELWPKGKSOWEIMFHEHVEEIIINOKILTYA 120
DB 61 QTGIGIAGKILGTGVPPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALSDLRGLGDALAVYHESLESWENNRNTRARSVVKQVIALELMFVQKLPSPFVSG 180
DB 121 RNKALTDKGLGDALAVHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPSPFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSCHCIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRAGDYSCHCVKWS 240
QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPIKTTSQLTREYVYTDI 300
DB 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQTREYVYTDI 300
QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRNSNTQYMMNW 360
DB 301 GTVHPNPSFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMMNW 360
QY 361 GGHRLSPRTGGALNTSTQGSTNTSINPVTLOFTSRDVRVTSAGLNFLTQPVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVTSAGLNFLTQPVNGVPR 420


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Qy 421 VDFHMKFPTLPIASDNFYILGYAGVGTQLQDSENELPPTTGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPTATGPQNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRITGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Db 601 TFRITGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 4
I39814
insecticidal protein cryVI - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: I39814
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:77933960
A;Accession: I39814
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: GB:L36338; NID:g540281; PIDN:AAC36999.1; PID:g540282
C;Genetics:
A;Gene: cryVI
C;Superfamily: parasporal crystal protein

Query Match 93.6%; Score 3503; DB 2; Length 719;
Best Local Similarity 92.5%; Pred. No. 3.2e-241;
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKMNEDYLRMSEHESIDPFVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKNSEYENVEPFVSASTI 60
Qy 61 QTGIGIAGKILGTGVPEAGQIASLYSFI LGELWPKGKQWEIFMEHVEEIIQKILTYA 120
Db 61 QTGIGIAGKILGTGVPEAGQIASLYSFI LGELWPKGKQWEIFMEHVEEIIQKISTYA 120
Qy 121 RNKALSDLRGLGDALAVYHESLESWVENNRNTRARSVVKQNYIALELMFVQKLPSPAVSG 180
Db 121 RNKALSDLRGLGDALAVYHESLESWVENNRNTRARSVVKQNYIALELMFVQKLPSPAVSG 180
Qy 181 EEVPLLPPIYAAQANLHLLLRDASIFGKEWGLSASEISFTYNQOVERTRDYSCHIKIKNYN 240
Db 181 EEVPLLPPIYAAQANLHLLLRDASIFGKEWGLSASEISFTYNQOVERTRDYSCHVKNYS 240
Qy 241 TGLNNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSYDTLVVPIKTTSQLTRVYTDAI 300
Db 241 TGLNNLRGTNAESWRYNQPRKDMTLMVLDLVALFPSYDTLVVPIKTTSQLTRVYTDAI 300
Qy 301 GTVHPNQAFSTTWYNNAPSFSAIEAAVRSRPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPNPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHRLLESRPICGALNTSTQGSTNTSINPVTLOFTSRDVRATESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPR 420
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Qy 421 VDFHMKFPTLPIASDNFYILGYAGVGTQLQDSENELPPTTGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPTATGPQNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRITGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Db 601 TFRITGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 5
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
tombacillus.
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094.1
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 62.0%; Score 2321.5; DB 2; Length 1228;
Best Local Similarity 63.6%; Pred. No. 1e-156;
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

Qy 23 TDSLKNETDI-----ELKMNEDYLRMSEHESIDPFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPACQIASLYSFI LGELWPKGKQWEIFMEHVEEIIQKILTYARNKALSRLG 130
Db 71 LGTLGVPPACQIASLYSFI LGELWPKGKQWEIFMEHVEEIIQKILTYARNKALSRLG 130
Qy 62 LGVLGVPPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQITENARNATALRLOQ 121
Db 62 LGVLGVPPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQITENARNATALRLOQ 121
Qy 131 LGDALAVYHESLESWVENNRNTRARSVVKQNYIALELMFVQKLPSPAVSGEYVPLLPPIYA 190
Db 131 LGDALAVYHESLESWVENNRNTRARSVVKQNYIALELMFVQKLPSPAVSGEYVPLLPPIYA 190
Qy 122 LGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181
Db 122 LGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181
Qy 191 QAAANLHLLLRDASIFGKEWGLSASEISFTYNQOVERTRDYSCHIKIKNYNTGLNNLRGTN 250
Db 191 QAAANLHLLLRDASIFGKEWGLSASEISFTYNQOVERTRDYSCHIKIKNYNTGLNNLRGTN 250
Qy 182 QAAANLHLLLRDASIFGSEFGLTSQEIQRYYERQVERTRDYSYCVWEYNTGLNLSRGTN 241
Db 182 QAAANLHLLLRDASIFGSEFGLTSQEIQRYYERQVERTRDYSYCVWEYNTGLNLSRGTN 241
Qy 251 AKSWRYNQPRKDMTLMVLDLVALFPSYDTLVVPIKTTSQLTRVYTDATIGTVHPNQAPA 310
Db 251 AKSWRYNQPRKDMTLMVLDLVALFPSYDTLVVPIKTTSQLTRVYTDATIGTVHPNQAPA 310
Qy 242 AASWRYNQPRKDMTLMVLDLVALFPSYDTLVVPIKTTSQLTRVYTDATIGTVHPNQAPA 299
Db 242 AASWRYNQPRKDMTLMVLDLVALFPSYDTLVVPIKTTSQLTRVYTDATIGTVHPNQAPA 299
Qy 311 STTWYNNAPSFSAIEAAVRSRPHLLDFLEKVTIYSLSRWSNTQYNNMWGHRLESRP 370
Db 311 STTWYNNAPSFSAIEAAVRSRPHLLDFLEKVTIYSLSRWSNTQYNNMWGHRLESRP 370
Qy 300 SMNTWYNNAPSFSAIEAAVRSRPHLLDFLEKVTIYSLSRWSNTQYNNMWGHRLESRP 359
Db 300 SMNTWYNNAPSFSAIEAAVRSRPHLLDFLEKVTIYSLSRWSNTQYNNMWGHRLESRP 359
Qy 371 GGALNTSTQGSTNTSINPVTLOFTSRDVRATESLAGLNLFLTQPVNGVPRVDFHMKFP 428
Db 371 GGALNTSTQGSTNTSINPVTLOFTSRDVRATESLAGLNLFLTQPVNGVPRVDFHMKFP 428
Qy 360 GGGALNTSTHGTATNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPRVDFHMKFP 419
Db 360 GGGALNTSTHGTATNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVPRVDFHMKFP 419
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QY	429	-TLPIASDNFYVLGAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLISASHVKAL	487
DB	420	QNISDRGTANYSQPYESPGIQLKXDSETELPPETTERPNYESYSHRLSHIGLISASHVKAL	479
QY	488	VYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFGDI	547
DB	480	VYSWTHRSADRTNTIIPNRITQIPWKASLPGFTGGDILRRNTGTFGDI	539
QY	548	RVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYKTFRTIGF	607
DB	540	RVTVNGPLTQRYIRIGFRYASTVDFFVSRGGITVNNFFLRMTWNGDELKYGNFVRRAF	599
QY	608	TPPFSFDVQSTFTICAWNFGSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTLFTST	667
DB	600	TPPFTTQIQDIIRTSIQGLSGNGEYVYIDKIEIIPVTATFEAEYDLERAQEAVALFTNT	659
QY	668	NPRGLTKVDYHIDOVSNLVESLSDFFYLDEKLEFEIVKYAKOIHIERNM	719
DB	660	NPRRLTKDVTYHIDQVSNLVACLSDFFCLDEKLEKVKYAKRLSDERNL	711

RESULT 6

B42459
 hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag
 C:Species: Bacillus thuringiensis
 C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
 C:Accession: B42459
 R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
 J. Bacteriol. 173, 3966-3976, 1991
 A:Title: Isolation and characterization of a novel insecticidal crystal protein gene fro
 A:Reference number: A42459; MUID:91286178; PMID:2061280
 A:Accession: B42459
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <CHA>
 A:Cross-references: UNIPROT:O8KY61; UNIPROT:Q45740; GB:M63897
 C:Superfamily: parasporal crystal protein

QY	1	MKLKNPDKHQSLSSNAKVYDIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFSASTI	60
DB	1	MKLKNPDKHQSLSSNAKVYDIATDSLKNETDIELQNIHEDCLKISEYENVEPFSASTI	60
QY	61	QTGIGIAGKILGTLGVPFAGQIASLYSIFILGELWPKGKSOMEIFMEHVEEIIQKILTVA	120
DB	61	QTGIGIAGKILGTLGVPFAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIQKILTVA	120
QY	121	RNKALSDLGLGDALAVYHESLESWENRNTARSVVKNQYIALELMFVOKLPSFAVSG	180
DB	121	RNKALTDLXGLGDALAVYHESLESWSVGNKNTARSVVKQYIALELMFVOKLPSFAVSG	180
QY	181	EEVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFFYNQVERTRDYSCHCKIKNYN	240
DB	181	EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSDHCVKWYS	240
QY	241	TGLNNLRGTNAKSWRYNPRKMTLMVLDLVALFPSPYDTLVPIKTTSQLTREYTDAL	300
DB	241	TGLNNLRGTNAKSWRYNPRKMTLMVLDLVALFPSPYDTLVPIKTTSQLTREYTDAL	300
QY	301	GTVHPNQAFASFTWYNNNAPSFAEAAVIRSPLLDFLEKVTIYSLSRWSNTQYNNMW	360
DB	301	GTVHPNPFASFTWYNNNAPSFTIESAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW	360
QY	361	GGHRLSPGICALNTSTQG	380
DB	361	GGHRLFPRTIGMLNTSTQG	380

Query Match 48.5%; Score 1813; DB 2; Length 380;
 Best Local Similarity 90.3%; Pred. No. 2.4e-121;
 Matches 343; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

S49247
parasporal crystal protein cryoCal [validated] - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIH
C;Species: Bacillus thuringiensis
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A59350; S49247
R;Lambert, B.; Buyasse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V.
Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity against
C;Reference number: A59350; MUID:96141404; PMID:8572715
A;Accession: A59350
A;Molecule type: DNA
A;Residues: 1-1157 <LAM>
A;Cross-references: UNIPROT:Q45733; EMBL:D37527; NID:g547554; PIDN:CAA85764.1; PID:g547554
A;Experimental source: serovar tolworthi
C;Comment: This parasporal crystal protein, active against corn borer and other insects,
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

	Query Match	40.3%; Score 1507; DB 1; Length 1157;
	Best Local Similarity	44.1%; Pred. No. 9e-99;
	Matches	Conservative 116; Mismatches 217; Indels 80; Gaps 15;
QY	26	LKNETDIELKNMNEDYLRMSEHSIDPFVSAS-----TTQTGIGIAGKILGTIGVPPF 78
DB	29	LASDPNAALQNMYKYQLQWTDDEYDYSINPSLSISGRDAVQTALTVVGRILGALGVPPF 88
QY	79	AQGIASLYSFITLGELMPKGKSQ-WEIFMEHVVEEIIQKILTAYRNKALSRLGLGDALAV 137
DB	89	SGQIVSFYQFLNTLTPNDTAIWFAFMQVEELVNQQITEFARNQALARLQGLGDSFNV 148
QY	138	YHESLESWVENNNTRARSVVKNOVIALMLFVQKLPSFAVSGBEVPLPIYAQAANLHL 197
DB	149	YQRSLQNLADNRNLNVVRRAQFIALDLDFVNAIFLPAVGQOVPLL SVTAAVNLHL 208
QY	198	LLLRDASIFGKEWGLSASEISTFFYNRQVERTRYSDHCIKWYNTGLNLRGNNAKSWRY 257
DB	209	LLLKDASLFGEWGFGTEIGEISTYYDRQLTAKTYNCETWYNTGLDRURGTWTESWLRY 268
QY	258	NQPRKDMTLMLDLVALFPSYDTLVYPKITSOLTREVTYDAIGTVHPNQAFASTTWYNN 317
DB	269	HQPRREMTLVLDVVALFPYYDVRLPYPTGSNPQLTREVTDPIVENPAPPANGLCRRWGTN 328
QY	318	NAPFSFAIEAAVIRSHLLDFLEKVITYILLSRW-S-NQVMNMGGHRLSRPIG-GALN 375
DB	329	PYNTFSELENAFIRPHFLFDRLNSLTISS--NRFPVSSNFMDYWSGHTLRRSYLNDSSAQV 386
QY	376	TSTQG---STNTSINP---VTLOFTSRDRVRTESLAGL-----NLF--LTQPYN 416
DB	387	EDSVGLITTTATINPGVDGINRIESTAVDFRSALIGIYGVNRASFVPGLFNGTTSPAN. 446
QY	417	GVPKRVDFHWKFPTLPFIASDNFYVLGYAGVTGLODSENEULPP-ETTGPNYVESYHRLSH 475
DB	447	GGCR-----DLYDINDLPPDESTG-----SSTHRLSH 474
QY	476	IGLIS-----ASHVKALVYSWTHRSADRNTNIEPNSTIQIPLVKAFNLSGAADV 526
DB	475	VTFPSFQTNQAGSIANAGSVPTVWTRRDVDLNTITPNRITQLPLVKASAPVSGTTVLK 534
QY	527	PGPTGGDILRRNTGTGDIRVINPINPPFAQRYRVRIRYASTTDLQFHTSINGKANQGN 586
DB	535	PGPFTGGGILRRNTGTGLTRVTVNSPLTQQYRLRVRFPAFTGNTFIRVLGGVSGDVR 594
QY	587	FSATNWRGDDLYKTFRTIGFTT-----PFSFSDVQSTFTIGAMNPFSSGNEVIYDRIEF 640
DB	595	LGSITMNRGQELTYESFFREFTTTGPFNPPFTTQAEILTVNAEGVSTGCGEYIIDRIEI 654
QY	641	VPVEVYEAHYDFEKAQEKVALTFTSTNPRGLTKTDVKDYHDIDQVSNLIVESDESDEFYDLEK 700
DB	655	VPVNPAREADELEAAKKAVASLFRTRD-GLQVNVTDYQVDQAANLVSCUSDEQYGHDK 713
QY	701	RELFEIVKVAQKHIERNM 719

C; Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text_change 09-Jul-2004
C; Accession: A90025; A91560; A90955; S14555; A36461; A24172; A29043; J00002
R; Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A; Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxins
A; Reference number: A90025
A; Accession: A90025
A; Molecule type: mRNA
A; Residues: 1-1155 <ON>
A; Cross-references: UNIPROT:P06578
A; Experimental source: subsp. kurstaki
R; Geisler, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A; Title: The hypervariable region in the genes coding for entomopathogenic
A; Reference number: A91560; MUID:87163505; PMID:3557124


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Db 228 RYNQFRRLTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPV-----L 273
Qy 316 NNNAPSP---SAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMMNWGGHRLSPIG 371
Db 274 ENFDGSPRGSQAQIEGS--IRSPHMLDILNSITIYTDHR--GEY--YWSGHQIMASPVG 327
Qy 372 -----GAL-NTSTQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVP 419
Db 328 FSGPEFTPLPGTMGNAAPQORIVAQLGQGVYRTLSSTLYRRPFENIGIN--NQQLSVLD 384
Qy 420 RVDHFWKFTPLPIASDNFYLYGAGVGTQQLQDSNELPPTTGPQNYESYSHRLSHIGLI 479
Db 385 GTEFAYG-----TSSNLPSSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMF 436
Qy 480 -----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTG 532
Db 437 RSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVYKPGPGFTG 496
Qy 533 GDILRRTNTGFDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMN 592
Db 497 GDILRRTSPQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMS 556
Qy 593 RGEDLDYKTRTIGTTPFSFSDVOSTFTIGAMNFFSSGNEVYIDRIEFPVVEVYEAAYD 652
Db 557 SCSNLQSGSFRVGTFTPFNSGSSVFTLSAHVFNNGNEVYIDRIEFPVPAEVTFEAYD 616
Qy 653 FEKAQEKVTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDDEFYLDKRELFIIVKYAKQ 712
Db 617 LERAQKAVNELFTSSNQIGLKTVDYHIDQVSNLVESLSDDEFYLDKRELSEKVKHAKR 676
Qy 713 IHIERNM 719
Db 677 LSDERNL 683

RESULT 12
A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 39.6%; Score 1480.5; DB 2; Length 1156;
Best Local Similarity 46.5%; Pred. No. 6.9e-97;
Matches 310; Conservative 105; Mismatches 195; Indels 57; Gaps 12;

Qy 76 VFPAGQIASLYSFILGELWPKGSKQWEIFMEHVEEIIINQKILTYARNKALSDLRGLGDAL 135
Db 51 VPGAGFVLGLVDIIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAISRLGLESLNLY 107

Qy 136 AVTHESLESVENNRNTRARVVKNQYIAELMFVQKLPFAVSGEEVPLLPYIAQANL 195
Db 108 QIYAESFREWEADPTNPALREEMRIQFNDKNSALTAPLFAVQNYQVPLLSVYVQAANL 167

Qy 196 HULLLRDASIFGKEMGLSASBISTFYNRQVRTRDYSDHCIKWNTGLNNLRGNTAKSWV 255
Db 168 HUSVLRDVSVFGQWGFDAATNSRYNDLRNLIGNYTDHVRWNTGLERWVGPDSDRWI 227

Qy 256 RYNQFRKDMTLMVLDLVALFSPYDYLVIYPIKTTSTQLTREVYTDAGTVPNQAFASITWY 315
Db 228 RYNQFRRLTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPV-----L 273

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Qy 316 NNNAPSF---SAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMMNWGGHRLSPIG 371
Db 274 ENFDGSPRGSQAQIEGS--IRSPHMLDILNSITIYTDHR--GEY--YWSGHQIMASPVG 327
Qy 372 -----GAL-NTSTQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVP 419
Db 328 FSGPEFTPLPGTMGNAAPQORIVAQLGQGVYRTLSSTLYRRPFENIGIN--NQQLSVLD 384
Qy 420 RVDHFWKFTPLPIASDNFYLYGAGVGTQQLQDSNELPPTTGPQNYESYSHRLSHIGLI 479
Db 385 GTEFAYG-----TSSNLPSSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMF 436
Qy 480 -----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTG 532
Db 437 RSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVYKPGPGFTG 496
Qy 533 GDILRRTNTGFDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMN 592
Db 497 GDILRRTSPQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMS 556
Qy 593 RGEDLDYKTRTIGTTPFSFSDVOSTFTIGAMNFFSSGNEVYIDRIEFPVVEVYEAAYD 652
Db 557 SCSNLQSGSFRVGTFTPFNSGSSVFTLSAHVFNNGNEVYIDRIEFPVPAEVTFEAYD 616
Qy 653 FEKAQEKVTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDDEFYLDKRELFIIVKYAKQ 712
Db 617 LERAQKAVNELFTSSNQIGLKTVDYHIDQVSNLVESLSDDEFYLDKRELSEKVKHAKR 676
Qy 713 IHIERNM 719
Db 677 LSDERNL 683

RESULT 13
S02134
parasporal crystal protein cryIc1 - Bacillus thuringiensis (strain aizawai IC1)
N:Alternate names: delta-endotoxin IC1; entomocidal crystal protein
C:Species: Bacillus thuringiensis
A:Variety: strain aizawai IC1
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S02134; S04994
R:Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A:Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal
A:Reference number: S02134; MUID:89083518; PMID:3205732
A:Accession: S02134
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1155 <HAI>
A:Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278
A:Experimental source: strain aizawai IC1
R:Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes
A:Reference number: S04994; MUID:89362455; PMID:2769751
A:Accession: S04994
A:Molecule type: DNA
A:Residues: 429-449, 'A', 451-724 <HAW>
A:Cross-references: EMBL:X16315
A:Experimental source: strain aizawai IC1
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 39.1%; Score 1463.5; DB 2; Length 1155;
Best Local Similarity 46.0%; Pred. No. 1.1e-95;
Matches 307; Conservative 105; Mismatches 198; Indels 57; Gaps 12;

Qy 76 VFPAGQIASLYSFILGELWPKGSKQWEIFMEHVEEIIINQKILTYARNKALSDLRGLGDAL 135
Db 51 VPGAGFVLGLVDIIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAISRLGLESLNLY 107

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds
(without alignments)
3909.384 Million cell updates/sec

Title: US-10-019-823B-59
Perfect score: 3742
Sequence: 1 MKLKNPKHQSLSSNAKVDC.....KRELFEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3520	94.1	719	16	US-10-782-020-10
2	3520	94.1	719	16	US-10-782-141-8
3	3368.5	90.0	710	15	US-10-428-961-42
4	2324.5	62.1	1228	16	US-10-809-953-10
5	2314.5	61.9	1207	10	US-09-988-462-7
6	2234	59.7	1227	15	US-10-428-961-63
7	2219	59.3	1186	9	US-09-826-660-23
8	2170.5	58.0	1228	15	US-10-428-961-38
9	2170.5	58.0	1228	15	US-10-614-524-2
10	1982	53.0	643	9	US-09-826-660-25
11	1734.5	46.4	1167	14	US-10-089-678-1
12	1683.5	45.0	653	15	US-10-428-961-6
13	1657.5	44.3	1157	16	US-10-782-141-16

14	1514	40.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1514	40.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1514	40.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1500.5	40.1	1156	14	US-10-099-285-72	Sequence 72, Appl
18	1500.5	40.1	1156	15	US-10-428-961-28	Sequence 28, Appl
19	1494	39.9	1210	13	US-10-032-717-4	Sequence 4, Appli
20	1494	39.9	1210	14	US-10-414-637-4	Sequence 4, Appli
21	1494	39.9	1210	15	US-10-606-320-4	Sequence 4, Appli
22	1480.5	39.6	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1480.5	39.6	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1480.5	39.6	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1480.5	39.6	1181	10	US-09-988-462-11	Sequence 11, Appl
26	1480.5	39.6	1181	10	US-09-988-462-13	Sequence 13, Appl
27	1480.5	39.6	1181	10	US-09-988-462-15	Sequence 15, Appl
28	1480.5	39.6	1181	10	US-09-988-462-17	Sequence 17, Appl
29	1480.5	39.6	1181	10	US-09-988-462-28	Sequence 28, Appl
30	1480.5	39.6	1181	15	US-10-136-998A-4	Sequence 4, Appli
31	1480.5	39.6	1181	15	US-10-136-998A-8	Sequence 8, Appli
32	1480.5	39.6	1181	15	US-10-136-998A-10	Sequence 10, Appl
33	1480.5	39.6	1181	15	US-10-136-998A-12	Sequence 12, Appl
34	1475.5	39.4	1177	14	US-10-035-060-6	Sequence 6, Appli
35	1472.5	39.4	1177	14	US-10-102-469-24	Sequence 24, Appl
36	1470.5	39.3	1177	14	US-10-035-060-2	Sequence 2, Appli
37	1470.5	39.3	1177	14	US-10-035-060-8	Sequence 8, Appli
38	1447	38.7	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1436.5	38.4	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1436.5	38.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1391	37.2	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1386.5	37.1	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1386.5	37.1	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1386.5	37.1	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1386.5	37.1	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 94.1%; Score 3520; DB 16; Length 719;
Best Local Similarity 92.9%; Pred. No. 5.4e-287;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

Qy	1	MKLKNPKHQSLSSNAKVDCIATSLKNETDIELKMNEDYLRMSEHSIDPFVSASTI	60
Db	1	MKLKNPKHQSLSSNAKVDCIATSLKNETDIELKMNEDYLRMSEHSIDPFVSASTI	60
Qy	61	QTGIGIAGKILGTGLVFPFAGQIASLYSFIILGELWPKGKQWEIFMEHVBEIINOKILTYA	120
Db	61	QTGIGIAGKILGTGLVFPFAGQIASLYSFIILGELWPKGKQWEIFMEHVBEIINOKILTYA	120

NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 90.0%; Score 3368.5; DB 15; Length 710;
Best Local Similarity 89.2%; Pred. No. 3e-274;
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;

Qy 1 MKLKNPKHQSLSSNAKVDKIATDSLKNDIELKNMNNEDYLRMSHEHSDPFSASTI 60
Db 1 MKSKNQMHQSLSSNAKVDKNTGSLNNTNTLQNFN-----HEGIEPFSVSTI 51
Qy 61 QTGIGIAGKIILGTGVPFAGQIASLYSIFILGELWPKGQWEIFMEHVEEIIINQKILTYA 120
Db 52 QTGIGIAGKILGNLGVFPAGQVAGSIFILGELWPKGQWEIFMEHVEELINQKISTYA 111
Qy 121 RNKALSDRLGLDALAVYHESLESWENRNNTARSVVKQYIALELMFVQKLPSFAVSG 180
Db 112 RNKALADLGLDALAVYHESLESWENRNNTARSVVKQYIALELMFVQKLPSFAVSG 171
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHIKWYN 240
Db 172 BEVPLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCWKYN 231
Qy 241 TGLNLRGCTNAKSWRYNQPKDWTLMVLDLVALFPSTYDLVPIKTTSQLTRVYTDAL 300
Db 232 TGLNRLGNNAESWRYNQPKDWTLMVLDLVALFPSTYDMYPIKTTAQLTRVYTDAL 291
Qy 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNW 360
Db 292 GTVHPNPSFTTWNNAAPSFTIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 351
Qy 361 GGHRLBSRPICGALNTSTOGSTNTSINPVTLOFTSRDVTYTESLAGLNLFLTOPVNGVPR 420
Db 352 GGHKLEFRITGTLNTSTOGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTOPVNGVPR 411
Qy 421 VDFHWKPEPLPIASDNFYILGYAGVGTQLODSENELPPETGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKFPVTHPIASDNFYYPGYAGVGTQLODSENELPPETGQPNYESYSHRLSHIGLIS 471
Qy 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRNTN 540
Db 472 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRKN 531
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 532 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 591
Qy 601 TERTIGTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660
Db 592 TERTIGTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDPEKAQEKV 651
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 652 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Botterman, Herman
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 62.1%; Score 2324.5; DB 16; Length 1228;
Best Local Similarity 63.6%; Pred. No. 5.3e-186;
Matches 454; Conservative 85; Mismatches 166; Indels 9; Gaps 5;

Qy 12 LSSNAKVDKIATDSLKNDIELKNMNNEDYLRMSHEHSDPFSASTIQTGIGIAG 68
Db 1 LSNKNEVEIINAVSNHSAQMDL-LPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAG 59
Qy 69 KILGTGVPFAGQIASLYSIFILGELWPKGQWEIFMEHVEEIIINQKILTYARNKALS 128
Db 60 RILGLVGPVFPAGQIASLYSIFILGELWPKGQWEIFLEHVEQLINQITENARTALARL 119
Qy 129 RGLGDALAVYHESLESWENRNNTARSVVKQYIALELMFVQKLPSFAVSGEVPPLPI 188
Db 120 QGLGDSFRAVQOQSLDLEWLNRRDARTSRVLHTQYIALELDLFLNAMPFAIRNQEVPLLMV 179
Qy 189 YQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHIKWYNGLNLRG 248
Db 180 YQAANLHLLLRDASLFGSEFGLTSQETQRYVERQVTRDYSQCYEWYNTGLNSLRG 239
Qy 249 TNAKSWRYNQPKDWTLMVLDLVALFPSTYDLVPIKTTSQLTRVYTDALGTVPHPNQ 308
Db 240 TNAASWRYNQPKDWTLMVLDLVALFPSTYDTRTPINTSAQLTRVYTDALGATGVN 297
Qy 309 FASTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNWGGHRLBSR 368
Db 298 MASMNWNNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNWGGHRLBSR 357
Qy 369 PIGGALNTSTOGSTNTSINPVTLOFTSRDVTYTESLAGLNLFLTOPVNGVPRVDFHWK 426
Db 358 PIGGGLTSTHGATNTSINPVTLPFASRDVYRTESYAGVLLWGLIYLEPIHGVPVFRNFT 417
Qy 427 FP-TLPIASDNFYILGYAGVGTQLODSENELPPETGQPNYESYSHRLSHIGLISASHVK 485
Db 418 NPQNSIDRGTYANSQPYESPGLQKDSLETLPETTERPNYESYSHRLSHIGLILQSRVN 477
Qy 486 ALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRNTNTGTFG 545
Db 478 VPVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRNTNTGTFG 537
Qy 546 DIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYKFTPTI 605
Db 538 PIRVTNGPLTQRYRIGRFRVASTVDVDFVSRGGTIVNNFRFLRTMNSGDELKXGNFVR 597
Qy 606 GFTTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDPEKAQEKVTALEFT 665
Db 598 AFTTTPFTTQIDIRTSIQGLSGNGEVYIDKIEIIPVATFAEYDLEKRAQEAVALFT 657
Qy 666 STNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 658 NTNPRRLKTDVTDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7
Query Match 61.9%; Score 2314.5; DB 10; Length 1207;
Best Local Similarity 65.4%; Pred. No. 3.6e-185;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

40 EYLRMEHESIDPFVASTQTGTGIGKILGVLGVPAGQIASLYSIFILGELWPKGS 99
10 EYLRMEHESIDPFVASTQTGTGIGKILGVLGVPAGQIASLYSIFILGELWPKGS 69

100 QWEIFMEHVEEIIINQKILTYARNKALSDRLGDLALAVHESLESWENNRTRARSVVK 159
70 QWEIFMEHVEEIIINQKILTYARNKALSDRLGDLALAVHESLESWENNRTRARSVVK 129

160 NOYIAELMFMVQKLPSPAVSGEVEPLPIYAQAANLHLLLRDASIFGKEWGLSASRIST 219
130 TQYIAELDLFNLAMPLFAIRNQEVPLLMVTAQAANLHLLLRDASIFGKEWGLSASRIST 189

220 FYNQVERTRDYSYDHCICWYNTGLNLRGTNAKSWVRYNQFRKDWTLMLVLDLVALFSSYD 279
190 YERQVERTRDYSYDHCICWYNTGLNLRGTNAKSWVRYNQFRKDWTLMLVLDLVALFSSYD 249

280 TLVPIKTTSQLTRVYTDAGTGVN--MASMWNVNNAPSFSAIEAAVIRSPHLLDFL 339

250 TRTYPINTSAQLTRVYTDAGTGVN--MASMWNVNNAPSFSAIEAAVIRSPHLLDFL 307
340 EKVTIYLSLRWSNTQYMMWGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVS 399
308 EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFSRDVS 367
400 RTESLAGLNLFF--LTQPVNGVPRVDFHWKFP-TLPIASDNFYLYGVAGVGTQLODSENEL 456
368 RTESYAGVLLWGIYLEPIHGVPVFRFNTNPQNISDRGTANYSQPYESPGQLKDSSETEL 427
457 PPETTPQPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAF 516
428 PPETTPQPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAF 487
517 NLSSGAAVVGPGFTGGDILRRNTGTGDIRVNNPFAQRYRVRIRYASTDLOFHTS 576
488 ELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNNPFAQRYRVRIRYASTDLOFHTS 547
577 INKAINQGNFSAATNRGDELDTYKTFRTIGFTTFFSFDVQSTFTTIGAWNFSSENEVID 636
548 RGGTTVNNFRFLRTWNSGDELKYGNFVRAFTTPTFTQIQDIIRTSIQGLSGNGEYIID 607
637 RIEFVPEVTEYAEYDFEKAQKVYALFTSTNPRGLKTDVYHIDQVSNLYESLSDEFY 696
608 KLEIIPVATFEAEYDLERAQEAVALFTNTNPRRLKTDVYHIDQVSNLYESLSDEFY 667
697 LDEKRELFEIVKYAKQIHIERNM 719
668 LDEKRELFEIVKYAKQIHIERNM 690

RESULT 6

US-10-428-961-63
Sequence 63, Application US/10428961
Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Donovan, William P.

APPLICANT: Gilmer, Amy J.

APPLICANT: Ruper, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201--1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PatentIn version 3.2

SEQ ID NO 63

LENGTH: 1227

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 59.7%; Score 2234; DB 15; Length 1227;

Best Local Similarity 60.8%; Pred. No. 2.2e-178;

Matches 434; Conservative 100; Mismatches 162; Indels 18; Gaps 3;

23 TDSLKNETDI---ELKNMNN-----EDYLRMEHESIDPFVASTQTGTG 65

2 TSNRKNENEIINALSIPAVNSHAQMNLSLDARIEDSLCAEGNNIDPFVASTQTGTG 61

66 IAGKILGTGVFPAGQIASLYSIFILGELWPKGSOWEIFMEHVEEIIINQKILTYARNKAL 125

62 IAGRILGVLGVPFAGQIASLYSIFILGELWPKGSOWEIFMEHVEEIIINQKILTYARNKAL 121

126 SDRLGDLALAVHESLESWENNRTRARSVYKNOYIAELMFMVQKLPSPAVSGEVEPL 185

Query Match 58.0%; Score 2170.5; DB 15; Length 1228;
Best Local Similarity 60.5%; Pred. No. 4.9e-173;
Matches 435; Conservative 98; Mismatches 171; Indels 15; Gaps 8;
US-10-614-524-2

12 LSSNAK-----VDKIATDSLKN-ETDIELK-MNMNEDYLRMSHEHESIDPFVFASTIQTGI 64
1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
65 GIAGKILGTGVFPAGQIASLYSFIIGELWPKGKQWEIEMFHEVVEEIIINQILTYARNKA 124
61 NIAGRIILGVLGVPAGQIASFYSLVGLWPRGRDQWEIEMFHEVVEEIIINQILTYARNKA 120
125 LSDRLGLDALAVHESLESWVENRNRTRSVVKNQYIALELMFVQKLPSPAVSGEVP 184
121 LARLQGLGDSFRAYQOSLEDWLENRDDARTSRVLTQYIALELDFLNAMPFLFAIRNOEVP 180
185 LLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCICKWYNTGLN 244
181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYVERQVEQTRDYSYCVWEYNTGLN 240
245 NLRGTNAKSWVRVYNQFRKDMTLMVLDLVALFPSYDTLVPIKTTSQLTREVYTDAGTVH 304
241 SLRGTNAASWVRVYNQFRDLTLGLVLDLVALFPSYDTLVPIKTTSQLTREVYTDAGTVH 300
305 PNOAFASWVRVYNQFRDLTLGLVLDLVALFPSYDTLVPIKTTSQLTREVYTDAGTVH 364
301 VN--MASMWNYNNAAPSAIEATAVIRSPHLLDFLEQITIFSTSRWSATRHMTYWRGHT 358
365 LESRPIGALNTSTOGSTNTSINPVTLOFTSRDVYRTESLAGLNL--LTQPVNGVPRVD 422
359 IQSRPIGGGLNTSTHGTNTSINPVLSPFSDRVYRTESLAGLNL--LTQPVNGVPRVD 418
423 FHWKFP--TLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS 480
419 FNRNPQNTFPGTAN--YSQPYESPLQKQDSELPETTERPNYESYSHRSLHIGLIS 477
481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
478 QSRVHVVPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 537
541 TGFGRDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
538 NGSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQ 597
601 TFRITGFTTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
598 SFRFAEPFVGISASGSQ--TAGISISNNAGRQTFHFDKIEFIPITATFEAYDLERAQEA 656
661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM 719
657 NALFTNTNPRRLKTDVTDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM 715

RESULT 9
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from *Bacillus thuringiensis*.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: *Bacillus thuringiensis*
US-10-614-524-2

Query Match 58.0%; Score 2170.5; DB 15; Length 1228;
Best Local Similarity 60.5%; Pred. No. 4.9e-173;
Matches 435; Conservative 98; Mismatches 171; Indels 15; Gaps 8;
US-10-614-524-2

12 LSSNAK-----VDKIATDSLKN-ETDIELK-MNMNEDYLRMSHEHESIDPFVFASTIQTGI 64
1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
65 GIAGKILGTGVFPAGQIASLYSFIIGELWPKGKQWEIEMFHEVVEEIIINQILTYARNKA 124
61 NIAGRIILGVLGVPAGQIASFYSLVGLWPRGRDQWEIEMFHEVVEEIIINQILTYARNKA 120
125 LSDRLGLDALAVHESLESWVENRNRTRSVVKNQYIALELMFVQKLPSPAVSGEVP 184
121 LARLQGLGDSFRAYQOSLEDWLENRDDARTSRVLTQYIALELDFLNAMPFLFAIRNOEVP 180
185 LLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCICKWYNTGLN 244
181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYVERQVEQTRDYSYCVWEYNTGLN 240
245 NLRGTNAKSWVRVYNQFRKDMTLMVLDLVALFPSYDTLVPIKTTSQLTREVYTDAGTVH 304
241 SLRGTNAASWVRVYNQFRDLTLGLVLDLVALFPSYDTLVPIKTTSQLTREVYTDAGTVH 300
305 PNOAFASWVRVYNQFRDLTLGLVLDLVALFPSYDTLVPIKTTSQLTREVYTDAGTVH 364
301 VN--MASMWNYNNAAPSAIEATAVIRSPHLLDFLEQITIFSTSRWSATRHMTYWRGHT 358
365 LESRPIGALNTSTOGSTNTSINPVTLOFTSRDVYRTESLAGLNL--LTQPVNGVPRVD 422
359 IQSRPIGGGLNTSTHGTNTSINPVLSPFSDRVYRTESLAGLNL--LTQPVNGVPRVD 418
423 FHWKFP--TLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS 480
419 FNRNPQNTFPGTAN--YSQPYESPLQKQDSELPETTERPNYESYSHRSLHIGLIS 477
481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
478 QSRVHVVPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 537
541 TGFGRDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
538 NGSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQ 597
601 TFRITGFTTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
598 SFRFAEPFVGISASGSQ--TAGISISNNAGRQTFHFDKIEFIPITATFEAYDLERAQEA 656
661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM 719
657 NALFTNTNPRRLKTDVTDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM 715

RESULT 10
US-09-826-660-25
; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardneau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05

;; PRIOR APPLICATION NUMBER: 09/178,252
;; PRIOR FILING DATE: 1998-10-23
;; PRIOR APPLICATION NUMBER: 60/065,215
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/076,445
;; PRIOR FILING DATE: 1998-03-02
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 25
;; LENGTH: 643
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match 53.0%; Score 1982; DB 9; Length 643;
Best Local Similarity 59.6%; Pred. No. 1.3e-157;
Matches 383; Conservative 94; Mismatches 148; Indels 18; Gaps 3;

Qy 23 TDSLKNETDI-----ELKMMN-----EDYLRMSEHSIDPFVSASTIQTGIG 65
Db 2 TSNRKNENIINALSIPAVNSHSAQWNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGIN 61

Qy 66 IAGKILGTGVPPFAGQIASLYFILGELWPKGSQWEIEMFHEVHEEIIINOKILTYARNKAL 125
Db 62 IAGRIILGVLPFAGQIASFYSLFGELWPKGRDPEWIEFHEVQEOLIRQVNTRETRTAL 121

Qy 126 SDLRGLGDALAVYHESLESWENRNNTRARSVVKNQYIALELMPVQKLPSPFAVSGEEVPL 185
Db 122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSVLTQYIALELDFLNPMLFAIRNQEVPL 181

Qy 186 LPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNRQVTRDYSCHIKWYNTGLNN 245
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIORYERQVEKREYSYCARWYNTGLNN 241

Qy 246 LRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTSQLTRREVYTDAGTWHV 305
Db 242 LRGTNAESWLRYNQFRDRLTLGVLDLVALPSPSYDTRVYPMNTSAQLTREIYTDPIGRNTA 301

Qy 306 NQAFASITWYNNAPSFSAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMWGGHRL 365
Db 302 PSGFASTNWFNNAPSFSAEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYNNYVWGHRL 361

Qy 366 ESRPIGALNTSTQGSTNTSINPVLQFTSRDVYRTESLAGLNLFLTOPVNGVPRVDFHW 425
Db 362 ESRTIRGSLSTSTHGNTSINPVLQFTSRDVYRTESFAGINILLTTPVNGVPPWAFNW 421

Qy 426 KPFTPLPIASDNFYLYAGVGTQLQDSENELPPTTGPQNYESYSHRLSHIGLISASHVK 485
Db 422 RNPLNSLRGSLLYTIGYTGVTQLDFDSELPPTTERPENYESYSHRLSIRLISGNTLR 481

Qy 486 ALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRKTNTGTFG 545
Db 482 APVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGTSVVGPGFTGGDIIRTNVNGSVL 541

Qy 546 DIRVNINPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRPTI 605
Db 542 SMGLNFNTSLQRYVRVRAASQTMVLRVTVGSTTFDQGFPSMTSAMESLTSQSFRFA 601

Qy 606 GFTPTTFSQSTFTTIGAMNFGSSGNEVYDRIEFVPPVEVTE 648
Db 602 EPPVGISASGSQ-TAGISISNAGKQTFHFDKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

;; FILE REFERENCE: Q68821
;; CURRENT APPLICATION NUMBER: US/10/089,678
;; CURRENT FILING DATE: 2002-05-02
;; PRIOR APPLICATION NUMBER: JP 2000-236140
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: PCT/JP01/06660
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 1167
;; TYPE: PRT
;; ORGANISM: Bacillus thuringiensis
US-10-089-678-1

Query Match 46.4%; Score 1734.5; DB 14; Length 1167;
Best Local Similarity 48.2%; Pred. No. 2.3e-136;
Matches 366; Conservative 123; Mismatches 210; Indels 61; Gaps 14;

Qy 1 MKNKPDKHQSL-----SSNAKVDTKIATDSLKNETDIELKMMNEDYLRMSEHE-----SI 51
Db 1 MSPNNQNEYBILDASSSTSVDSNSVRYPLANDQTTLQNMNVDYLRMSEGENPELFGNP 60

Qy 52 DPFVSASTIOTGIGIAGKILGTGVPPFAGQIASLYFILGELWPKGK-SQWEIEMFHEV 110
Db 61 ETFISSTVOTGIGIVGVQVGLGALGVPPFAGQIASFYFIVGQLWPSSTVSVWEMIMKQVED 120

Qy 111 IINQKILTVAARNKALSRLGLGDALAVYHESLESWENRNNTRARSVVKNQYIALELMFV 170
Db 121 LIDQKITDSVRKTTALAGLQGLGDGLDVYQSKLWLENRNDTRARSVVVQTYIALELDFV 180

Qy 171 QKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNRQVTRD 230
Db 181 AKIPSPAISQOEVLPLSVYAQAANLHLLLRDASIFGAEWGFTPEGEISTFYDRQVTRTAQ 240

Qy 231 YSDHCIKWYNTGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTSQ 290
Db 241 YSDYCVKWTNTGLDKLGTNAASWLKYHQRREMTLLVLDLVALFPNVDTRYPIETTAQ 300

Qy 291 LTREVYTDAGTWHVNPQAFASITWYNNAPSFSAEAAVIRSPHLLDFLEKVTIYSLLS- 349
Db 301 LTREVYTDPIVFNRETSGFCRRWSLNSDISFSEVESAVIRSPHLLDFLSEIEFYTTTAAQ 360

Qy 350 -RWSNTQYNNMWGGHRLSRRPIGALNTSTQGSTNTSINPVT-----LQFTSRDVYRTE 402
Db 361 LPLNNTLEYVWVGHSIKYK-----NINASSALERNYGTITSNKIKYDLANKDIFQVR 414

Qy 403 SL-AGLNLFLTOPVNGVPRVDFHWKFPPLPIASDNFYLYAGVGT-----T 447
Db 415 SLGADLANVYAQ-VYGVYPASF-----TLDDKN---TSGSGVGGFTYKPHHTMQVCT 463

Qy 448 QLQDSENELPPTTGPQNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRSADRT 499
Db 464 QNYNTIDEIPPE--NEPLSRGYSHRLSHITSYSPSKNASSPARYGNLVPFAWTHRSADVT 521

Qy 500 NTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRKTNTGTFGDIRVNINPPFAQRY 559
Db 522 NTVYSDKITQIPVVKAKHTLVSGTTVKGPGFTGNNILKRTSSGPLAVTSVSKSPLSQRY 581

Qy 560 RVRIYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRPTTPTTSPFSQVST 619
Db 582 RARIYASTTNLRFLVFTISGTRIYSINVNKTMKGGDDLTFTNTFDLATIGTATFTSNTSDS 641

Qy 620 FTIGAWNFGSSGNEVYDRIEFVPPVEVTEAEYDFEKAQKVTALFTSTNPRGLKTDVKDY 679
Db 642 LTVGADSFASGGEVYVDKFLIPVNATFAEEDLDVAKAVNGLFTSKKD-ALQTSVTDY 700

Qy 680 HIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719
Db 701 QVNOAANLVECLSDLEYLPNEKRLMLMDAVKEAKRLVQARNL 740

RESULT 12

u8-10-019-823b-59.rapb

[illegible]

Db 527 TQIPAVKGMVLYLGGVVQPGFTGGDILKRTNPSILGTFAVTNGLSQRVVRIRVAS 586
Qy 568 TTDLQFHTSINGKAINQGNFSATMRGDLDTKPTRTIGTFTTSPFSVDQSTFTIGAWNF 627
Db 587 TTDPER-TLYLGDTEIKRNFKNMTDNGASUYETFKFASFITDQFRETQDKILLSWGDF 645
Qy 628 SSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKVKTALFTSTNPRGLKTDVKVDHIDQVSNL 687
Db 646 SSGQEVYIDRIEFVPEVVEVYAEYDFEKAQEKVKTALFTSTNPRGLKTDVKVDHIDQVSNL 704
Qy 688 VESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 705 VECLSDDLYPNEKRLLFDAVREAKRLSGARNL 736
RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2
Query Match 40.5%; Score 1514; DB 13; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.7e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;
Qy 1 MKLKPNPKHQSLSSNAKVDKIATDS---LKNETDIELKNNMEDYLRMSHESID---- 52
Db 1 MSPNNQNEYEIIDATPST-SVNSDNRYPFANEPTNALQNMMDYKDYKMSAGNASEYPGS 59
Qy 53 PFVSAS---TIQTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKG-KSQWEIFMEHV 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQV 119
Qy 109 EEIINQKILTYARNKALSDRLGLDALAVTHESLESWENNRNTRARSVVVKQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNRSLRDLVRNRFELDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVERT 228
Db 180 FTQYMPFSRVNTFEVFPFLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYYDRQMKLT 239
Qy 229 RDSYDHCIKWNTGLNLRGNTAKSWRVYNOFRKDMTLMVLDLVALFSPYDYLVPYIKTT 288
Db 240 AEYSDDHCWKYETGLAKLKGTSKQWVDVYQFRREMTLAVLDVVALFPNYDTRTPMETK 299
Qy 289 SOLTREYVTDAGTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLDFLEKVTIYSL 348
Db 300 AQLTREYVTDPLGAVNV---SIGSWY-DKAPSGFVIESVIRPHVFDYITGLTVYVTS 355
Qy 349 SRWSNTQYMMWGGHRLSRPIGGALNTSTQGSTNTSINPV-TLQFTSRDVRVRESLAGL 407
Db 356 RSISSARYIRHWAGHQISYHRVSRGSLNQMYGTQNQLHSTSTDFDTYDIYKTLKSDAV 415

Qy 408 NLFLTOP-----VNGVPRVDPHW-----KFPTL---PIASDNFYFLGYAGVGTQLODSE 453
Db 416 LLDIVYFGYTYIFFGMEVEFFMVNQLNTRKTLKYNPVS KD-----IIASTRDSE 466
Qy 454 NELPPTTGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIENPSITQI 510
Db 467 LELPPTSDQPNYESYSHRLCHITSIPAGNTTGLVPVFSWTHRSADLNNTIYSDKITQI 526
Qy 511 PLVKAFNLSSGAAVVRGPGTGGDILR-RTNTGTGFDI---RVNINPPFAQRYRVRIRYA 566
Db 527 PAVKWDNLFPVVPVVGPGHTGGDLLQVNRSTGSGVTGLFLARYGLALEKAGKRVRLRYA 586
Qy 567 STTDLQFHTSINGKAINQGNFSATMRGDLDTKPTRTIGTFTTSPFS- 614
Db 587 TDADIVLH--VNDQAI---QMPKTMNPGEDLTSTKTFKVADAITTLNLTATDSSLAKHNLG 641
Qy 615 -DVQSTFTICAWNFSSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKVKTALFTSTNPRGLK 673
Db 642 EDPNSTLS-----GIVYVDRIEFIPVDETVEAEQDLEAAKAVNALFTNTKD-GLR 691
Qy 674 TDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 692 PGVTYEVNQAAANLVECLSDDLYPNEKRLLFDAVREAKRLSEARNL 737
RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2
Query Match 40.5%; Score 1514; DB 14; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.7e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;
Qy 1 MKLKPNPKHQSLSSNAKVDKIATDS---LKNETDIELKNNMEDYLRMSHESID---- 52
Db 1 MSPNNQNEYEIIDATPST-SVNSDNRYPFANEPTNALQNMMDYKDYKMSAGNASEYPGS 59
Qy 53 PFVSAS---TIQTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKG-KSQWEIFMEHV 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQV 119
Qy 109 EEIINQKILTYARNKALSDRLGLDALAVTHESLESWENNRNTRARSVVVKQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGLGNNYQLYLTALAEWEENPNRSLRDLVRNRFELDLSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVERT 228
Db 180 FTQYMPFSRVNTFEVFPFLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYYDRQMKLT 239

Tue Feb 15 10:07:57 2005

QY	229	RDYSDHC	IKWYNTGL	NNLRGT	NAKSWV	RYNQFR	KDWTML	VLVDF	PSDYDTL	VYPIKT	288																																											
Db	240	AEYSDHC	VKWYETGL	AKUKGT	SAKQW	DYNOFR	REMTL	AVLDV	VALFP	VNDTRYPMETK	299																																											
QY	289	SQLTRE	VYTD	DAIGTV	HPNQAF	ASTTWY	NNAP	SFSA	IAEAA	VIRSHPLL	FLFKVTIYSLL	348																																										
Db	300	AQLTRE	VYDPL	GA	VNVS--	SIGSWY	-DKAP	SFGV	IESSVIR	PPHFVDYIT	GLTVYITQS	355																																										
QY	349	SRWNTQ	YQNMW	GCHRL	ESR	PIG	GALNT	STQ	STNTS	INPV-TL	QFTSRD	VYRTESLAGL	407																																									
Db	356	RSISSA	RYIRH	WAGH	QISY	HRVSR	GSLNQ	MYGT	QNQLH	STSTF	DTNYDI	YKTLSDAV	415																																									
QY	408	NLFLT	QTP-----	VNGV	PRVD	FHW-----	KPTL	---PIA	SDNFY	YLVG	AGVG	QTQLODSE	453																																									
Db	416	LLDI	VY	PGV	TYIF	FGME	VEF	FMV	NQLN	TRKT	LYNP	VS	466																																									
QY	454	NELP	ETTQ	OP	NYES	SYSH	RLSH	IGL	ISAS	-HV	KAL--VY	SWTH	RSADR	TNTIE	PN	SITOI	510																																					
Db	467	LELP	PET	SQ	PNYES	SYSH	RLCH	ITSI	PAT	NTNT	GLV	PV	FSW	TH	RSAD	LNNTI	YS	DKITQI	526																																			
QY	511	PLVKA	FN	LSS	GAAV	VR	PG	FT	G	GDIL	-RT	NTGT	FG	DI---	R	VN	NP	PPA	QRYR	IR	RYA	566																																
Db	527	PAVK	CW	DN	LPFV	PV	VK	PG	H	TG	GDLLQ	YN	RS	TG	SV	GLTFL	ARY	GLA	E	KAK	G	YR	RL	RYA	586																													
QY	567	STTD	LQ	FHT	S	ING	KA	IN	Q	GN	FS	AT	M	N	R	G	EDL	D	Y	K	T	F	---	T	G	F	T	P	P	S	F	S	---	614																				
Db	587	TDAD	I	VLH--	-V	ND	QI---	-Q	M	P	K	T	W	N	P	G	E	D	L	T	S	K	T	F	K	V	A	D	A	I	T	T	L	N	L	A	T	D	S	S	L	A	K	H	N	L	G	641						
QY	615	-DVQ	ST	F	T	I	G	A	N	F	S	S	G	N	E	Y	I	D	R	I	E	F	P	V	E	V	T	E	A	E	Y	D	F	E	K	A	E	K	V	T	A	L	T	F	T	S	T	N	P	R	G	L	K	673
Db	642	EDP	N	S	T	L	S-----	G	I	V	Y	D	R	I	E	F	P	V	D	E	T	E	A	E	Q	D	L	E	A	K	K	A	V	N	A	L	T	N	T	K	D	-G	L	R	691									
QY	674	TDV	K	D	X	H	I	D	O	V	S	N	L	V	E	S	L	S	D	E	F	Y	L	D	E	K	R	E	L	F	E	I	V	K	A	Q	I	H	I	E	R	N	719											
Db	692	PGV	T	D	E	V	N	Q	A	N	L	V	E	C	L	S	D	D	L	Y	P	N	E	K	R	L	L	F	D	V	A	R	E	K	R	L	S	E	A	R	N	737												

Search completed: February 14, 2005, 20:56:50
Job time : 62.0945 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds
(without alignments)
2403.590 Million cell updates/sec

Title: US-10-019-823B-59
Perfect score: 3742
Sequence: 1 MKLKNPDKHQSLSSNAKVVK.....KRELFEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3546	94.8	719	2	US-09-003-217-2
2	3541	94.6	719	3	US-09-218-942-2
3	3516	94.0	719	3	US-08-286-870A-8
4	3368	90.0	710	4	US-09-661-322A-42
5	3160	84.4	648	3	US-08-286-870A-4
6	2573	68.8	535	3	US-08-286-870A-6
7	2459	65.7	1229	1	US-08-100-709-4
8	2459	65.7	1229	1	US-08-176-865-4
9	2459	65.7	1229	1	US-08-474-038-4
10	2459	65.7	1229	2	US-08-779-046-4
11	2459	65.7	1229	2	US-08-881-340-4
12	2314.5	61.9	1207	1	US-07-951-715A-7
13	2314.5	61.9	1207	1	US-08-459-448A-7
14	2314.5	61.9	1207	3	US-08-459-595A-7
15	2314.5	61.9	1207	3	US-08-459-504B-7
16	2314.5	61.9	1207	3	US-08-459-444-7
17	2314.5	61.9	1207	3	US-09-053-549-8
18	2314.5	61.9	1207	3	US-09-547-422-7
19	2314.5	61.9	1207	4	US-09-988-462-7
20	2308.5	61.7	1227	3	US-09-053-549-2
21	2243	59.9	1227	1	US-08-448-170-8
22	2243	59.9	1227	3	US-08-961-803-9
23	2234	59.7	1227	4	US-09-661-322A-63
24	2233.5	59.7	488	1	US-08-448-170-10
25	2233.5	59.7	488	3	US-08-961-803-10
26	2219	59.3	1186	3	US-09-178-252-23
27	2219	59.3	1186	4	US-09-826-660-23

28	2168.5	58.0	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1982	53.0	643	3	US-09-178-252-25	Sequence 25, Appl
30	1982	53.0	643	4	US-09-826-660-25	Sequence 25, Appl
31	1813	48.5	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1683.5	45.0	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1657.5	44.3	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1657.5	44.3	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1657.5	44.3	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1657.5	44.3	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1519.5	40.6	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1507	40.3	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1507	40.3	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1507	40.3	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1507	40.3	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1507	40.3	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1507	40.3	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1506.5	40.3	1168	1	US-08-291-368-4	Sequence 4, Appl
45	1506.5	40.3	1168	2	US-08-962-190-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia A.
; APPLICANT: Madkour, Magdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003.217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2302
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-003-217-2

Query Match 94.8%; Score 3546; DB 2; Length 719;
Best Local Similarity 95.0%; Pred. No. 6,le-318;
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MKLKNPDKHQSLSSNAKVVKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60
Db 1 MKLKNPDKHQSLSSNAKVVKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQIASLYSFIILGELWPKGKSQWEIFMEHVEEIIINOKILTYA 120
Db 61 QTGIGIAGKILGTGVPAGQIASLYSFIILGELWPKGKSQWEIFMEHVEEIIINOKILTYA 120
QY 121 RNKALSDRLGGLDALAVHESLESWENNRNTRARSVVKQNYIALELMFVQKLPFAVSG 180
Db 121 RNKALSDRLGGLDALAVHESLESWENNRNTRARSVVKQNYIALELMFVQKLPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSHCICKWYN 240
Db 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSHCICKWYN 240
QY 241 TGLNLRGNTAKSWVRYNQFRKDIELMVLVLRVFPYSYDILVPIKTTSQLTRVYTDAL 300
Db 241 TGLNLRGNTAKSWVRYNQFRKDIELMVLVLRVFPYSYDILVPIKTTSQLTRVYTDAL 300
QY 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360
QY 361 GGHRLSRPIGGALNTSTQSTNTSINPVTLOFTSRDVRYSAGLNFLTPQVNGVPR 420
Db 361 GGHRLSRPIGGALNTSTQSTNTSINPVTLOFTSRDVRYSAGLNFLTPQVNGVPR 420
QY 421 VDFHWKFPPLPIASDNFYLYGAGVGTOLQDSNELPPTTGPQNYESYSHRSLHIGLIS 480
Db 421 VDFHWKFPPLPIASDNFYLYGAGVGTOLQDSNELPPTTGPQNYESYSHRSLHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDLDYK 600
QY 601 TFRGTGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
Db 601 TFRGTGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 2
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; TITLE OF INVENTION: Activity
; FILE REFERENCE: C1V1
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

Query Match 94.6%; Score 3541; DB 3; Length 719;
Best Local Similarity 95.0%; Pred. No. 1.4e-317;
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
QY 1 MKLKNPKHQSLSSNAKVDTATDSUKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60

Db 1 MKLKNPKHQSLSSNAKVDTATDSUKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPAGQIASLYSFIILGELWPKGKSQWEIFMEHVEEIIINOKILTYA 120
Db 61 QTGIGIAGKILGTGVPAGQIASLYSFIILGELWPKGKSQWEIFMEHVEEIIINOKILTYA 120
QY 121 RNKALSDRLGGLDALAVHESLESWENNRNTRARSVVKQNYIALELMFVQKLPFAVSG 180
Db 121 RNKALSDRLGGLDALAVHESLESWENNRNTRARSVVKQNYIALELMFVQKLPFAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSHCICKWYN 240
Db 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSHCICKWYN 240
QY 241 TGLNLRGNTAKSWVRYNQFRKDIELMVLVLRVFPYSYDILVPIKTTSQLTRVYTDAL 300
Db 241 TGLNLRGNTAKSWVRYNQFRKDIELMVLVLRVFPYSYDILVPIKTTSQLTRVYTDAL 300
QY 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360
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Db 361 GGHRLSRPIGGALNTSTQSTNTSINPVTLOFTSRDVRYSAGLNFLTPQVNGVPR 420
QY 421 VDFHWKFPPLPIASDNFYLYGAGVGTOLQDSNELPPTTGPQNYESYSHRSLHIGLIS 480
Db 421 VDFHWKFPPLPIASDNFYLYGAGVGTOLQDSNELPPTTGPQNYESYSHRSLHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDLDYK 600
QY 601 TFRGTGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
Db 601 TFRGTGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 3
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/286,870A
 ; FILING DATE: 05-AUG-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/520228
 ; FILING DATE: 09-MAY-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 8910624.9
 ; FILING DATE: 09-MAY-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PAUL N. KOKULIS
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 70608/220720
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0944
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 719 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-286-870A-8

[illegible]

Qy	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM	719
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Db	661	TALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
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RESULT 4			
US-09-661-322A-42			
; Sequence 42, Application US/09661322A			
; Patent No. 6593293			
; GENERAL INFORMATION:			
; APPLICANT: Baum, James A.			
; APPLICANT: Chu, Chih-Rei			
; APPLICANT: Donovan, William P.			
; APPLICANT: Gilmer, Amy J.			
; APPLICANT: Rupar, Mark J.			
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin			
; TITLE OF INVENTION: and Methods of Use			
; FILE REFERENCE: MECO201			
; CURRENT APPLICATION NUMBER: US/09/661.322A			
; CURRENT FILING DATE: 2000-09-13			
; NUMBER OF SEQ ID NOS: 63			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 42			
; LENGTH: 710			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (200)..(200)			
; OTHER INFORMATION: No. 6593293-Coding			
US-09-661-322A-42			
Query Match 90.0%; Score 3368.5; DB 4; Length 710;			
Best Local Similarity 89.2%; Pred. No. 1.2e-301;			
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;			
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Db	1	MSKQNNHQSLSSNATVDKNFTGSLNNTNTELQNFN-----HEGIEPFVSVSTI	51
		: : : : : : : : :	
Qy	61	QTGIGIAGKILGTGVPPAGQIASLYSFILGELMPKGSQWEIFMEHVEEIIINOKILTYA	120
		: : : : : : : : :	
Db	52	QTGIGIAGKILGNLGVPPAGQVASLYSFILGELMPKGSQWEIFMEHVEELINQKISTYA	111
		: : : : : : : : :	
Qy	121	RNKALSDRLGDLALAVYHESLESWTENRNTRARSVVKQYIALELMFVQKLPSPAVSG	180
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Db	112	RNKALADLKGLDALAVYHESLESWIENRNTRRSVVKSQYITLELMFVQSLPSPAVSG	171
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Qy	181	EEVPLLPPIYAQANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHICKWYN	240
		: : : : : : : : :	
Db	172	EEVPLLPPIYAQANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKEYSDHCWKWYN	231
		: : : : : : : : :	
Qy	241	TGLNNLRGNTNAKSWRYNQFRKDMTLMVLVLDLVALFPSYDTLVYPIKTTTSQLTREVTDAI	300
		: : : : : : : : :	
Db	232	TGLNRLMGNAESWRYNQFRDRMTLMVLVLDLVALFPSYDTQWYPIKTTAQLTREVTDAI	291
		: : : : : : : : :	
Qy	301	GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYNNMW	360
		: : : : : : : : :	
Db	292	GTVHPHPSFTSTWYNNAPSPSTIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQYNNMW	351
		: : : : : : : : :	
Qy	361	GGHRLSRPIGGALNTSTQGSTNTSINPVTIQTSTRDVYRTESLAGLNFLTQPVNGVPR	420
		: : : : : : : : :	
Db	352	GGHKLPRFTIGTTLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTQPVNGVPR	411
		: : : : : : : : :	
Qy	421	VDPHWKFTPLIASDNFYYLGVAGVGTQLQDSENELEPPETTGQPNYESYSHRLSHIGLIS	480
		: : : : : : : : :	
Db	412	VDPHWKFTVTHPIASDNFYYPGVAGIGTQLQDSENELEPPETTGQPNYESYSHRLSHIGLIS	471
		: : : : : : : : :	
Qy	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAADVVRGPGFTGGDILRRTN	540
		: : : : : : : : :	
Db	472	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAADVVRGPGFTGGDILRRKN	531
		: : : : : : : : :	
Qy	541	TGTFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNRRGEDLDYK	600

Db 532 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGDLKY 591
QY 601 TPTGIGTTPPSFSDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYTYEABYDFEKAQEV 660
Db 592 TPTGIGTTPPSFSDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYTYEABYDFEKAQEV 651
QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719
Db 652 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 710

RESULT 5
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 84.4%; Score 3160; DB 3; Length 648;
Best Local Similarity 92.3%; Pred. No. 1.8e-282;
Matches 598; Conservative 30; Mismatches 20; Indels 0; Gaps 0;
QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPPFVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQIASLYSFTILGELWPKGKSGWEIFMEHVEEIIINOKILTVA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASLYSFTILGELWPKGKSGWEIFMEHVEEIIINOKISTVA 120

QY 121 RNKALSDLRGDGLALAVYHBSLESWVENNRNTRARSVVKNQYIALELMFVQKLPSPFAVSG 180
Db 121 RNKALTDLKGDLALAVYHDSLESWVGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
QY 181 EKVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
Db 181 EKVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYS 240
QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDLYVPLKTTTSQLTREYVYTDAL 300
Db 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSPYDLYVPLKTTTQALTRVYVYTDAL 300
QY 301 GTVHPNQAFATTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMNW 360
Db 301 GTVHPNPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGGTNLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTQPVNGVPR 420
QY 421 VDFHWKFTPLPIASDNFYILGYAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGDLKY 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGDLKY 600
QY 601 TPTGIGTTPPSFSDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYTYE 648
Db 601 TPTGIGTTPPSFSDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVYTYE 648

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989


```
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-6

Query Match      68.8%; Score 2573; DB 3; Length 535;
Best Local Similarity 91.0%; Pred. No. 2e-228;
Matches 487; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKLKNPKHQSLSSNAKVDTKATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTI 60
DB 1 MKLKNQDKHQSPSSNAKVDTKISTDSLKNETDIELQNHEDCLKXSEVENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTLGVFPAGQIASLYSFIIGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGIGIAGKILGTLGVFPAGQIASLYSFIIGELWPKGKQWEIFMEHVEEIIINQKISFYA 120

QY 121 RNKALSDLRLGDLALAVYHESLESVENNRNTRARSVKNQYIALELMFVQKLPSPFAVSG 180
DB 121 RNKALSDLRLGDLALAVYHESLESVENNRNTRARSVKNQYIALELMFVQKLPSPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVQRTDYSDHCKIKNYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVQRTDYSDHCKIKNYN 240

QY 241 TGLNLRGTNAKSWRYNQFRDMLMVLDLVALPSPSYDTLVYPIKTTSQLTRVYTDAL 300
DB 241 TGLNLRGTNAKSWRYNQFRDMLMVLDLVALPSPSYDTLVYPIKTTSQLTRVYTDAL 300

QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPNPFSTFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360

QY 361 GGHRLSRPIGALNTSTQGSTNTSINPVTIQTSDRVYRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHRLSRPIGALNTSTQGSTNTSINPVTIQTSDRVYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTPLTASDNFYLYGAGVGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTPLTASDNFYLYGAGVGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS c1YET4 AND c1YETS
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
```

```
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match      65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKHQSLSSNAKVDTKATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTIQT 62
DB 20 VSNPSTQMNLSPDARI-----EDSLCVAEVDNIDPFVSASTVQT 58

QY 63 GIGIAGKILGTLGVFPAGQIASLYSFIIGELWPKGKQWEIFMEHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVFPAGQIASLYSFIIGELWPKGKQWEIFMEHVEEIIINQKILTYARN 118

QY 123 KALSDLRLGDLALAVYHESLESVENNRNTRARSVKNQYIALELMFVQKLPSPFAVSGEE 182
DB 119 TAIARLEGLGRYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVQRTDYSDHCKIKNYNTG 242
DB 179 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVQRTDYSDHCKIKNYNTG 238

QY 243 LNNLRGTNAKSWRYNQFRDMLMVLDLVALPSPSYDTLVYPIKTTSQLTRVYTDALGT 302
DB 239 LNNLRGTNAKSWRYNQFRDMLMVLDLVALPSPSYDTLVYPIKTTSQLTRVYTDALGT 298

QY 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWGG 362
DB 299 TNAPSGFASTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWGG 358

QY 363 HRLESRPIGALNTSTQGST-NTSINPVTIQTSDRVYRTESLAGLNLFLTQPVNGVPRV 421
DB 359 HRLNFRPIGGLNTSTQGLTNTSINPVTIQTSDRVYRTESLAGLNLFLTQPVNGVPRV 418

QY 422 DFHWKFTPLTASDNFYLYG-----YAGVGTQDSENELPPEATGQPNYESYSHRLS 474
DB 419 RFNF-----INPQNIYERGATTSQYQGVGIQIQLFDSSETLPPEATGQPNYESYSHRLS 472

QY 475 HIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
DB 473 HIGLIGNTLRAPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 532

QY 535 ILRRNTGTGDIRVNIINPPFAQYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRG 594
DB 533 ILRRNTGTGDIRVNIINPPFAQYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRG 592

QY 595 EDLDYKTFRTIGFTTFFSFDVQSTFTIGAWNFSNGNEVYIDRIEFPVVEVTVYEAEDFE 654
DB 593 DNLEYSFRTAGFSTPFNFNLAQSTFTLGAQSFNS-QEVYIDRIEFPVVEVTVYEAEDFE 651
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179 VPLLMVYQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYETEEYHNCHVQWYNTG 238
243 LNNLRGTNAKSWRYNQFRKMDLWLDLVALFPSYDVLVPIKTTSQLTREVYTDAGT 302
239 LNNLRGTNAESWLRNQFRDLTLGLVLDLVALFPSYDTRTYPIINTSAQLTREIYTDPIGR 298
303 VHPNQAFSTWYNNNAPSFAIEAAVIRSPHLLDPLEKVTIYSLLSRWNTQVNMWVG 362
299 TNAPSGFASTWYNNNAPSFAIEAAVIRSPHLLDPLEKVTIYSLLSRWNTQVNMWVG 358
363 HRLSRPIGGALNTSTQST-NTSINPVTLQFTSRDVRVTSAGLNLFLTPQVNGVPRV 421
359 HRLNRPPIGGTLNTSTQGLTNTSINPVTLQFTSRDVRVTSAGLNLFLTPQVNGVPRV 418
422 DFHWKFPPTLPIASDNFYVILG-----YAGVGTQLQDSNELPPETTGQPNYESYSHRLS 474
419 RNFN-----INPQNIYERGATTVSQYQGVGLQDFSETLPPETTERPNYESYSHRLS 472
475 HIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
473 HIGLIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGD 532
535 ILRRTNTGTDIRVNVNPPFAQRYRVIRYASTDQLQFHTSINGKAINQGNFSATMNRG 594
533 ILRRTNTGTDIRVNVNPPFAQRYRVIRYASTDQLQFHTSINGKAINQGNFSATMNRG 592
595 EBLDYKTRTIGTTPFPFSDVQSTFTTGAMNFSNGEVIIDRIEFPVVEYEAEDFE 654
593 DNLEYSFRTAGFTFPFNLNAQSTFTLGAQSPFN-QEYVIDRVEFPVPAEVTFAEYDLE 651
655 KAOEKVTALFTSTNPRGLTKDVKYHIDQVSNLVESLSEDFYLDKEKELFEIVKYAKQIH 714
652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLSEDFCLDEKELFEIVKYAKRLS 711
715 IERNM 719
712 DERNL 716

RESULT 9
US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709

655 KAOEKVTALFTSTNPRGLTKDVKYHIDQVSNLVESLSEDFYLDKEKELFEIVKYAKQIH 714
652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLSEDFCLDEKELFEIVKYAKRLS 711
715 IERNM 719
712 DERNL 716

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;
3 LKNPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFVSASTIQT 62
20 VSNPSTQWNLSPDARI-----EDSLCVAEVNNDIPFVSASTVQT 58
63 GIGTAGKILGTGVPFAGQIASLYSTILGELWPKGSKQWEIFMEHVEEIIQKILTYARN 122
59 GINIAGRILGLVLPFAGQLASFYSLVGLWPSGRDPWEIFLHVEQLIQVQVNTN 118
123 KALSDLRGLDALAVHESLESVENNTRARSVVKNOYIALELMFVKLPSPFAVSCEE 182
119 TATARLEGIGRGYRSYQOALETWLDNRDARSILERYVALELDITTAIPLRIRNEE 178
183 VPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFFYNRQVTRDYSCHICKWYNTG 242


```

; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

Qy 3 LKNPKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTIQT 62
Db 20 VSNPSTQMNLSPDARI-----EDSLCAEVNNDIDPFVSASTVQT 58

Qy 63 GIGIAGKILGTGVFPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEELINQKILTYARN 122
Db 59 GINIAGRILGVLGVFPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQVNTNRN 118

Qy 123 KALSDRLGLDALAVYHESLESWVENNRNTRRSVVKNOYIALELMFVKLPFAVSCEE 182
Db 119 TAIARLEGLRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

Qy 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVQERTRDYSDHCIKWYNTG 242
Db 179 VPLLMYVAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEESYHNHCQWYNTG 238

Qy 243 LNNLRGTNAKSWVRNQFRKDMTLMVLDLVALFPSYDILVYPIKTTSQLTREYVTDIGT 302
Db 239 LNNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGR 298

Qy 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLDDFLEKVTIYSLLSRWSNTQYMMNWGG 362
Db 299 TNAPSGFASTWFWNNNAPSFAIEAAIRPPLHLLDFPEQLTIYSASSRWSSTQHMNYWVG 358

Qy 363 HRLESRPIGGALNTSTQGST-NTSINPVTIQTSDRVYRTESLAGNLFLTPQVNGVPRV 421
Db 359 HRLNFRPIGGTLNTSTQGLTNTSINPVTIQTSDRVYRTESNAGTNILFTTPVNGVPWA 418

Qy 422 DFHWKPTLPTASDNFYLG-----YAGVGTQLQDSNELPPETTPGPNYESYSHRLS 474
Db 419 RNF-----INPQNIYERGATTYSQYQGVGIQIQLFDSETELPEPETERPNYESYSHRLS 472

Qy 475 HIGLISASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
Db 473 HIGLIIGNTLRAPVYSWTHRSADRTNTEIPNRIITQIPLVKALNLHSGVTVVGPGFTGGD 532

Qy 535 ILRRTNTGTGDIRVNNPPAQRVRIYASVTTDLQHTSINGKALNQGNFSATWNRG 594
Db 533 ILRRTNTGTGDIRLNNVPLSQRYRIRYASVTTDLQFTTRNGTNNIGNFSRTWNRG 592

Qy 595 EDLDYKTFRTIGFTTFPSFSDVQSTFTIGAWNPFSGNEVYIDRETFVPVEVTEAEYDFE 654
Db 593 DNLEYSRFTAGFTSTFNFNLAQSTFTLGAQSFSN-QEVYIDRVFVPAEVTFAEYDLE 651

Qy 655 KAQEKVYALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIH 714
Db 652 RAQKAVNALFTSTNPRGLKTDVTHIDQVSNMVACLSDEFCLDEKRELFEKVKYAKKLS 711

Qy 715 IERNM 719
Db 712 DERNL 716
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US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match 65.7%; Score 2459; DB 2; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

Qy 3 LKNPKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTIQT 62
Db 20 VSNPSTQMNLSPDARI-----EDSLCAEVNNDIDPFVSASTVQT 58

Qy 63 GIGIAGKILGTGVFPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEELINQKILTYARN 122
Db 59 GINIAGRILGVLGVFPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQVNTNRN 118

Qy 123 KALSDRLGLDALAVYHESLESWVENNRNTRRSVVKNOYIALELMFVKLPFAVSCEE 182
Db 119 TAIARLEGLRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

Qy 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVQERTRDYSDHCIKWYNTG 242
Db 179 VPLLMYVAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEESYHNHCQWYNTG 238

Qy 243 LNNLRGTNAKSWVRNQFRKDMTLMVLDLVALFPSYDILVYPIKTTSQLTREYVTDIGT 302
Db 239 LNNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGR 298

Qy 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLDDFLEKVTIYSLLSRWSNTQYMMNWGG 362
Db 299 TNAPSGFASTWFWNNNAPSFAIEAAIRPPLHLLDFPEQLTIYSASSRWSSTQHMNYWVG 358
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363 HRLSRPIGGALNTSTQGST-NTSINPVTLQFTSRDVRVYTESLAGNLFLTOPVNGVPRV 421
359 HRLNFRPIGGTLNTSTOGLTNTSINPVTLQFTSRDVRVYTESNAGTNILFTTPVNGVFWA 418
422 DFHWKFTPLPIASDNFYLLG-----YAGVGTQLQDSNELPPTTGPQNYESYSHRLS 474
419 RFNF-----INPQNIYERGATYSQYQGVGIQFDSETELPPTTGPQNYESYSHRLS 472
475 HIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
473 HIGLIIGNTLRAPVYSWTHRSADRTNTEPNSITQIPLVKALNLHSGVTVVGGPGFTGGD 532
535 ILRRTNTGTFDIRVNIINPFPFAQRYVRIRYASTTDLQFTSINGKAINQGNFSATMNRG 594
533 ILRRTNTGTFDIRVNIINPFPFAQRYVRIRYASTTDLQFTSINGKAINQGNFSATMNRG 592
595 EDLYKTFRTIGTTPFSQVSTFTIGAMNFSNGEVYIDRIEFVPEVVEAEYDFE 654
593 DNLEYSFRTAGSTPFPFLNAQSTFTLGAQSFN-QEVYIDRVFVPAEVTPEAEYDLE 651
655 KAOEKVTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIH 714
652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLDEFCLDEKRELFEKVKYAKRLS 711
715 IERNM 719
712 DERNL 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS c1yE4 AND c1yE5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSES: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-881-340-4
Query Match 65.7%; Score 2459; DB 2; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;
QY 3 LKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFVSASTIQT 62
DB 20 VSNFSTQNLSPDARI-----EDSLCVAEAVNNIDPFVSASTVQT 58
QY 63 GIGIAGKILGTLGVFPFAGQIASLYSFTLGLWPKGSKQWEIPMEHVEEIIINOKILTYARN 122
DB 59 GINIAGRILGLVGVFPFAGQIASLYSFTLGLWPKGSKQWEIPMEHVEEIIINOKILTYARN 118
QY 123 KALSRLRGDGLAVYHESLESWVENNTRARSVVKQNYIALELMFVQKLPFAVSGEE 182
DB 119 TAIARLEGGLRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFIRNEE 178
QY 183 VPLLPIYQAANLHLLLRDASIFGKWLGLSASEISTFYNNQVETRDYSDHCHIKWYNTG 242
DB 179 VPLLPMVYQAANLHLLLRDASIFGSEWGMASDVNQYQSQIRYTYEYSNHCWYNTG 238
QY 243 LNNLGTNAKSWRYNQPRKDMTLMVLDLVALPSPYDVLVPIKTTSQLTREYVYDAIGT 302
DB 239 LNNLGTNAESWLRYNQPRRDLTLGLVLDLVALPSPYDTRTPINTSAQLTREYVYDPIGR 298
QY 303 VHPNOAFSTWYNNNAPSFAIEAAVTRSPHLLDFLEKVTIYSLSRWSNTQYNNMWGG 362
DB 299 TNAPSGFASTWYNNNAPSFAIEAAIFRPHLLDPPEQLTIYSSASSRWSSTQHMNYWVG 358
QY 363 HRLSRPIGGALNTSTQGST-NTSINPVTLQFTSRDVRVYTESLAGNLFLTOPVNGVPRV 421
DB 359 HRLNFRPIGGTLNTSTOGLTNTSINPVTLQFTSRDVRVYTESNAGTNILFTTPVNGVFWA 418
QY 422 DFHWKFTPLPIASDNFYLLG-----YAGVGTQLQDSNELPPTTGPQNYESYSHRLS 474
DB 419 RFNF-----INPQNIYERGATYSQYQGVGIQFDSETELPPTTGPQNYESYSHRLS 472
QY 475 HIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
DB 473 HIGLIIGNTLRAPVYSWTHRSADRTNTEPNSITQIPLVKALNLHSGVTVVGGPGFTGGD 532
QY 535 ILRRTNTGTFDIRVNIINPFPFAQRYVRIRYASTTDLQFTSINGKAINQGNFSATMNRG 594
DB 533 ILRRTNTGTFDIRVNIINPFPFAQRYVRIRYASTTDLQFTSINGKAINQGNFSATMNRG 592
QY 595 EDLYKTFRTIGTTPFSQVSTFTIGAMNFSNGEVYIDRIEFVPEVVEAEYDFE 654
DB 593 DNLEYSFRTAGSTPFPFLNAQSTFTLGAQSFN-QEVYIDRVFVPAEVTPEAEYDLE 651
QY 655 KAOEKVTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIH 714
DB 652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLDEFCLDEKRELFEKVKYAKRLS 711
715 IERNM 719
712 DERNL 716

RESULT 12
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.


```

; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

Query Match 61.9%; Score 2314.5; DB 1; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

Qy 40 EDYLRMSEHESIDPFVSASTQTGTGIGIAGKILGTIGVPPAGQIASLYSIFILGELWPKGKS 99
Dy 10 EDSLCTAEGNIDPFVSASTVQTGINIAGRIILVGLVPPAGQLASFSYFLVGLWPKGRD 69
Qy 100 QWEIFMEHVEEIIINOKILTYARNKALSDLRLGDLALAVYHESLESWENNNTRARSVVK 159
Dy 70 QWEIFLEHVEQLINQITENARTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLY 129
Qy 160 NOYIAELMFVQKLPFAVSGEEVPLPIYAQAANLHLRLDASIFGKEWGLSASEIST 219
Dy 130 TOYIAELDFLNPALFAIRNQEVPLMVYAQAANLHLRLDASLFGSEFGLTSQEIQR 189
Qy 220 FYNRQVERTRDYSCHICKWNTGLNNLRGTNAKSWRVYRQFRKDMTLMVLDLVALFPSYD 279
Dy 190 YTERQVERTRDYSYCVWYNTGLNSLRGTNAASWRYRQFRDLTLGLVDLVALFPSYD 249
Qy 280 TLVYPIKTSQLTREYVTDAGTVHNPQAFASSTWYNNAPSFSAIEAAVIRSPHLLDFL 339
Dy 250 TRYPINTSAQLTREYVTDAGTGVN--MASMWNYNNAAPSFSAIEAAIRSPHLLDFL 307
Qy 340 EKVITYLLSRWSNTQYMMWGGHRLSRIPIGGALNTSQGSTWTSINPVTLOFTSRDVI 399
Dy 308 EQLTIFASRRSNTHTMYRGTIQSRPIGGGLNTSTHGTWTSINPVTLRFASRDVI 367
Qy 400 RTESLAGLNLFF--LTQPVNGVRVDFHWKFF--TLPIASDNFYILYAGVGTQLQDSENEL 456

; Db 368 RTESYAGVLLWGIYLEPIHGVPVTRFNFNPNQISDRGTANYSQPYESFGLQKDSDEL 427
; Qy 457 PPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAF 516
; Db 428 PPETTERPNYESYSHRLSHIGIILQSRVNVVPVYSWTHRSADRTNTEPNSITQIPLVKAS 487
; Qy 517 NLSSGAANVRGPGFTGGDIILRRNTGTGDIRVNNINPFAORVRYRIRYASITDLOFHTS 576
; Db 488 ELPOGTTVVRGPGFTGGDIILRRNTGTGDIRVNNINPFAORVRYRIRYASITDLOFHTS 547
; Qy 577 INKAINQGNFSATNVRGEBLDYKTFRTIGFTTFFSDVQSTFTTIGAWNFSGNEVVID 636
; Db 548 RGGTTVNNFRFLRTWNSGDELKYGNFVRRAFTTFFFTQIQDIIRTSIQGLSGNGEVVID 607
; Qy 637 RIEFVPEVTEYAEYDFEKAQEKVLTALFTSTNPRGLKTDVYKHIDQVSNLVESLSDEFY 696
; Db 608 KIEIIPVTATFEAYDLEAQAQAVNALFTNTNPRRLKTDVTDYKHIDQVSNLVACLSDEFY 667
; Qy 697 LDEKRELFVIVKAKQIHIERNM 719
; Db 668 LDEKRELFVIVKAKRLSDERNL 690

RESULT 13
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dawson, Cindy G.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
```


REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-448A-7

Query Match 61.9%; Score 2314.5; DB 2; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;
QY 40 EDYLRMSHESIDPFVVSASTIQTGTGIGIAGKILGTGVPPFAGQIASLYSFLGELWPKGKS 99
Db 10 EDSLCAEAGNNIDPFVVSASTVQTGINAGILGVLGVPPFAGQLASFYSLVGLWPRGRD 69
QY 100 QWEIFMEHVEEIIINQKILTYARNKALSDRLGLGDALAVYHESLESWVENRNTARSVVK 159
Db 70 QWEIFLEHVEQLINQITENARTALRQLGDSFRAYQOOSLEDWLENRDDARTRSVLY 129
QY 160 NOYIALELMFVQKLPSPAVSGVEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEIST 219
Db 130 TOYIALELDFLNAMPFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIOR 189
QY 220 FYNQOVERTRDYSCHCIKWYNTGLNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSSYD 279
Db 190 YERQVERTRDYSYCVENYNTGLNSLRGTNAASWRYNQPRKDLTLGVLDLVALFPSSYD 249
QY 280 TLVYPIKTSQLTREYTDATGTVHPNQAFSTWYNNAPSFSAEAAVIRSPHLLDFL 339
Db 250 TRYPINTSAQLTREYTDATGTVN--MASMNWYNNAPSFSAEAAVIRSPHLLDFL 307
QY 340 EKVTYLLSRWSNTQYNNMWGHRLEPIGGALNTSTQSTNTSINPVTLOFTSRDVI 399
Db 308 EQLTFSASRWSNTRHMYWRTGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFSRDVI 367
QY 400 RTESLAGLNLFP--LTQPVNGVPRVDFHWKFP--TLPIASDNFYLYGVAGVGTQLQDSNEL 456
Db 368 RTESYAGVLLWGIYLEPIHGVTFRFNTNPQNISDRGTANYQPYESPGLQKDSSETL 427
QY 457 PPETTCQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAF 516
Db 428 PPETTERPNYESYSHRLSHIGLILQSRVNVVSVWTHRSADRTNTIGPNRITQIPMVKAS 487
QY 517 NLSSGAARVVRGPGFTGGDILRRTNTGTGDIRVNNINPFAQVRVIRYASTDLOFHTS 576
Db 488 ELPGQITVVRGPGFTGGDILRRTNTGTGDIRVNTGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVS 547
QY 577 INKAINQGNFSATMNRGDLDTFTRTGFTTTPSFSDVQSTFTIGAWNFSNGNEVYID 636
Db 548 RGTGVNNFRRLTWNMGDELKYGNGFVRAFTTPTFTQIDIRTSIQGLSGNGEYVYID 607
QY 637 RIEFVPEVTVYAEYDFEKAQKVTALFTSTNPRGLKTDVXYHIDQVSNLVESLDEFY 696
Db 608 KIEIIPVTATFAEYDLERAQEAVALFTNTNPRKLTDTVDTHIDQVSNLVACLSDFEFC 667
QY 697 LDEKRELFEIVKAKQIHIERNM 719
Db 668 LDEKRELLEKVKYAKRLSDERNL 690

RESULT 14
US-08-459-595A-7
Sequence 7, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-595A-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;
QY 40 EDYLRMSHESIDPFVVSASTIQTGTGIGIAGKILGTGVPPFAGQIASLYSFLGELWPKGKS 99
Db 10 EDSLCAEAGNNIDPFVVSASTVQTGINAGILGVLGVPPFAGQLASFYSLVGLWPRGRD 69
QY 100 QWEIFMEHVEEIIINQKILTYARNKALSDRLGLGDALAVYHESLESWVENRNTARSVVK 159
Db 70 QWEIFLEHVEQLINQITENARTALRQLGDSFRAYQOOSLEDWLENRDDARTRSVLY 129
QY 160 NOYIALELMFVQKLPSPAVSGVEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEIST 219
Db 130 TOYIALELDFLNAMPFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIOR 189
QY 220 FYNQOVERTRDYSCHCIKWYNTGLNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSSYD 279

Db 190 YVERQVTRDYSYCVWYNTGLNSLRTGNTAASWVRYNQFRRLDTLGLVLDLVALFPSVD 249
Qy 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFSTTWNNAAPSFSAIEAAVIRSPHLLDFL 339
Db 250 TRYPINTSAQLTREVYTDAGTGVN--MASMWNNAAPSFSAIEAAVIRSPHLLDFL 307
Qy 340 EKVITYLLSRNSNTQYMMNGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVS 399
Db 308 EQITFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGAINTSINPVTLPASRDVY 367
Qy 400 RTESLAGNLF--LTQPVNGVPRVDHFKFP-TLPIASDNFYLYGAGVGTQLODSENEL 456
Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNI SDRGTANYSPQYESPGLQKDSFEL 427
Qy 457 PPETGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAF 516
Db 428 PPETTERPNYESYSHRLSHIGLILQSRVNPVYSWTHRSADRTNTEPNSITQIPLVKAS 487
Qy 517 NLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNINPPFAQRYRIRYASTTDLQFHTS 576
Db 488 ELPOGTTVVRGPGFTGGDILRRNTGTGDIRVNINPPFAQRYRIRYASTTDLQFHTS 547
Qy 577 INKAINQGNFSAATNRGEDIYKTRTIGTTPFSFSDVQSTTIGAWNFSSGNEVYID 636
Db 548 RGGTTVNNFRFLRTNWSGDELKYGNEVRRAFTTPTFTQIQDIIRTSIQGLSGNGEVYID 607
Qy 637 RIEFVPEVTEAEYDFEKAQEKVTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFY 696
Db 608 KIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFY 667
Qy 697 LDEKRELFEIKYAKQIHIERNM 719
Db 668 LDEKRELLEKVKYAKRLSDERNL 690

RESULT 15

US-08-459-504B-7

Sequence 7, Application US/08459504B

Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,504B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-459-504B-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;

Best Local Similarity 65.4%; Pred. No. 5.7e-204;

Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

Qy 40 EDYLRMSEHSIDPFVSASTIQTGTGAGKILGTGVPPAGQIASLYSILGSLWPKGKS 99
Db 10 EDSLCTAEGNIDPFVSASTVQTGINIAGRLGVLPAGQIASLYSILGSLWPKGSRD 69
Qy 100 QWEIFMEHVEIINOKILTATNKALESRLGLDALAVVHESLESWENNRNTRARSVVK 159
Db 70 QWEIFLEHVEQLINQOITENARNTALARLQGLGDSFRAYQQLSDWLENRRDARTSLV 129
Qy 160 NOYIALELMFVOKLPFAVSGEEVPLLPYAAQANLHLLLRDASIFGKEWGLSASEIST 219
Db 130 TQYIALELDFLNPMLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189
Qy 220 FYNQVETRDYSDHCIKWYNTGLNLRGNAKSWVRYNQFRKDMTLMVLDLVALFPSVD 279
Db 190 YVERQVTRDYSYCVWYNTGLNSLRTGNTAASWVRYNQFRRLDTLGLVLDLVALFPSVD 249
Qy 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFSTTWNNAAPSFSAIEAAVIRSPHLLDFL 339
Db 250 TRYPINTSAQLTREVYTDAGTGVN--MASMWNNAAPSFSAIEAAVIRSPHLLDFL 307
Qy 340 EKVITYLLSRNSNTQYMMNGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVS 399
Db 308 EQITFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGAINTSINPVTLPASRDVY 367
Qy 400 RTESLAGNLF--LTQPVNGVPRVDHFKFP-TLPIASDNFYLYGAGVGTQLODSENEL 456
Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNI SDRGTANYSPQYESPGLQKDSFEL 427
Qy 457 PPETGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAF 516
Db 428 PPETTERPNYESYSHRLSHIGLILQSRVNPVYSWTHRSADRTNTEPNSITQIPLVKAS 487
Qy 517 NLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNINPPFAQRYRIRYASTTDLQFHTS 576
Db 488 ELPOGTTVVRGPGFTGGDILRRNTGTGDIRVNINPPFAQRYRIRYASTTDLQFHTS 547
Qy 577 INKAINQGNFSAATNRGEDIYKTRTIGTTPFSFSDVQSTTIGAWNFSSGNEVYID 636
Db 548 RGGTTVNNFRFLRTNWSGDELKYGNEVRRAFTTPTFTQIQDIIRTSIQGLSGNGEVYID 607
Qy 637 RIEFVPEVTEAEYDFEKAQEKVTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFY 696
Db 608 KIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFY 667

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds
(without alignments)
2827.419 Million cell updates/sec

Title: US-10-019-823B-59
Perfect score: 3742
Sequence: 1 MKLKNPKHQSLSSNAKVDK.....KRELPEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	719	6	AAB66912 Insectici
2	3742	100.0	719	6	AAB66912 Insectici
3	3598	96.2	719	7	Adm/4717 B. thurin
4	3546	94.8	719	2	Aaw49089 Bacillus
5	3520	94.1	719	4	AAB66908 Insectici
6	3520	94.1	719	6	AAB66908 Insectici
7	3520	94.1	719	8	Adr89421 crylia. 1
8	3516	94.0	719	4	AAB66910 Insectici
9	3516	94.0	719	6	AAB66910 Insectici
10	3511	93.8	719	4	Aau02095 Bacillus
11	3509	93.8	719	4	AAB66911 Insectici
12	3509	93.8	719	6	AAB66911 Insectici
13	3503	93.6	719	4	AAB66909 Insectici
14	3503	93.6	719	6	AAB66909 Insectici
15	3499	93.5	719	2	AAR08041 81 kd end
16	3488.5	93.2	718	6	AAB66907 Insectici
17	3482.5	93.1	718	4	AAB66907 Insectici
18	3368.5	90.0	710	4	Aau02041 B. thurin
19	3311	88.5	719	3	Abb07073 Bacillus
20	3060	81.8	1217	4	Aau02092 Bacillus
21	2645	70.7	1208	4	Aau02093 Bacillus
22	2460	65.7	1230	8	Adk98489 B thuring
23	2460	65.7	1230	8	Adk98489 B thuring
24	2460	65.7	1230	8	Adk98481 B thuring
25	2460	65.7	1230	8	Adk98491 B thuring

26	2460	65.7	1230	8	ADK98487
27	2459	65.7	1229	2	AAR54074
28	2459	65.7	1229	2	AAW35259
29	2459	65.7	1229	2	AAW17699
30	2459	65.7	1229	2	AAW87633
31	2459	65.7	1229	2	AAW87633
32	2459	65.7	1229	8	ADK98479
33	2322.5	62.1	1228	2	AAR50955
34	2317.5	61.9	1209	4	Aau02094
35	2308.5	61.7	1227	2	AAW31990
36	2243	59.9	1227	2	AAW44321
37	2243	59.9	1227	4	AAB19950
38	2234	59.7	1227	4	AAU02046
39	2233.5	59.7	488	2	AAW44322
40	2233.5	59.7	488	4	AAB19947
41	2219	59.3	1186	2	AAW16796
42	2198.5	58.8	1221	4	AAU00421
43	2184.5	58.4	1221	4	AAU00420
44	2170.5	58.0	1228	4	AAB84628
45	2168.5	58.0	1228	4	AAU02039

ALIGNMENTS

RESULT 1
AAB66912
ID AAB66912 standard; protein; 719 AA.
XX
AC AAB66912;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIb1.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
(ZENE) ZENECA LTD.
XX
PI Griffin J., Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
PS Claim 14; Page 64-66; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66912 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
SQ Sequence 719 AA;

Query Match 100.0%; Score 3742; DB 4; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.1e-300;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60
DB 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGIGIAGKILGTLGVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120
QY 121 RNKALSDLRGLGDALAVYHESLESWVENRNTRARSVVKNQYIALELMFVKQLPSPAVSG 180
DB 121 RNKALSDLRGLGDALAVYHESLESWVENRNTRARSVVKNQYIALELMFVKQLPSPAVSG 180
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
DB 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
QY 241 TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPPSYDTLVPIKTTSQLTREYVYTDAL 300
DB 241 TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPPSYDTLVPIKTTSQLTREYVYTDAL 300
QY 301 GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFTQPVNGVPR 420
QY 421 VDFHMKFPTLPASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFPTLPASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
QY 601 TFRITGFTTFFSDFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TFRITGFTTFFSDFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 2
AAE36276
ID AAE36276 standard; protein; 719 AA.
AC AAE36276;
XX AAE36276;
DT 26-JUN-2003 (first entry)
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
OS Bacillus thuringiensis.
XX WO200298911-A2.
PN 12-DEC-2002.
XX 30-MAY-2002; 2002WO-GB002666.
PF 07-JUN-2001; 2001GB-00013900.
XX (SYGN) SYNGENTA LTD.
PA XX

Vincent JL, Viner R;
WPI; 2003-175137/17.
New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
Claim 12; Page 56-58; 67pp; English.
The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
Sequence 719 AA;
Query Match 100.0%; Score 3742; DB 6; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.1e-300;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60
DB 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGIGIAGKILGTLGVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120
QY 121 RNKALSDLRGLGDALAVYHESLESWVENRNTRARSVVKNQYIALELMFVKQLPSPAVSG 180
DB 121 RNKALSDLRGLGDALAVYHESLESWVENRNTRARSVVKNQYIALELMFVKQLPSPAVSG 180
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
DB 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
QY 241 TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPPSYDTLVPIKTTSQLTREYVYTDAL 300
DB 241 TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPPSYDTLVPIKTTSQLTREYVYTDAL 300
QY 301 GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFTQPVNGVPR 420
QY 421 VDFHMKFPTLPASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFPTLPASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
QY 601 TFRITGFTTFFSDFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TFRITGFTTFFSDFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

CC strain which produces at least three different types of crystal proteins
CC and is therefore claimed to be capable of killing insects from at least
CC three orders, thus providing a suitable alternative for broad-spectrum
CC agricultural pest control. The isolated crystal proteins, for e.g. CryII
CC protein, can also be applied to control pests (alone or with e.g. other
CC insecticidal proteins) and is useful to produce antibodies to isolate
CC similar proteins from other strains/organisms. The invention also
CC provides a BtC-18 toxin protein which is active against rootworms. The
CC Cry encoding nucleic acids are claimed to be useful for expressing the
CC plant products, to produce pest-resistant transgenic plants and
CC plant products, or in micro-organisms, which can be applied to protect
CC agricultural crops. They are also useful to isolate nucleic acids
CC encoding potentially pesticidal proteins from other strains/organisms by
CC hybridisation
XX
XX Sequence 719 AA;

Query Match		94.8%;	Score 3546;	DB 2;	Length 719;
Best Local Similarity		95.0%;	Pred. No. 3.5e-284;		
Matches 683;		Conservative 11;	Mismatches 25;	Indels 0;	Gaps 0;
QY	1	MKLKNDKHSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHSDIPFVSASTI	60		
DB	1	MKLKNDKHSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHSDIPFVSASTI	60		
QY	61	QTGIGIAGKILGTGVPFAGQIASLYSFIIGELWPKGKQWEIFMEHVVEIINOKILTYA	120		
DB	61	QTGIGIAGKILGTGVPFAGQIASLYSFIIGELWPKGKQWEIFMEHVVEIINOKILTYA	120		
QY	121	RNKALSDRLGLDALAVYHESLESWVENRNNTRARSVVKNOYIALELMFVQKLPFAVSG	180		
DB	121	RNKALTDKGLDALAVYHESLESWVENRNNTRARSVVKNOYIALELMFVQKLPFAVSG	180		
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN	240		
DB	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN	240		
QY	241	TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDILVPIKTTSQLTRVYTDAL	300		
DB	241	TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDILVPIKTTSQLTRVYTDAL	300		
QY	301	GTVHPNOAFSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW	360		
DB	301	GTVDPNQALRSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW	360		
QY	361	GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYRTESLAGNLFILTPQVNGVPR	420		
DB	361	GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYRTESLAGNLFILTPQVNGVPR	420		
QY	421	VDFHWKEPTLPASDNFYILGYAGVGTQLQDSNELPPTTGQPNYESYSHRLSHGLIS	480		
DB	421	VDFHWKEPTLPASDNFYILGYAGVGTQLQDSNELPPTTGQPNYESYSHRLSHGLIS	480		
QY	481	ASHVKALVSWTHRSADRTNTEPNSTIQLPLVKAFLNLSGAAVVRGPGFTGGDILRTN	540		
DB	481	GSVHKALVSWTHRSADRTNTEPNSTIQLPLVKAFLNLSGAAVVRGPGFTGGHILRTK	540		
QY	541	TGTFGDIRVNIINPPFAQYRVRIRYASTTDLOFHTSINGKAINQGNFATMNGEDLDYK	600		
DB	541	SGTFGHIRVNIINPPFAQYRVRIRYASTTDLOFHTSINGKAINQGNFATMNGEDLDYK	600		
QY	601	TFRTIGFTTPFSDVQSTFTTGAMFSSGNEVYIDRIEFPVPEVTEYAEYDEKAQEKV	660		
DB	601	TFRTVGTTPFSDVQSTFTTGAMFSSGNEVYIGRIEFPVPEVTEYAEYDEKAQEKV	660		
QY	661	TALETSTNPRGLTKDVKDHYIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM	719		
DB	661	TALFTSTNPRGLTKDVKDHYIDQVSNLVSLSDEFLYDEKRELFEIVKYAKQIHIERNM	719		

RESULT 5
AAB66908
ID AAB66908 standard; protein; 719 AA.

XX AAB66908;
XX 12-APR-2001 (first entry)
XX Insecticidal protein cryIIa2.
XX Insecticide; transgenic plant; insect-resistance.
XX Paecilomyces sp.
XX WO200100841-A1.
XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-GB002457.
XX 29-JUN-1999; 99GB-00015215.
XX 23-DEC-1999; 99GB-00030536.
XX (ZENE) ZENECA LTD.
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
XX Vincent JL, Lee MD;
XX WPI; 2001-123015/13.
XX Novel insecticidal protein obtained from species of Paecilomyces for
XX controlling insects, and for insect-resistant transgenic plant
XX production.
XX Claim 14; Page 55-57; 72pp; English.
XX The present invention relates to novel insecticidal proteins obtained
XX from Paecilomyces sp. (see AAB66901 and AAB66913). The
XX insecticidal proteins can be used to produce transgenic plants, which are
XX insect-resistant. Also, the insecticidal proteins are useful for
XX controlling insects by providing them at a locus where insects feed
XX Sequence 719 AA;

Query Match		94.1%;	Score 3520;	DB 4;	Length 719;
Best Local Similarity		92.9%;	Pred. No. 5e-282;		
Matches 668;		Conservative 31;	Mismatches 20;	Indels 0;	Gaps 0;
QY	1	MKLKNDKHSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHSDIPFVSASTI	60		
DB	1	MKLKNDKHSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHSDIPFVSASTI	60		
QY	61	QTGIGIAGKILGTGVPFAGQIASLYSFIIGELWPKGKQWEIFMEHVVEIINOKILTYA	120		
DB	61	QTGIGIAGKILGTGVPFAGQIASLYSFIIGELWPKGKQWEIFMEHVVEIINOKILTYA	120		
QY	121	RNKALSDRLGLDALAVYHESLESWVENRNNTRARSVVKNOYIALELMFVQKLPFAVSG	180		
DB	121	RNKALTDKGLDALAVYHESLESWVENRNNTRARSVVKNOYIALELMFVQKLPFAVSG	180		
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN	240		
DB	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN	240		
QY	241	TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDILVPIKTTSQLTRVYTDAL	300		
DB	241	TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDILVPIKTTSQLTRVYTDAL	300		
QY	301	GTVHPNOAFSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW	360		
DB	301	GTVHPNPSFTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW	360		
QY	361	GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYRTESLAGNLFILTPQVNGVPR	420		
DB	361	GGHLEFRITGTLNISTOGSTNTSINPVTLPFTSRDYRTESLAGNLFILTPQVNGVPR	420		

QY 421 VDFHMKFPTLPPIASDNFYILGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYILGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAATMRGDLGYK 600
DB 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAATMRGDLGYK 600
QY 601 TFRITGFTTSPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
DB 601 TFRITGFTTSPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 6
AAE36272
ID AAE36272 standard; protein; 719 AA.
XX
AC AAE36272;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 44-47; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 719 AA;

Query Match 94.1%; Score 3520; DB 6; Length 719;
Best Local Similarity 92.9%; Pred. No. 5e-282;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;
QY 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKMNEDYLRMSEHESIDPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCIKWSENVBPVFSASTI 60

QY 61 QTGIGIAGKILGTGLGVPPAGQIASLYSIFLGLWPKGSKQWEIFMEHVVEIINQKILTYA 120
DB 61 QTGIGIAGKILGTGLGVPPAGQIASLYSIFLGLWPKGSKQWEIFMEHVVEIINQKILTYA 120
QY 121 RNKALSDRLGLDALAVYHESLESWVENRNTRARSVVKNQYIALELMFVQKLPSPFAVSG 180
DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNTRARSVVKSQYIALELMFVQKLPSPFAVSG 180
QY 181 BEVPLLPPIYQAANLHLLLRDASIFGKEMGLSASEISFYNQROVERTRDYSCHCIKWYN 240
DB 181 BEVPLLPPIYQAANLHLLLRDASIFGKEMGLSASEISFYNQROVERTRDYSCHCIKWYN 240
QY 241 TGLNNLRGTNAKSWRYNQPRKMTLMVLDLVALPPSDTLVYPIKTTQSOLTREVYTDAL 300
DB 241 TGLNNLRGTNAESWRYNQPRKMTLMVLDLVALPPSDTLVYPIKTTQSOLTREVYTDAL 300
QY 301 GTVHPNQAFASFTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
QY 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDQVYRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDQVYRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHMKFPTLPPIASDNFYILGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
DB 421 VDFHMKFVTHPIASDNFYILGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAATMRGDLGYK 600
DB 541 TGTFGDIRVINPPEAQRVRIYASTTDLQFHTSINGKAINQGNFSAATMRGDLGYK 600
QY 601 TFRITGFTTSPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
DB 601 TFRITGFTTSPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 7
ADR89421
ID ADR89421 standard; protein; 719 AA.
XX
AC ADR89421;
XX
DT 18-NOV-2004 (first entry)
XX
DE cryIIa.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.

Db 61 QTGIGIAGKILGTLGVFFAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALSDLRGDGLDALAVYHESLESWVENNRNTRARSVKNOYIALELMFVKQLPSFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWVGNRNTRARSVKSYIALELMFVKQLPSFAVSG 180
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVTRDYSDHCHIKWYN 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVTRDYSDHCHIKWYS 240
Qy 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTSQLTRVYTDAL 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALPSPSYDTQMYPIKTTAQLTRVYTDAL 300
Qy 301 GTVHPNQAFSTTWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Qy 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVRATESLAGLNLFLTOPVNGVPR 420
Db 361 GGHKLEFRTTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPR 420
Qy 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Qy 601 TPRTIGTTPPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Db 601 TPRTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELPEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELPEIVKYAKQIHIERNM 719

RESULT 9
AAE36274
ID AAE36274 standard; protein; 719 AA.
XX
AC AAE36274;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.
XX
XW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
XX WO200298911-A2.
XX
PD 12-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
XX (SYGN) SYNGENTA LTD.
PI Vincent JL, Viner R;
XX
XX WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-

PT terminus, useful as an active ingredient of a pesticide.
XX Claim 12; Page 50-53; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
CC sequence is used in the invention
XX Sequence 719 AA;
SQ
Query Match 94.0%; Score 3516; DB 6; Length 719;
Best Local Similarity 92.8%; Pred. No. 1.1e-281;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKQMNEDYLRMSEHESIDPFVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCLKMSYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTLGVFFAGQIASLYSFIILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120
Db 61 QTGIGIAGKILGTLGVFFAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALSDLRGDGLDALAVYHESLESWVENNRNTRARSVKNOYIALELMFVKQLPSFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWVGNRNTRARSVKSYIALELMFVKQLPSFAVSG 180
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVTRDYSDHCHIKWYN 240
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVTRDYSDHCHIKWYS 240
Qy 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPSYDTLVYPIKTTSQLTRVYTDAL 300
Db 241 TGLNNLRGTNAESWRYNQFRDMLMVLDLVALPSPSYDTQMYPIKTTAQLTRVYTDAL 300
Qy 301 GTVHPNQAFSTTWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Qy 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVRATESLAGLNLFLTOPVNGVPR 420
Db 361 GGHKLEFRTTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPR 420
Qy 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
Qy 601 TPRTIGTTPPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Db 601 TPRTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELPEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELPEIVKYAKQIHIERNM 719
RESULT 10
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX

AAU02095;	QY	301	GTVPNQAFAS	GTVPNQAFAS	360
07-SEP-2001 (first entry)	Db	301	GTVPHPST	GTVPHPST	360
Bacillus thuringiensis partial mutant CryIIa.	QY	361	GGHLESRPIG	GGHLESRPIG	420
CryIIa; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle; mutant; mutein.	Db	361	GGHLEFRITG	GGHLEFRITG	420
Bacillus thuringiensis.	QY	421	VDFHWKFP	VDFHWKFP	480
Key	Db	421	VDFHWKFP	VDFHWKFP	480
Location/Qualifiers	QY	481	ASHVKALV	ASHVKALV	540
1..19	Db	481	ASHVKALV	ASHVKALV	540
/label= Signal_peptide	QY	541	TGTFGDIR	TGTFGDIR	600
20..719	Db	541	TGTFGDIR	TGTFGDIR	600
/label= Mature_CryIIa	QY	601	TFRTIGFT	TFRTIGFT	660
EP1099760-A1.	Db	601	TFRTIGFT	TFRTIGFT	660
16-MAY-2001.	QY	661	TALFTSTN	TALFTSTN	719
09-NOV-1999; 99EP-00203723.	Db	661	TALFTSTN	TALFTSTN	719
09-NOV-1999; 99EP-00203723.	QY	719	AAAB66911	AAAB66911	719
(CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.	Db	719	AAAB66911	AAAB66911	719
De Maagd RA, Bosch HJ;	QY	719	AAAB66911	AAAB66911	719
WPI; 2001-337141/36.	Db	719	AAAB66911	AAAB66911	719
N-PSDB; AAS04855.	QY	719	AAAB66911	AAAB66911	719
New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as CryIIa and CryIIb, and having insecticidal activity, useful for combating insects.	Db	719	AAAB66911	AAAB66911	719
Example; Page 30-32; 43pp; English.	QY	719	AAAB66911	AAAB66911	719
The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA encoding which was mutated to allow cloning of domain III or domains I and II, to make the hybrid proteins of the invention. The hybrid toxins of the invention, having structural domains I, II and III in this order starting from the N-terminal derived from at least 2 different crystal proteins, are useful for protecting plants against pest insects, e.g. moths, butterflies and Colorado potato beetle or for combating insects	Db	719	AAAB66911	AAAB66911	719
Sequence 719 AA;	QY	719	AAAB66911	AAAB66911	719
Query Match	Db	719	AAAB66911	AAAB66911	719
Best Local Similarity 93.8%; Score 3511; DB 4; Length 719;	QY	719	AAAB66911	AAAB66911	719
Mismatches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;	Db	719	AAAB66911	AAAB66911	719
1 MKLKNPKHQSLSSNAKVDKIATDSLNKNETDIELKNMNNEDYLRMSEHSDPFSASTI 60	QY	719	AAAB66911	AAAB66911	719
1 MKLKNPKHQSLSSNAKVDKIATDSLNKNETDIELKNMNNEDYLRMSEHSDPFSASTI 60	Db	719	AAAB66911	AAAB66911	719
61 QTGIGIAGKILGTGVPFAGQIASLYSFLIGELWPKGSKQWEIFMEHVEEIIINQKILTYA 120	QY	719	AAAB66911	AAAB66911	719
61 QTGIGIAGKILGTGVPFAGQIASLYSFLIGELWPKGSKQWEIFMEHVEEIIINQKILTYA 120	Db	719	AAAB66911	AAAB66911	719
121 RNKALSDLRGLGDALAVYHESLESWVENNNTRARSVKNQYIALELMFVQKLPFAVSG 180	QY	719	AAAB66911	AAAB66911	719
121 RNKALSDLRGLGDALAVYHESLESWVENNNTRARSVKNQYIALELMFVQKLPFAVSG 180	Db	719	AAAB66911	AAAB66911	719
181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISFYNNQVTRDYSCHIKWYN 240	QY	719	AAAB66911	AAAB66911	719
181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISFYNNQVTRDYSCHIKWYN 240	Db	719	AAAB66911	AAAB66911	719
241 TGLNNLRGTNAKSWVRNQFRKDMTLMVLVALPFSYDTLVYPIKTTSQLTRVYTDAT 300	QY	719	AAAB66911	AAAB66911	719
241 TGLNNLRGTNAKSWVRNQFRKDMTLMVLVALPFSYDTLVYPIKTTSQLTRVYTDAT 300	Db	719	AAAB66911	AAAB66911	719

Sequence 719 AA;

[illegible]

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKOIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719

RESULT 13
ID AAB66909 standard; protein; 719 AA.
XX AAB66909;
AC AAB66909;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa3.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
XX
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE) ZENECA LTD.
XX
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
PI
XX WPI; 2001-123015/13.
XX
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
PS Claim 14; Page 57-59; 72pp; English.
XX
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66909 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 719 AA;

Query Match 93.6%; Score 3503; DB 4; Length 719;
Best Local Similarity 92.5%; Pred. NO. 1.3e-280;
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKMNEDYLRMSEHESIDPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60

QY 61 QTGGIAGKILGTGVFPAGQIASLYSIFILGELWPKGSKQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGGIAGKILGTGVFPAGQIASLYSIFILGELWPKGSKQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALSDLGLDALAVVHESLESWYENNRNTRSVVKNQYIALELMFVQKLPSFAVSG 180
DB 121 RNKALTDLKGLDALAVVHDSLESWYGNRNTRSVVKSQYIALELMFVQKLPSFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCIIKWN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGNTNAKSWRYNQFRKDMTLMVLDLVALFSDYTLVYPIKTTSLTREVYTDAT 300
DB 241 TGLNNLRGNTNAESWRYNQFRDWTLMVLDLVALFSDYDTQMPYIKTTAQLTREVYTDAT 300

QY 301 GTVHPNQAFASSTWYNNAPSFSAIEAAVIRSPHLLDLEKVTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPNPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMW 360

QY 361 GGHRLSPIGGALNTSTQGSTNTSINPVTILOFTSRDVYRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLODSENELPPEPTTQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYLYGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDIQLFHTSINGKAINQGNFSATMNRGDDLYK 600
DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDIQLFHTSINGKAINQGNFSATMNRGDDLYK 600

QY 601 TFRITGFTTFFSFDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TFRITGFTTFFSFDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKOIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719

RESULT 14
ID AAE36273 standard; protein; 719 AA.
XX
AC AAE36273;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 47-50; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

SQ Sequence 719 AA;

XX	09-MAY-1989;	89GB-00010624.			
PF					
XX	09-MAY-1989;	89GB-00010624.			
PR					
XX	(ICIL)	IMPERIAL CHEM IND PLC.			
PA					
PI	Blenk RG,	Ely S, Tailor RH, Tippett JM;			
XX	WPI;	1990-361486/48.			
DR	N-PSDB;	AAQ06636.			
XX	Bacillus thuringiensis strains -	used for producing an endotoxin for			
PT	protecting plants against insects,	partic. Lepidoptera and Coleoptera.			
XX	Claim 5;	Fig 5-10; 66pp; English.			
PS					
XX	The sequence carried on pJH12	which was isolated from B. thurin- giensis			
CC	strains JHCC4835 and JHCC 4353	(NCIB 40091 and 40090 resp.). The DNA can			
CC	be used to produce transformants	E.coli strain MC12022/pJH12 (NCIB 40278,			
CC	or bacteriophage EMBL4 vector	(NCIB 40279) or E.coli strain BL21/pJH11			
CC	(NCIB 40275). The delta-endo-	toxin produced by the transformants can be			
CC	used in formulations for	combattling Lepidoptera and Coleoptera pests.			
CC	(Updated on 25-MAR-2003	to correct PA field.) (Updated on 24-OCT-2003 to			
CC	standardise OS field)				
XX	SQ	Sequence 719 AA;			
	Query Match	93.5%; Score 3499; DB 2; Length 719;			
	Best Local Similarity	92.5%; Pred. No. 2.8e-280;			
	Matches 665; Conservative 31; Mismatches 23; Indels 0; Gaps 0;				
Qy	1	MKLKNDPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI	60		
Db	1	MKLKNDKQKHSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFVSASTI	60		
Qy	61	QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGQWEIFMEHVEEIIINQKILTYA	120		
Db	61	QTGIGIAGKILGTGVPFAGQVASYLSIFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120		
Qy	121	RNKALSDLRIGDALAVHYHESLESWVENNTRARSVVKQYIALELMFVQKLPSPAVSG	180		
Db	121	RNKALTDLKGGLDALAVYHDSLESWVGNNRNRARSVVKSQYIALELMFVQKLPSPAVSG	180		
Qy	181	BEVPLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNQVERTRDYSCHIKWYN	240		
Db	181	BEVPLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNQVERAGDYSYHCVKWS	240		
Qy	241	TGLNNLRGTNAKSWRYNQFRKDMTLMVLVDLVALFPSPYDVLVPIKTTSQLTREYVTDAL	300		
Db	241	TGLNNLRGTNAESWRYNQFRDMTLMVLVDLVALFPSPYDTQMPYIKTTAQLTREYVTDAL	300		
Qy	301	GTVHPNQAFASFTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW	360		
Db	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360		
Qy	361	GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNLFLTQPVNGVPR	420		
Db	361	GGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR	420		
Qy	421	VDFHWKFPPTLP IASDNFFYLYGAGVGTQLQDSENELPPTTGPQNYESYSHRLSHIGLIS	480		
Db	421	VDFHWKFVTHPIASDNFFYYPGYAGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS	480		
Qy	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540		
Db	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540		
Qy	541	TGTFGDIRVNNPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600		
Db	541	TGTFGDIRVNNPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600		
Qy	601	TFRTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDEKAQEKV	660		
Db	601	TFRTVGTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDEKAQEKV	660		
Qy	661	TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM	719		
Db	661	TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719		
	RESULT 15				
	AAR08041				
	AAR08041	standard; protein; 719 AA.			
	IID	XX			
	AC	AAR08041;			
	XX	XX			
	24-OCT-2003	(revised)			
	25-MAR-2003	(revised)			
	27-FEB-1991	(first entry)			
	XX	XX			
	81 kD endotoxin deduced from DNA	carried on pJH12.			
	DE	DE			
	XX	XX			
	Crystal; insecticide; toxin; delta	endotoxin.			
	XX	XX			
	Bacillus thuringiensis; JHCC 4353	and 4835.			
	OS	OS			
	XX	XX			
	PN	W09013651-A.			
	XX	XX			
	15-NOV-1990.				
	PD				

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(without alignments)
4539.261 Million cell updates/sec

Title: US-10-019-823B-59
Perfect score: 3742
Sequence: 1 MKLKNPDKQSLSSNAKVDK.....KRELPEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	719	1 C1IB_BACTE	Q45709 bacillus th
2	3598	96.2	719	2 Q9F0P8	Q9F0P8 bacillus th
3	3546	94.8	719	1 C1IC_BACTU	O87404 bacillus th
4	3520	94.1	719	1 C1IA_BACTK	Q45752 bacillus th
5	3520	94.1	719	2 Q6X1B1	Q6X1B1 bacillus th
6	3515	93.9	719	2 Q93NJ5	Q93nj5 bacillus th
7	3514	93.9	719	2 Q85796	O85796 bacillus th
8	3510	93.8	719	2 Q8KY61	Q8KY61 bacillus th
9	3311	88.5	719	1 C1ID_BACTU	Q9xd11 bacillus th
10	2459	65.7	1229	1 C1BB_BACTU	Q45739 bacillus th
11	2459	65.7	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2322.5	62.1	1228	2 Q93T75	Q93t75 bacillus th
13	2321.5	62.0	1228	1 C1BA_BACTK	P05517 bacillus th
14	2313.5	61.8	1228	2 Q93NM5	Q93nm5 bacillus th
15	2243	59.9	849	2 Q6PYW8	Q6Pyw8 bacillus th
16	2243	59.9	1227	1 C1BE_BACTU	O85805 bacillus th
17	2129	56.9	1231	2 Q8KNY2	Q8kny2 bacillus th
18	2116	56.5	1231	1 C1BD_BACT2	Q9raz5 bacillus th
19	1963	52.5	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1817	48.6	381	2 Q45740	Q45740 bacillus th
21	1670	44.6	1144	2 Q8KZL7	Q8kz17 bacillus th
22	1657.5	44.3	1157	1 C8AA_BACUK	Q45704 bacillus th
23	1507	40.3	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1503.5	40.2	1166	1 C1GA_BACTU	Q45746 bacillus th
25	1497.5	40.0	1169	1 C1FB_BACTM	O66377 bacillus th
26	1491.5	39.9	1174	2 Q45749	Q45749 bacillus th
27	1484.5	39.7	1169	1 C8BA_BACUK	Q45705 bacillus th
28	1480.5	39.6	1155	1 C1AB_BACTK	P06578 bacillus th
29	1480.5	39.6	1155	2 Q7BE98	O7be98 bacillus th
30	1480.5	39.6	1155	2 Q9F296	Q9F296 bacillus th
31	1475.5	39.4	1156	2 Q6GUA7	Q6gua7 bacillus th

RESULT 1
CLIB_BACTE
ID C1IB_BACTE STANDARD; PRT; 719 AA.
AC Q45709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin
DE CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name-cryIIb; Synonyms=cryII(b), cryV, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U07642; AAA82114.1; -
CC PIR; I40590; I40590.
CC HSSP; P02965; ICIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
CC SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

ALIGNMENTS

32	1473.5	39.4	1118	2	Q9AM83	Q9am83 bacillus th
33	1470.5	39.3	793	2	Q6PYW7	Q6pyw7 bacillus th
34	1470.5	39.3	1177	2	Q6EIX3	Q6eix3 bacillus th
35	1468.5	39.2	1155	2	Q93T21	Q93t21 bacillus th
36	1468	39.2	1167	1	C1JA_BACTU	Q45738 bacillus th
37	1463.5	39.1	1181	1	C1AE_BACTL	Q03748 bacillus th
38	1459	39.0	1180	2	Q9S5V8	Q9s5v8 bacillus th
39	1457	38.9	1176	2	Q7WZT9	Q7wzt9 bacillus th
40	1451	38.8	1176	2	Q45736	Q45736 bacillus th
41	1447	38.7	1176	1	C1AA_BACTK	P02965 bacillus th
42	1447	38.7	1176	2	Q9RCJ0	Q9rc30 bacillus th
43	1436.5	38.4	1179	1	C1AD_BACTA	Q03744 bacillus th
44	1419.5	37.9	1118	2	Q9AM82	Q9am82 bacillus th
45	1416	37.8	1169	2	Q8GHE8	Q8ghe8 bacillus th

"Identification of cryII-type genes from *Bacillus thuringiensis* strains and characterization of a novel cryII-type gene.";
Appl. Environ. Microbiol. 69:5207-5211(2003).
EMBL; AF211190; AAG43526.1; -.
HSSP; P02965; 1CIY.
GO; GO:0005102; P:receptor binding; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
Plasmid.
SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

RT	Query Match	100.0%;	Score 3742;	DB 1;	Length 719;				
RT	Best Local Similarity	100.0%;	Pred. No. 1.4e-249;						
RL	Matches 719;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
DR	1	MKLKPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTI	60						
DR	1	MKLKPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTI	60						
DR	61	QTGIGIAGKILGTGVPFAGQIASLSYFILGELWPKGSQWEIFMEHVEEIIINQILTYA	120						
DR	61	QTGIGIAGKILGTGVPFAGQIASLSYFILGELWPKGSQWEIFMEHVEEIIINQILTYA	120						
DR	121	RNKALSDRLGLDALAVYHESLESWENRNTRARSVVKQYIALELMFVQKLPSPFVSG	180						
DR	121	RNKALSDRLGLDALAVYHESLESWENRNTRARSVVKQYIALELMFVQKLPSPFVSG	180						
DR	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSABISITFYNRQVTRDYSDHCIKWYN	240						
DR	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSABISITFYNRQVTRDYSDHCIKWYN	240						
DR	241	TGLNLRGTNAKSWRVYRQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL	300						
DR	241	TGLNLRGTNAKSWRVYRQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL	300						
DR	301	GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYNNMW	360						
DR	301	GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYNNMW	360						
DR	361	GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNFLTPQVNGVPR	420						
DR	361	GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNFLTPQVNGVPR	420						
DR	421	VDFHWKFPTLPASDNFYLYGAGVGTQLQDSENELPPTTQPNYESYSHRLSHIGLIS	480						
DR	421	VDFHWKFPTLPASDNFYLYGAGVGTQLQDSENELPPTTQPNYESYSHRLSHIGLIS	480						
DR	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540						
DR	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540						
DR	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAIWMNRGEDLDYK	600						
DR	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAIWMNRGEDLDYK	600						
DR	601	TFRTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV	660						
DR	601	TFRTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV	660						
DR	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIVKAKQIHIERNM	719						
DR	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIVKAKQIHIERNM	719						

RESULT 2									
Q9F0P8	PRELIMINARY;	PRT;	719 AA.						
AC	Q9F0P8;								
DT	01-MAR-2001 (Tremblrel. 16, Created)								
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)								
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)								
DE	CryII.								
GN	Name=cryII;								
OS	<i>Bacillus thuringiensis</i> .								
OG	Plasmid pBTC19.								
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .								
OX	NCBI_TaxID=1428;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=BTC007;								
RX	MEDLINE=22837682; PubMed=12957903;								
RA	DOI=10.1128/AEM.69.9.5207-5211.2003;								
RA	Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,								
RA	Hu Y., Li G., Huang D.								

RESULT 3
CLIC_BACTU

ID CLIC BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OC Bacterioides; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF056933; AAC62933.1; --
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 94.8%; Score 3546; DB 1; Length 719;
Best Local Similarity 95.0%; Pred. No. 4.8e-236;
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHSIDPPVSASTI 60
DB 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHSIDPPVSASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQIASLYSIFILGELWPKGKSQWEIFMEHVBEIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQIASLYSIFILGELWPKGKSQWEIFMEHVBEIINQKILTYA 120

QY 121 RNKALSDLRLGDLALAVYHESLESWYENRNTRRSVKNQYIALELMFVKLPSPFVSG 180
DB 121 RNKALSDLRLGDLALAVYHESLESWYENRNTRRSVKNQYIALELMFVKLPSPFVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSASEISTPNRQVTRDYSHCIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSASEISTPNRQVTRDYSHCIKWYN 240

QY 241 TGLNNLRGTNAKSWVRNQFRKDMVLVLDLVALPSPDYTLVPIKTTSQLTRVYTDAI 300
DB 241 TGLNNLRGTNAKSWVRNQFRKDMVLVLDLVALPSPDYTLVPIKTTSQLTRVYTDAI 300

QY 301 GTVHPNOAFASFTWYNNAPSPSAIAAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPNOAFASFTWYNNAPSPSAIAAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360

QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVTSTESLAGLNFLTPQVNGVPR 420
DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVTSTESLAGLNFLTPQVNGVPR 420

QY 421 VDFHWKFPPTLPFASDNFYLYGYAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFPPTLPFASDNFYLYGYAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TCTFGDIRVININPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
DB 541 TCTFGDIRVININPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600

QY 601 TPTTGTTPFSDVQSTFTIGAWNFSSGNEVIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TPTTGTTPFSDVQSTFTIGAWNFSSGNEVIDRIEFVPEVTEYAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 4
CLIA_BACTK STANDARD; PRT; 719 AA.
ID CLIA_BACTK STANDARD; PRT; 719 AA.
AC Q45752; P71092; Q45750; Q45751; Q45756;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin
DE CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryV1;
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSIR732;
RX MEDLINE=93298009; PubMed=8517758;
RA Gleave A.P., Williams R., Hedges R.J.;
RT "Screening by polymerase chain reaction of Bacillus thuringiensis
RT serotypes for the presence of cryV-like insecticidal protein genes and
RT characterization of a cryV gene cloned from B. thuringiensis subsp.
RT kurstaki.";
RL Appl. Environ. Microbiol. 59:1683-1687 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JHCC4835;
RX MEDLINE=92269582; PubMed=1588820;
RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;
RT "Identification and characterization of a novel Bacillus thuringiensis
RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";
RL Mol. Microbiol. 6:1211-1217 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407 (1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=AB88;
RX MEDLINE=96178985; PubMed=8606196;
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
RA Craig J.A., Koziel M.G., Estruch J.J.;

Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPSPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISFYNQVERTRDYSCHIKWYN 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISFYNQVERTRDYSCHIKWYN 240
Qy 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDAI 300
Db 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDAI 300
Qy 301 GTVHPNQAFSTTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPNPSFTTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHRLSRPIGALNTSTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420
Db 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420
Qy 421 VDFHWKFPPTLIASDNFYLYGAGVGTQLODSENELPPTTGPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYLYGAGVGTQLODSENELPPTTGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TPTTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660
Db 601 TPTVGTGTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 6

Q93NJ5 ID Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5; Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cryllia.
GN Name=Cryllia;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1] SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 93.9%; Score 3515; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 6.7e-234;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEFPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGKSQWEIFMEHVVEEIIINOKILTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGKSQWEIFMEHVVEEIIINOKISITYA 120
Qy 121 RNKALSRLGLGDALAVYHDSLESWGNRNTRARSVKNQYIALELMFVQKLPSPFAVSG 180
Db 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVKNQYIALELMFVQKLPSPFAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISFYNQVERTRDYSCHIKWYN 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSEISFYNQVERTRDYSCHIKWYS 240
Qy 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDAI 300
Db 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTSQLTRVYTDAI 300
Qy 301 GTVHPNQAFSTTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPNPSFTTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHRLSRPIGALNTSTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420
Db 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420
Qy 421 VDFHWKFPPTLIASDNFYLYGAGVGTQLODSENELPPTTGPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYLYGAGVGTQLODSENELPPTTGPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TPTTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660
Db 601 TPTVGTGTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 7

O85796 ID O85796 PRELIMINARY; PRT; 719 AA.
AC O85796; Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryVI01;
OS Bacillus thuringiensis (subsp. kurstaki).
OC Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=S101;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.

DR	InterPro; IPR001178; Endotoxin.	
DR	InterPro; IPR005638; endotoxin_C.	
DR	InterPro; IPR005639; endotoxin_N.	
DR	InterPro; IPR008979; Gal_bind_like.	
DR	Pfam; PF03944; Endotoxin_C; 1.	
DR	Pfam; PF00555; Endotoxin_M; 1.	
DR	Pfam; PF03945; Endotoxin_N; 1.	
KW	Plasmid.	
SEQ	SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;	
	Query Match 93.9%; Score 3514; DB 2; Length 719;	
	Best Local Similarity 92.8%; Pred. No. 7.8e-234;	
	Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;	
QY	1	MKLKNDPKHQSLGSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFFVSASTI 60
DB	1	MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKSEYENVEPFFVSASTI 60
QY	61	QTGIGIAGKILGTGLGVPFAGQIASLYSFIIGELWPKGKSOWEIFMEHVEEIIINQILTYA 120
DB	61	QTGIGIAGKILGTGLGVPFAGQVASLYSFIIGELWPKGKNQWEIFMEHVEEIIINQIKISTYA 120
QY	121	RNKALSDLGLGDALAVHYESLSBVENRNNTRARSVVKNQVIALEIMFVKQLPSFAVSG 180
DB	121	RNKALTDLGLGDALAVHDSLSBVGVRNNTRARSVVKSQVIALEIMFVKQLPSFAVSG 180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDCIKWYN 240
DB	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRDYSDCIKWYS 240
QY	241	TGLNLRGNTNAKSWRYNQFRKDMTLMVLDLVALFPSTDTLYPIKTTSQLTRVYTDAI 300
DB	241	TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYKTTAQLTRVYTDAI 300
QY	301	GTVHPNQAFASSTWYNNNAPSFAIEAAVIRSPHLLDLEKVTIYSLLSRWSNTQYNNMW 360
DB	301	GTVHPHPSPFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMW 360
QY	361	GGHRLSRPTGGALNTSTOGSTNTSINPVTLQFTSRDYVYRTESLAGNLFLTQPVNGVPR 420
DB	361	GGHKLFRFTTGGTLNISTOGSTNTSINPVTLPFTSRDYVYRTESLAGNLFLTQPVNGVPR 420
QY	421	VDHFWKPTPIASDNFYLYGAGVGTQLQDSENELPPTTGQPNYESYSHRLSHIGLIS 480
DB	421	VDHFWKFVTPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY	481	ASHVKALVYSWTHRSADRTNTIENSIITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB	481	ASHVKALVYSWTHRSADRTNTIENSIITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY	541	TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB	541	TGTFGDIRVNIKPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY	601	TFTIGFTTTPFSFSDVQSTFTIGAWNFSGNEVYIDRTIEFVPVEVTYEAAYDFEKAQEKV 660
DB	601	TFTRTVGFTTTPFSFLDVQSTFTIGAWNFSGNEVYIDRTIEFVPVEVTYEAAYDFEKAQEKV 660
QY	661	TALFTSTNPRGLKTDVKDYHDQVNLVESLSDFYLDKRELFEIVKYAKQIHIERNM 719
DB	661	TALFTSTNPRGLKTDVKDYHDQVNLVESLSDFYLDKRELFEIVKYAKQIHIERNM 719
RESULT	8	
Q8KY61	PRELIMINARY;	PRT; 719 AA.
ID	Q8KY61	
AC	Q8KY61;	
DT	01-OCT-2002 (TrEMBLrel. 22, Created)	
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Cry.	
OS	Bacillus thuringiensis.	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	


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RESULT 9
CLID_BACTU
ID CLID_BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin
DE CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIId; Synonyms=cryII(d), NRCryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RX MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
RT gene.";
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae. Active on Plutella
CC xylostella and on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AF047579; AAD44366.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 88.5%; Score 3311; DB 1; Length 719;
Best Local Similarity 87.2%; Pred. No. 8.1e-220;
Matches 627; Conservative 50; Mismatches 42; Indels 0; Gaps 0;

QY 1 MKLKNPKHQSLSSNAKVDKIATDSIKNETDIELKNMNEIDYLRMSSEHSDPFSVASTI 60
DB 1 MKSKQNMYSFSSNATVDKSFDTPLEHNTNMELQNSHEDCLKMSYESVEPFSVSTI 60

QY 61 QTGIGIAGKILGTLPVFPAGQIASLYSIFILGELWPKGQWEIPMEHVEEIIHQKILTYA 120
DB 61 QTGIGIAGKILGNLGVFPAGQVASLYSIFILGELWPKGQWEIPMEHVEELINQKISTYA 120

QY 121 RNKALSDRLGLDALAVHYHESLESWENRNTRARSVVKNQYIALELMFVQKLPFAVSG 180
DB 121 RNKALADLKGGLDALAVHYHESLESWENRNTRVRSVKNQYIALELMFVQKLPFAVSG 180

QY 181 BEVPLLPYQAANLHLLLRDASIFGKGLSASEISTPNYRQVTRDYSCHIKWYN 240
DB 181 EEVPLLPYQAANLHLLLRDASIFGKGLSESEISTFYNRQSSQTEYSYDCEWYN 240

QY 241 TGLNLRGNTNAESWRYNQFRDWTLMVLDLVALFPSYDTRMYPPIPTSAQLTREYTDAL 300
DB 241 TGLNLRGNTNAESWRYNQFRDWTLMVLDLVALFPSYDTRMYPPIPTSAQLTREYTDAL 300

RESULT 10
CLIBB_BACTU
ID CLIBB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbB (Insecticidal delta-endotoxin
DE CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbB; Synonyms=cryET5, cryIB(b);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
```



```
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 1.2e-160;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKDHQSLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPFVSASTIQT 62
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 20 VSNPSTQWNLSPDARI-----EDSLCVAEVNNDIDPFVSASTVQT 58
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 GIGIAGKILGTGVPPAGQIASLYSFLGELWPKGSKSQWEIFMEHVEEIIKILTYARN 122
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 59 GINIAGRILGVLGVPPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRN 118
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 123 KALSDRLGLDALAVTHESLESVVENNTRARSVKNQYIALELMFVQKLPSFAVSGEE 182
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 TAIARLEGLGRGYSYQQALETWLDNRDARSRIILERYVALELDITTAIPLFRIRNEE 178
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYNTG 242
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 179 VPLLMVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEESNHCQWYNTG 238
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 243 LNNLRGTNAKSVRYNQFRKDMTLMVLDLVALFSPSYDTLVYPIKTTSQLTREVYDAIGT 302
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 239 LNNLRGTNAESWLRYNQFRRLDTLGLVDLVALFSPSYDTRTPINTSAQLTREIYTDPIGR 298
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 303 VHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYMMWGG 362
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 299 TNAPSGFASTNWFNNNAPSFAIEAAIFRPPHLLDPPEQLTIYSASSRWSSTQHMNYWVG 358
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 363 HRLESRPFGALNTSTQGST-NTSINPVTLOFTSRDVRTYESLAGNLFLTQPVNGVPRV 421
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 359 HRLNFRPIGGTLNTSTQGLTNNTSINPVTLOFTSRDVRTYESNAGTNILFTTPVNGVPA 418
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 422 DFHWKFPPLPIASDNFYVLG-----YAGVGTQLQDSSENELPPTTGPNYESYSHRLS 474
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 419 RFNF-----INPQNIYERGATTYSQYQGVGIQLFDSSETLPPETTERNYESYSHRLS 472
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

DR EMBL; Z46442; CAA86568.1; -.
DR HSPP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 65.7%; Score 2459; DB 1; Length 1233;
Best Local Similarity 64.8%; Pred. No. 1.2e-160;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKDHQSLSSNAKVDKIATDSLKNETDIELKNNMNNEDYLRMSHESIDPFVSASTIQT 62
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 20 VSNPSTQWNLSPDARI-----EDSLCVAEVNNDIDPFVSASTVQT 58
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 GIGIAGKILGTGVPPAGQIASLYSFLGELWPKGSKSQWEIFMEHVEEIIKILTYARN 122
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 59 GINIAGRILGVLGVPPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRN 118
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 123 KALSDRLGLDALAVTHESLESVVENNTRARSVKNQYIALELMFVQKLPSFAVSGEE 182
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 TAIARLEGLGRGYSYQQALETWLDNRDARSRIILERYVALELDITTAIPLFRIRNEE 178
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYNTG 242
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 179 VPLLMVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEESNHCQWYNTG 238
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 243 LNNLRGTNAKSVRYNQFRKDMTLMVLDLVALFSPSYDTLVYPIKTTSQLTREVYDAIGT 302
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 239 LNNLRGTNAESWLRYNQFRRLDTLGLVDLVALFSPSYDTRTPINTSAQLTREIYTDPIGR 298
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 303 VHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYMMWGG 362
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 299 TNAPSGFASTNWFNNNAPSFAIEAAIFRPPHLLDPPEQLTIYSASSRWSSTQHMNYWVG 358
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 363 HRLESRPFGALNTSTQGST-NTSINPVTLOFTSRDVRTYESLAGNLFLTQPVNGVPRV 421
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 359 HRLNFRPIGGTLNTSTQGLTNNTSINPVTLOFTSRDVRTYESNAGTNILFTTPVNGVPA 418
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 422 DFHWKFPPLPIASDNFYVLG-----YAGVGTQLQDSSENELPPTTGPNYESYSHRLS 474
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 419 RFNF-----INPQNIYERGATTYSQYQGVGIQLFDSSETLPPETTERNYESYSHRLS 472
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
CIBC_BACTM STANDARD; PRT; 1233 AA.
AC Q45774;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin
DE CryIb(c)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
```


Qy	475	HIGLISASHVVALVSWTHRSADRTNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGD	534
Dd	473	HIGLIIGNTLRAPVSWTHRSADRTNTIGNRITQIPLVKALNLSHSGVTVVGGPGFTGGD	532
Qy	535	ILRRTNTGTFGDIRVNINPPPAQRVRIYASRTDLOFHTSINGKAINQGNFSATMNRG	594
Dd	533	ILRRTNTGTFGDIRVNINPLSQRVRIYASRTDLOFHTSINGKAINQGNFSATMNRG	592
Qy	595	EDLDYKTFRTTGTTPESFSDVQSTFTIGAMNFSNGEVYIDRIEFVPEVTEAEYDPE	654
Dd	593	DNLEYSFRTAGFTFPFNLAQSTFTLGAQSFN-QEYVIDRVEFPAEVTPEAEYDLE	651
Qy	655	KAQEKYATLFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIH	714
Dd	652	RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEIVKYAKRLS	711
Qy	715	IERNM 719	
Dd	712	DERNL 716	
RESULT 12			
Q93T75	PRELIMINARY; PRT; 1228 AA.		
AC	Q93T75		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Delta-endotoxin CryIa2.		
GN	Name=cryIa2;		
OS	Bacillus thuringiensis (subsp. entomocidus).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1436;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=HD-9;		
RA	Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF363025; AAK51084.1; -		
DR	HSSP; P07130; IDLC.		
DR	GO: 0005102; F:receptor binding; IEA.		
DR	GO: 0006952; P:defense response; IEA.		
DR	GO: 0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;		
Query Match 62.1%; Score 2322.5; DB 2; Length 1228;			
Best Local Similarity 63.6%; Pred. No. 3.2e-151;			
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;			
Qy	23	TDSLKNETDI-----ELKMNEDYLRMSEHSDIPFVSASTIQTGIGIAGKI	70
Dd	2	TSNRKNEEII NAVSNHSAQMDLLPDARIEDSLCIAEGNNDIPFVSASTVQTGINIAGRI	61
Qy	71	LGTGVFPAGQIASLYSPILGELWPKGSQWEIFMEHVEEIIINOKILTYARNKALSDLRG	130
Dd	62	LGVGVFPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQQTENARNTALRLQG	121
Qy	131	LGDAVYHESLESWENNRNTRSVVKQYIALELMFVQKLPSFAVSGEVPPLPIYA	190
Dd	122	LGDSFRAYQOSLEDWLENRRDARTSVLHTQYIALELDFLNPFLAIRNQEVPLLMVYA	181
Qy	191	QAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYNTGLNLRGTN	250
Dd	182	QAANLHLLLRDASLFGSEFGLTSQEIQRYRQVTRDYSDYCVWEYNTGLNLRGTN	241
RESULT 13			
CL1BA_BACTK	STANDARD; PRT; 1228 AA.		
AC	P05517; Q45731;		
DT	01-NOV-1988	(Rel. 09, Created)	
DT	01-FEB-1996	(Rel. 33, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Pesticidal crystal protein cryIaB (insecticidal delta-endotoxin		
DE	CryIaB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).		
GN	Name=cryIaB; Synonyms=cryA4, cryIa(a);		
OS	Bacillus thuringiensis (subsp. kurstaki), and		
OS	Bacillus thuringiensis (subsp. entomocidus).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339, 1436;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=B.t.kurstaki; STRAIN=HD-2;		
RX	MEDLINE=88203216; PubMed=3362680;		
RA	Brizzard B.L., Whiteley H.R.;		
RT	"Nucleotide sequence of an additional crystal protein gene cloned from		
RL	Bacillus thuringiensis subsp. thuringiensis.";		
RV	Nucleic Acids Res. 16:2723-2723(1988).		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=B.t.entomocidus; STRAIN=HD-110;		
RA	Soetaert P.;		
RL	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut		
CC	epithelial cells of insects.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X06711; CAA29898.1; -
DR EMBL; X95704; CAA65003.1; -
DR PIR; S00873; S00873.
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 62.0%; Score 2321.5; DB 1; Length 1228;
Best Local Similarity 63.6%; Pred. No. 3.7e-151;
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY	23	TDLSKNETDI-----ELKNNMNEYLRMSSEHSIDPFVSASTIQTGIGIAGKI	70
Db	2	TSNRKNEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI	61
QY	71	LGTGVFPFAGQIASLYSFLGELWPKGSKQWEIFMEHVEEIIINQKILTYARNKALSDLRG	130
Db	62	LGVLPFAGQLASFSYFLVGLWPRGRDQWEIFLEHVEQLINQITENARNTALARQG	121
QY	131	LGDALAVYHESLESWVENNRNTRARVVKNQYIALELMFVQKLPFAVSSEVPLPIYA	190
Db	122	LGDSFRAYQOSLEDWLENRDDARTSVLYTQYIALELDFLNAPLFAIRNQEVPLLMVYA	181
QY	191	QAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCICKWYNTGLNLRGTN	250
Db	182	QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVTRDYSDYCVWYNTGLNLRGTN	241
QY	251	AKSWRYNQFRKDMTLVLDLVALFPSYDTLVYPIKTSQLTREVYTDATGTVHPNQAF	310
Db	242	AASWRYNQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREYITDAIGATGVN--MA	299
QY	311	STTWYNNAPSFSAIEAAVTRSPHLLDFLEKVTIYSLSRWSNTQYMNWGGHRESRPI	370
Db	300	SMWYNNAPSFSAIEAAVTRSPHLLDFLEKVTIYSLSRWSNTRHMTYWRGHTIQSRPI	359
QY	371	GGALNTSTQGSTNTSINPVTLOFTSRDVRRTESLAGNLF--LTQPVNGVPRVDFHWKFP	428
Db	360	GGGLNTSTHGATNTSINPVTIRFASRDVYRTESYAGVLLWGIYLEPIHGVPTRFNTNP	419
QY	429	-TLPIASDNFYLYGAGVGTQLODSENELEPPETTGQPNYESYSHRLSHIGLISASHVKAL	487
Db	420	QNISDRGTANTSQPYSPGLQKDSSETLPETTERPNYESYSHRLSHIGIILQSRVNP	479
QY	488	VYSWTHSADRTNTIENPSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTGFDI	547
Db	480	VYSWTHSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRNTGTGFGPI	539
QY	548	RVINPFPQAQRVRYRYASTDLQFTSINGKAINQGNFSATMNRGDDLDYKTFRTIGF	607
Db	540	RVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYNFVRRAF	599
QY	608	TFPFSFSDVQSTFTIGAWNFSSGNEVIIDRIEFVPEVVEYAEVDFEKAQKVTALFTST	667
Db	600	TFPFTFTQIDIRTSTQGLSGNGEYVIDKIEIIPVATFAEAYDLERAQEAVALFTNT	659
QY	668	NPRGLKTDVKYHIDQVNLVESLSDEFYLDKRELFEIVKYAKQIHTERM 719	
Db	660	NPRRLKTDVTDYHIDQVNLVACLSDSEFCLDEKRELLEKVKYAKLSDBNL 711	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.6029 Seconds
(without alignments)
3350.901 Million cell updates/sec

Title: US-10-019-823B-59
Perfect score: 3742
Sequence: 1 MKLKNPDKHQSLSSNAKVDK.....KRELFEIVKYAKOIHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:**
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:**
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:**
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:**
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:**
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:**
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:**
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:**
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:**
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:**
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:**
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:**
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:**
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:**
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3520	94.1	719	16	US-10-782-020-10
2	3520	94.1	719	16	US-10-782-141-8
3	3368.5	90.0	710	15	US-10-428-961-42
4	2324.5	62.1	1228	16	US-10-809-953-10
5	2314.5	61.9	1207	10	US-09-988-462-7
6	2234	59.7	1227	15	US-10-428-961-63
7	2219	59.3	1186	9	US-09-826-660-23
8	2170.5	58.0	1228	15	US-10-428-961-38
9	2170.5	58.0	1228	15	US-10-614-524-2
10	1982	53.0	643	9	US-09-826-660-25
11	1734.5	46.4	1167	14	US-10-089-678-1
12	1683.5	45.0	653	15	US-10-428-961-6
13	1657.5	44.3	1157	16	US-10-782-141-16

14	1514	40.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1514	40.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1514	40.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1500.5	40.1	1156	14	US-10-099-285-72	Sequence 72, Appl
18	1500.5	40.1	1156	15	US-10-428-961-28	Sequence 28, Appl
19	1494	39.9	1210	13	US-10-032-717-4	Sequence 4, Appli
20	1494	39.9	1210	14	US-10-414-637-4	Sequence 4, Appli
21	1494	39.9	1210	15	US-10-606-320-4	Sequence 4, Appli
22	1480.5	39.6	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1480.5	39.6	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1480.5	39.6	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1480.5	39.6	1181	10	US-09-988-462-11	Sequence 11, Appl
26	1480.5	39.6	1181	10	US-09-988-462-13	Sequence 13, Appl
27	1480.5	39.6	1181	10	US-09-988-462-15	Sequence 15, Appl
28	1480.5	39.6	1181	10	US-09-988-462-17	Sequence 17, Appl
29	1480.5	39.6	1181	10	US-09-988-462-28	Sequence 28, Appl
30	1480.5	39.6	1181	15	US-10-136-998A-4	Sequence 4, Appli
31	1480.5	39.6	1181	15	US-10-136-998A-8	Sequence 8, Appli
32	1480.5	39.6	1181	15	US-10-136-998A-10	Sequence 10, Appl
33	1480.5	39.6	1181	15	US-10-136-998A-12	Sequence 12, Appl
34	1475.5	39.4	1177	14	US-10-035-060-6	Sequence 6, Appli
35	1472.5	39.4	1177	14	US-10-102-469-24	Sequence 24, Appl
36	1470.5	39.3	1177	14	US-10-035-060-2	Sequence 2, Appli
37	1470.5	39.3	1177	14	US-10-035-060-8	Sequence 8, Appli
38	1447	38.7	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1436.5	38.4	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1436.5	38.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1391	37.2	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1386.5	37.1	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1386.5	37.1	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1386.5	37.1	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1386.5	37.1	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10
; Sequence 10, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-10

Query Match 94.1%; Score 3520; DB 16; Length 719;
Best Local Similarity 92.9%; Pred. No. 4.7e-287;
Matches 669; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

Qy	1	MKLKNPDKHQSLSSNAKVDKIATDSLKNVETIELKNNNEDYLRMSHESIDPFVSA	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNVETIELQNHEDCLKMSYENVEPFVSA	60
Qy	61	QTGIGIAGKILGTIGVPPAGQIASLYSPILGELWPKGKSQWEIFMEHVEEINQILTYA	120
Db	61	QTGIGIAGKILGTIGVPPAGQVASLYSPILGELWPKGKNQWEIFMEHVEEINQIKISTYA	120

121 RNKALDRLGLDALAVYHESLESWVENNTRARSVVKNOYIALELMFVKLPFAVSG 180
121 RNKALDRLGLDALAVYHDSLESWGNRNTRARSVVKNOYIALELMFVKLPFAVSG 180
181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDRYSDHCWKYN 240
181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRDRYSDHCWKYS 240
241 TGLNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSYDTLVPIKTTTSOLTREVYTDI 300
241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTLVPIKTTTAQLTREVYTDI 300
301 GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
361 GGHKLEFRITGGTTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
421 VDFHWKFPPLPIASDNFYLYGYAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVTHPIASDNFYLYGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK 600
541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK 600
601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHERNM 719
661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHERNM 719

RESULT 2
US-10-782-141-8
; Sequence 8, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

US-10-782-141-8
Query Match 94.1%; Score 3520; DB 16; Length 719;
Best Local Similarity 92.9%; Pred. No. 4.7e-287;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

1 MKLKNQDKHQSFSSNAKVDKISTDLSLKNETDIELQNIHEDCLMKSEYENVEPFSASTI 60

1 MKLKNQDKHQSFSSNAKVDKISTDLSLKNETDIELQNIHEDCLMKSEYENVEPFSASTI 60
61 QTGIGIAGKILGTLGVPPFAGQIASLYSFTLGLMWPKGSKQWEIFMEHVVEEIIINQKILTYA 120
61 QTGIGIAGKILGTLGVPPFAGQVASLYSFTLGLMWPKGKNQWEIFMEHVVEEIIINQKISTYA 120
121 RNKALDRLGLDALAVYHESLESWVENNTRARSVVKNOYIALELMFVKLPFAVSG 180
121 RNKALDRLGLDALAVYHDSLESWGNRNTRARSVVKNOYIALELMFVKLPFAVSG 180
181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDRYSDHCWKYN 240
181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRDRYSDHCWKYS 240
241 TGLNLRGTNAKSWRYNQFRDMTLMVLDLVALFPSYDTLVPIKTTTSOLTREVYTDI 300
241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTLVPIKTTTAQLTREVYTDI 300
301 GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
361 GGHKLEFRITGGTTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
421 VDFHWKFPPLPIASDNFYLYGYAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVTHPIASDNFYLYGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
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541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK 600
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601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
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RESULT 3
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:

NAME/KEY: misc feature
LOCATION: (200) (200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match 90.0%; Score 3368.5; DB 15; Length 710;
Best Local Similarity 89.2%; Pred. No. 2.6e-274;
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;

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DB 1 MKSKQNMHQSLSNATVDKNFTGSLNNTNLTQNFY-----HEGIEPFVSASTI 51
QY 61 QTGIGIAGKILGTPFAGQIASLYSFIIGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120
DB 52 QTGIGIAGKILGTPFAGQIASLYSFIIGELWPKGKSQWEIFMEHVEEIIINQKISTYA 111
QY 121 RNKALSDRLGDLALAVYHESLESWVENRNTFRSVVKNQYIALELMFVQKLPSPAVSG 180
DB 112 RNKALADLGLDALAVYHESLESWVENRNTFRSVVKSQYITLLELMFVQSLPSPAVSG 171
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDHCIKWYN 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDHCIKWYN 231
QY 241 TGLNLRGTTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL 300
DB 232 TGLNLRGTTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL 291
QY 301 GTVHPNQAFSTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360
DB 292 GTVHPNPSFTTWNAPSFSTIEAAVVRNPHLLDFLEKVTIYSLLSRWSNTQYNNMW 351
QY 361 GGHRLSPGIGALNTSTOGSTNTSINPVTLOFTSRDYRTESLAGNLFPLTPQVNGVPR 420
DB 352 GGHKLEFRIGTNTSTOGSTNTSINPVTLOFTSRDYRTESLAGNLFPLTPQVNGVPR 411
QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENLPEPTTQPNYESYSHRLSHIGLIS 480
DB 412 VDFHWKFTVTHPIASDNFYLYGAGVGTQLODSENLPEPTTQPNYESYSHRLSHIGLIS 471
QY 481 ASHKALVTSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
DB 472 ASHKALVTSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRKN 531
QY 541 TGTGDIRVNINPPFAQRVRYRYASTDLOPHTSINGKAINQGNFSAATMNRGDLDDYK 600
DB 532 TGTGDIRVNINPPFAQRVRYRYASTDLOPHTSINGKAINQGNFSAATMNRGDLDDYK 591
QY 601 TFRITGTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 592 TFRITGTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 651
QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 652 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 710

RESULT 4
US-10-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
APPLICANT: Van Mellaert, Herman
APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bc INSECT
TITLE OF INVENTION: CRYSTAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 1990-05-30
PRIOR APPLICATION NUMBER: GB 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1228
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 62.1%; Score 2324.5; DB 16; Length 1228;
Best Local Similarity 63.6%; Pred. No. 4.9e-186;
Matches 454; Conservative 85; Mismatches 166; Indels 9; Gaps 5;

QY 12 LSSNAKVDKIATDSLKN---ETDIELKNNMNNEDYLRMSHEHESIDPPFVSASTIQTGIGIAG 68
DB 1 LTSNRKNEEIIINAVSNHSAQMDL-LPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAG 59
QY 69 KILGTLPVFPAGQIASLYSFIIGELWPKGKSQWEIFMEHVEEIIINQKILTYARNKALS 128
DB 60 RILGVLGVPFAGQIASLYSFIIGELWPKGKSQWEIFMEHVEEIIINQKILTYARNKALS 119
QY 129 RGLGDALAVYHESLESWVENRNTFRSVVKNQYIALELMFVQKLPSPAVSGEVEPLLP 188
DB 120 QGLGDSFRAYQQSLEDWLENRDARTSVLHTQYIALELDFLNPMLFAIRNQEVEPLLMV 179
QY 189 YQAANLHLLLRDASIFGKWLGSASEISTFYNRQVTRDYSDHCIKWNTGLNLRG 248
DB 180 YQAANLHLLLRDASIFGSEGLTSQBIQRYRYQVTRDYSDYCVWYNTGLNLRG 239
QY 249 TNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDALGTVHPNQ 308
DB 240 TNAASWRYNQFRDLTLGLVLDLVALFPSYDTLVYPIKTTSQLTRVYTDALGTATGN-- 297
QY 309 FASTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMWGHRLES 368
DB 298 MASMNWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTRHMTYWRGHTIQSR 357
QY 369 PIGGALNTSTOGSTNTSINPVTLOFTSRDYRTESLAGNLF--LTQPVNGVPRVDFHWK 426
DB 358 PIGGALNTSTOGSTNTSINPVTLOFTSRDYRTESLAGNLF--LTQPVNGVPRVDFHWK 417
QY 427 FP-TLPIASDNFYLYGAGVGTQLODSENLPEPTTQPNYESYSHRLSHIGLISASHVK 485
DB 418 NPQNISDRGTANTYQSPESGLQKDSSETLPEPTTERPNYESYSHRLSHIGLISQSRVN 477
QY 486 ALVTSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNRTGTFG 545
DB 478 VPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNRTGTFG 537
QY 546 DIRVNINPPFAQRVRYRYASTDLOPHTSINGKAINQGNFSAATMNRGDLDDYKTRTI 605
DB 538 PIRVTNGPLTQRYRIGFRYASTVDFVSRGGTTVNNFRFRTMNSGDELKYGNFVRR 597
QY 606 GFTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 665
DB 598 AFTTPFTTQIQDIIRTSIQGLSGNGEYVYIDKIEIIPVTATFAEYDLERAEVVALFT 657
QY 666 STNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 658 NTNPRRLKTDVTDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKRSLDERNL 711

RESULT 5
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nallini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauais, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sygenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-988-462-7
Query Match 61.9%; Score 2314.5; DB 10; Length 1207;
Best Local Similarity 65.4%; Pred. No. 3.3e-185;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;
QY 40 EDYLRMSEHESIDPFVSASTIQTGIGIAGKILGILGVPAGQIASLYSIFILGLWPKGKS 99
DB 10 EDLSIAGNNIDPFVSASTIQTGINIAGILGILGVPAGQIASLYSIFILGLWPGRGD 69
QY 100 QWEIFMEHVEEIIINQKILTYARNKALSGLGLDALAVYHESLESWVENNTRARSVK 159
DB 70 QWEIFLEHVEQLINQITENARTALARLQGLGDSFRAVQOSLEDWLENRDDARTSVLY 129
QY 160 NQYTALELMFVQKLPSPAVSGBEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEIST 219
DB 130 TQYIALELDLFLNAMPFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEQIR 189
QY 220 FYNRQVTRDYSYDCHCQWYNTGLNIRGNTAKSVRYNQFRKDMTLMVLDLVALFPSSYD 279
DB 190 YERQVTRDYSYDCHCQWYNTGLNIRGNTAKSVRYNQFRKDMTLMVLDLVALFPSSYD 249
QY 280 TLVYPIKTTSQLTREYVTDAGTGVN--MASNMWYNNAPSFSAIEAAIRSPHLLDFL 339

DB 250 TRTYPINTSAQLTREYVTDAGTGVN--MASNMWYNNAPSFSAIEAAIRSPHLLDFL 307
QY 340 EKVTIYSLLSRWSTNTQYMMWGGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTRSDVY 399
DB 308 EQLTIFSSASSRWSNRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDVY 367
QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFP-TLPIASDNFYVLGVAGVGTQLOQDSNEL 456
DB 368 RTESYAGVLLWGIYLEPIHGVTFRFNTPNQNISDRGTANTYQPYSPGLQKDSSETEL 427
QY 457 PPETGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIENPNSITQIPLVKAF 516
DB 428 PPETTERPNYESYSHRLSHIGLIIQSRVNVVYSWTHRSADRTNTIGPNRITQIPMKAS 487
QY 517 NLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPPFAQRYRVRIRYASTDLOQHTS 576
DB 488 ELPOGTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVS 547
QY 577 INGKAINQGNFSATMNRGEBLDYKTFRTTGFSTPFSDVQSTFTTIGAMNFSNGEYVID 636
DB 548 RGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTFTTQIOTIIRTSIQGLSGNGEYVID 607
QY 637 RIEFVPEVETTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFY 696
DB 608 KIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFY 667
QY 697 LDEKRELFEIVKYAKQIHIERNM 719
DB 668 LDEKRELLEKVKYAKLSDERNL 690

RESULT 6
US-10-428-961-63
; Sequence 63, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 63
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-428-961-63

Query Match 59.7%; Score 2234; DB 15; Length 1227;
Best Local Similarity 60.8%; Pred. No. 2e-178;
Matches 434; Conservative 100; Mismatches 162; Indels 18; Gaps 3;
QY 23 TDSLKNETDI---ELKNMNN-----EDYLRMSEHESIDPFVSASTIQTGIG 65
DB 2 TSNRKNENEINALSIPAVSNHSAQNNLSTDAIEDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQIASLYSIFILGLWPKGKSQWEIFMEHVEEIIINQKILTYARNKAL 125
DB 62 IAGRILGVLGVPFAGQIASLYSIFILGLWPGRDPEWIFLEHVEHLIRQVNTEDTAL 121
QY 126 SDLRGLGDALAVYHESLESWVENNTRARSVVKVQVIALELMFVQKLPSPAVSGBEVPL 185


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; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match          53.0%; Score 1982; DB 9; Length 643;
Best Local Similarity 59.6%; Pred. No. 1.2e-157;
Matches 383; Conservative 94; Mismatches 148; Indels 18; Gaps 3;

QY 23 TDSLKNETDI-----ELKMNW-----EDYLRMSEHESIDPFVSASTIQTGIG 65
DB 2 TSNRKNENEINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTGVPPAGQIASYSLFELGELWPKGSKWEIFMEHVEEIIINQKILTYARNKAL 125
DB 62 IAGRILGVLGVPPAGQIASYSLFVLGELWPRGRDPWEIPLFHEVQELLRQQVTENTDIAL 121

QY 126 SDLRGLGDALAVYHESLESVENNRNTRARSVVKNQYIALELMFVQKLPSFAVSGREVPL 185
DB 122 ARLOGLGNSPRAYQOSLEDWLENRDDARTRSVLYTOYIALELDPLNAMPLFAIRNQEVPL 181

QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYNTGLNN 245
DB 182 LMVYAQAANLHLLLRDASIFGSEGLTSQEIQRYERQVREKTRYSYDCARWYNTGLNN 241

QY 246 LRGTNAKSWRYNQFRKQMTLWLDLVALFPSPYDTLVYPIKTTSQLTREVYTDAGTVHP 305
DB 242 LRGTNAESWRYNQFRDLTLGVLDLVALFPSPYDTRVYPMNTSAQLTREIYTDPIGRNA 301

QY 306 NQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYNNMVGSHRL 365
DB 302 PSGFASITWYNNNAPSFAIEAAVIRPPHLLDFPEQLTIFSVLSRWNTQYNNYVVGSHRL 361

QY 366 ESRPGCALNTSTQSTNTSINPVTLOFTSRDYRTESLAGLNLFLTPVNGVPRVDVFW 425
DB 362 ESRITRGLSTSTHGTNTSINPVTLOFTSRDYRTESFAGINILLTPVNGVPRVAREFW 421

QY 426 KFTPLPIASDNFYLYAGVGTQLQDSNELPPTGPNYSESYSHRLSHGLISASHVK 485
DB 422 RNPLSLRGSLLYITIGYGTQQLFDSELTPELPTETTERPNYSESYSHRLSLISGNLIR 481

QY 486 ALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFG 545
DB 482 APVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTVNGSVL 541

QY 546 DIRVNPVPPAQRVRYRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRTI 605
DB 542 SMGLNFNNTSLQRYRVRYRYAASQTMVLRTVCGSTTDDQGPSTMSANESLTSQSFRFA 601

QY 606 GFTTTPFSFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTVYE 648
DB 602 EFPVGISASGSQ-TAGISISNNAGRQTFHFDKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
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; FILE REFERENCE: Q68921
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1

Query Match          46.4%; Score 1734.5; DB 14; Length 1167;
Best Local Similarity 48.2%; Pred. No. 2.1e-136;
Matches 366; Conservative 123; Mismatches 210; Indels 61; Gaps 14;

QY 1 MKLKNDPKHQSL---SSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHE-----SI 51
DB 1 MSPNNQNEYIELDASSSTVSNDNSVRYPLANDQTTTLQNNMYKDYLRMSEGENPELFGNP 60

QY 52 DPFVSASTTQTGIGIAGKILGTGVPPAGQIASYSLFELGELWPKGK-SQWEIFMEHVEE 110
DB 61 ETFISSSTVQTGIGIVGVLGVPAGQIASFYSFIVGQLWSPSTVSVMEMIMKQVED 120

QY 111 IINOKILTYARNKALSDLRGLGDALAVYHESLESVENNRNTRARSVVKNQYIALELMFV 170
DB 121 LIQOKITDSVRKTAGLQGLDGLDVYQKSLKNWLENRNDTRARSVVVTQVIALELDV 180

QY 171 OKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRD 230
DB 181 AKIPSAISQGEVPELLSVYAQAANLHLLLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240

QY 231 YSDHCIKWYNTGLNNLRGTNAKSWRYNQFRKQMTLWLDLVALFPSPYDTLVYPIKTT 290
DB 241 YSDYCVKWYNTGLDKLKGTAASWLKYHQFRREMTLLVLDLVALFPYVDTTRYPIETTAQ 300

QY 291 LTREYVYTDAGTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLS- 349
DB 301 LTREYVYTDPIVFNRETSCGFCRRWSLNSDISFSEVESAVIRSPHLPILSEIFYETTRAG 360

QY 350 -RWSNTQYNNMVGSHRLSRRPIGGALNTSTQSTNTSINPVT-----LQFTSRDYVRTE 402
DB 361 LPLANNTEYLYWVGHSIKYK-----NTNASSALERNYGTITSNKIKYYDLANKDIFQVR 414

QY 403 SL-AGLNLFLTPVNGVPRVDVFWKFTPLPIASDNFYLYAGVAG-----T 447
DB 415 SLGADLANVYQAQ-VYGVVPYASF-----TLDDKN---TSGSGVGGFTYKPHHTMQVCT 463

QY 448 QLODSENELPPTGPNYSESYSHRLSHGLIS-----ASHVKALVYSWTHRSADRT 499
DB 464 QNYNTIDEIPPE--NEPLSRGYSHRLSHITSYFSKXASSPARYGNLPVFAWTHRSADVT 521

QY 500 NTIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFGDIRVNPVPPAQRV 559
DB 522 NTVYSDKITQIPVYKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSKSPLSQRY 581

QY 560 RVIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRTIGTFTTTPFSFSDVQST 619
DB 582 RARIRYASTTNLRLFVTISGTRIYSINVKNTWKNKDDLTFTNTFDLATIGTFTTTPFSNYS 641

QY 620 FTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEYDFEKAQEKVYALFTSTNPRGLKTDVKDY 679
DB 642 LTVGADSFASGGEVYVDKFEIIPVNAFEEAEEDLDVAKKANGLFTSKKD-ALQTSVTDY 700

QY 680 HIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 701 QVNOQAANLVESLSDELYPNEKRMLMDAVKAKRLVQARNL 740

RESULT 12
```


Db 527 TQIPAVKGMVLYLGGSVVQPGFTGGDILKRTNPSILGTFAVTNGSLSQRYRVRIRYAS 586
QY 568 TTDLPQHTSINGKAINQGNFSAWNRGDLDTYKTRFRTIGFTTTPFSDVQSTFTTGAMNF 627
Db 587 TTDPEF-TLYLGDIEKRNKMTDNGASLTETFEKASFIIDFQFRETQDKILLSMGDF 645
QY 628 SSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTAFTSTNPRGLKTDVVDKDYHIDQVSNL 687
Db 646 SSGQEVYIDRIEFIPVDEYAEQDLEAKKAVNALFTNTKD-GLRPGVTDYEVNQANL 704
QY 688 VESISDEFYLDKELEFEIVKYAKQIHIERNM 719
Db 705 VECLSDLLYPNEKRLFLDAVREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 40.5%; Score 1514; DB 13; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.3e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;

QY 1 MCLKNPDKHQSLSSNAKVDKIATDS----LKNETDIELKNNMNEYLRMSHESID- 52
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPFANEPTNALQNDYKOYLKMSAGNASEYPGS 59
QY 53 PFVSAS---TIQTGIGIAGKILGTGLVPPFAGQIASLYSIFILGELWPKG-KSOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGKSGQWEIFMEQV 119
QY 109 EEINQKILTYARNKALSDRLGDLALAVYHESLESWENNRNTRARSVVKQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGNGNYYQLYLTAAEEENPNRGRALRDVNRFRFELDSL 179
QY 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFFYNQVVERT 228
Db 180 FTQYMPSPRVTFNEVFPFLTVYAMAANLHLLLRDASIFGEEGWSTTTINNYYDQMKLT 239
QY 229 RYSDHCIKWYTNGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYDVLVPIKTT 288
Db 240 AEYSDHCVKWYETGLAKLGTSAKWVDYNQFRREMTLAVLDVVALFPYDTRTYPMETK 299
QY 289 SOLTREYVTDAGTVHPNQAFSTWYNNAPFSFAEAAVIRSPHLLDFLEKVTIYSL 348
Db 300 AQLTREYVTDPLGAVNVS---SIGSWY-DKAPSGVIESSVIRPPHVFYDITGLTYTQS 355
QY 349 SRWSNTQYMMWGGHRLSRPIGALNTSTQGSTNTSINPV-TLQTSRDVYRTESLAGL 407
Db 356 RSISSARYIRHWAGHQISYHRVSRGNSNLQOMYGTQNQLHSTSTFDFTNYDIYKTLSDOAV 415

QY 408 NLFLTQP-----VNGVPRVDFHW-----KFTPL----PIASDNFYVLGYAGVGTQLQDSE 453
Db 416 LLDIVYPGYTYIFGMPVEFEFFMVNQNNTRKTLKYNPVSVD-----IIASTRDS 466
QY 454 NELPPTTCQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNIEPNSITQI 510
Db 467 LELPPTSQPNYESYSHRLCHITSIPATGNTTGLVFPVSWTHRSADLNNIYSDKITQI 526
QY 511 PLVKAFLSSGAAVVRGPGFTGGDILR-RTNTGTGFDI---RVNINPPFAQRYRVRIRYA 566
Db 527 PAVKWDNLFPFVVKVKGHTGGDLLQVNRSTGSGVGTFLFLARYGLALEKAGKYRVLRYA 586
QY 567 STTDLPQHTSINGKAINQGNFSAWNRGDLDTYKTRF-----TIGFTTTPFS 614
Db 587 TDADIVLH--VNDQAI---QMPKTMNPGEDLTSKTFKVADAITTLNLTADSSLALKHNLG 641
QY 615 -DVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTAFTSTNPRGLK 673
Db 642 EDPNSTLS-----GIVYVDRIEFIPVDEYAEQDLEAKKAVNALFTNTKD-GLR 691
QY 674 TDVKDYHIDQVSNLVSLSDEFYLDKEKRELFEIVKYAKQIHIERNM 719
Db 692 PGVTDYEVNQANLVECLSDLLYPNEKRLFLDAVREAKRLSEARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 40.5%; Score 1514; DB 14; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.3e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;

QY 1 MCLKNPDKHQSLSSNAKVDKIATDS----LKNETDIELKNNMNEYLRMSHESID- 52
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPFANEPTNALQNDYKOYLKMSAGNASEYPGS 59
QY 53 PFVSAS---TIQTGIGIAGKILGTGLVPPFAGQIASLYSIFILGELWPKG-KSOWEIFMEHV 108
Db 60 PEVLVSGQDAAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGKSGQWEIFMEQV 119
QY 109 EEINQKILTYARNKALSDRLGDLALAVYHESLESWENNRNTRARSVVKQYIALELM 168
Db 120 EELINQKIAEYARNKALSELEGNGNYYQLYLTAAEEENPNRGRALRDVNRFRFELDSL 179
QY 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFFYNQVVERT 228
Db 180 FTQYMPSPRVTFNEVFPFLTVYAMAANLHLLLRDASIFGEEGWSTTTINNYYDQMKLT 239

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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds
(without alignments)
2318.356 Million cell updates/sec

Title: US-10-019-823B-59
Perfect score: 3742
Sequence: 1 MKLKNPDKHQSLSSNAKVDK.....KRELFEIVKVKQIHIERNM 719

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3546	94.8	719	2	US-09-003-217-2
2	3541	94.6	719	3	US-09-218-942-2
3	3516	94.0	719	3	US-08-286-870A-8
4	3368.5	90.0	710	4	US-09-661-322A-42
5	3160	84.4	648	3	US-08-286-870A-4
6	2573	68.8	535	3	US-08-286-870A-6
7	2459	65.7	1229	1	US-08-100-709-4
8	2459	65.7	1229	1	US-08-176-865-4
9	2459	65.7	1229	2	US-08-474-038-4
10	2459	65.7	1229	2	US-08-779-046-4
11	2459	65.7	1229	2	US-08-881-340-4
12	2314.5	61.9	1207	1	US-07-951-715A-7
13	2314.5	61.9	1207	2	US-08-459-448A-7
14	2314.5	61.9	1207	3	US-08-459-595A-7
15	2314.5	61.9	1207	3	US-08-459-504B-7
16	2314.5	61.9	1207	3	US-08-459-444-7
17	2314.5	61.9	1207	3	US-09-053-549-8
18	2314.5	61.9	1207	3	US-09-547-422-7
19	2314.5	61.9	1207	4	US-09-988-462-7
20	2308.5	61.7	1227	3	US-09-053-549-2
21	2243	59.9	1227	1	US-08-448-170-8
22	2243	59.9	1227	3	US-08-961-803-9
23	2234	59.7	1227	4	US-09-661-322A-63
24	2233.5	59.7	488	1	US-08-448-170-10
25	2233.5	59.7	488	3	US-08-961-803-10
26	2219	58.3	1186	3	US-09-178-252-23
27	2219	59.3	1186	4	US-09-826-660-23

28	2168.5	58.0	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1982	53.0	643	3	US-09-178-252-25	Sequence 25, Appl
30	1982	53.0	643	4	US-09-826-660-25	Sequence 25, Appl
31	1813	48.5	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1683.5	45.0	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1657.5	44.3	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1657.5	44.3	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1657.5	44.3	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1657.5	44.3	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1519.5	40.6	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1507	40.3	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1507	40.3	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1507	40.3	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1507	40.3	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1507	40.3	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1507	40.3	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1506.5	40.3	1168	1	US-08-291-368-4	Sequence 4, Appl
45	1506.5	40.3	1168	2	US-08-962-190-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia A.
; APPLICANT: Madkour, Magdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-003-217-2

Query Match 94.8%; Score 3546; DB 2; Length 719;
Best Local Similarity 95.0%; Pred. No. 6.1e-318;
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
Qy 1 MKLKNPDKHQSLSSNAKVDKIAATDSLKNETDIELKNNNEDYLRMSHESIDPFVSASTI 60
Db 1 MKLKNPDKHQTLSSNAKVDKIAATDSLKNETDIELKNNNEDYLRMSHESIDPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKSOWEIFMEHVEEIIINOKILTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKSOWEIFMEHVEEIIINOKILTYA 120
QY 121 RNKALSDRLGLGDALAVYHESLESWVNRNTRARSVVKNOYIALELMFVKQLPSFAVSG 180
DB 121 RNKALSDRLGLGDALAVYHESLESWVNRNTRARSVVKNOYIALELMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSCHCIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSCHCIKWYN 240
QY 241 TGLNLRGNTAKSWRYNQFRKDIEMVLDLVRVFPSTYDILVPIKTTSQLTREYVTDAL 300
DB 241 TGLNLRGNTAKSWRYNQFRKDIEMVLDLVRVFPSTYDILVPIKTTSQLTREYVTDAL 300
QY 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRYSAGLNLFLTQPVNGVPR 420
DB 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRYSAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFPPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFPPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
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DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
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DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
QY 601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
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QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 2
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: CryII
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2
Query Match 94.6%; Score 3541; DB 3; Length 719;
Best Local Similarity 95.0%; Pred. No. 1.4e-317;
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNEYLRMSEHESIDPFVSASTI 60

DB 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNEYLRMSEHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKSOWEIFMEHVEEIIINOKILTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKSOWEIFMEHVEEIIINOKILTYA 120
QY 121 RNKALSDRLGLGDALAVYHESLESWVNRNTRARSVVKNOYIALELMFVKQLPSFAVSG 180
DB 121 RNKALSDRLGLGDALAVYHESLESWVNRNTRARSVVKNOYIALELMFVKQLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSCHCIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSCHCIKWYN 240
QY 241 TGLNLRGNTAKSWRYNQFRKDIEMVLDLVRVFPSTYDILVPIKTTSQLTREYVTDAL 300
DB 241 TGLNLRGNTAKSWRYNQFRKDIEMVLDLVRVFPSTYDILVPIKTTSQLTREYVTDAL 300
QY 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPNQAFASITWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRYSAGLNLFLTQPVNGVPR 420
DB 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRYSAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFPPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFPPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480
QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
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DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
QY 601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 3
US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-8

Query Match 94.0%; Score 3516; DB 3; Length 719;
Best Local Similarity 92.8%; Pred. No. 3e-315;
Matches 667; Conservative 32; Mismatches 20; Indels 0; Gaps 0;

QY 1 MRLKNDKQKQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSHESIDPFVSASTI 60
DB 1 MRLKNDKQKQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
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DB 121 RNKALSDLRGLDALAVYHESLESWEVNRNTRARSVVKNQVIALELMFVQKLPSPAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
QY 241 TGLNLRGNTNAKSWVRYNQFRDMTLMVLDLVALFPSTYDTQYPIKTTAQTREVYTDAI 300
DB 241 TGLNLRGNTNAKSWVRYNQFRDMTLMVLDLVALFPSTYDTQYPIKTTAQTREVYTDAI 300
QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRKSNTOYMNW 360
DB 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRKSNTOYMNW 360
QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPQVNGVPR 420
DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPQVNGVPR 420
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DB 421 VDFHWKFPFTPIASDNFYLYGAGVGTQDSENELPPTTGPQNYESYSHRLSHIGLIS 480
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DB 541 TGTGDIRVNINPPAQRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRITGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TFRITGFTTFFSFDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
RESULT 4
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupaar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661.322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: No. 6593293-Coding
; US-09-661-322A-42

Query Match 90.0%; Score 3368.5; DB 4; Length 710;
Best Local Similarity 89.2%; Pred. No. 1.2e-301;
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;

QY 1 MRLKNDKQKQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSHESIDPFVSASTI 60
DB 1 MRLKNDKQKQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
QY 121 RNKALSDLRGLDALAVYHESLESWEVNRNTRARSVVKNQVIALELMFVQKLPSPAVSG 180
DB 121 RNKALSDLRGLDALAVYHESLESWEVNRNTRARSVVKNQVIALELMFVQKLPSPAVSG 180
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCWKYN 240
QY 241 TGLNLRGNTNAKSWVRYNQFRDMTLMVLDLVALFPSTYDTQYPIKTTAQTREVYTDAI 300
DB 241 TGLNLRGNTNAKSWVRYNQFRDMTLMVLDLVALFPSTYDTQYPIKTTAQTREVYTDAI 300
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DB 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRKSNTOYMNW 360
QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPQVNGVPR 420
DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPQVNGVPR 420
QY 421 VDFHWKFPFTPIASDNFYLYGAGVGTQDSENELPPTTGPQNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFPFTPIASDNFYLYGAGVGTQDSENELPPTTGPQNYESYSHRLSHIGLIS 480
QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVNINPPAQRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGEDLDYK 600

Db 532 TGTFGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 591
 Qy 601 TFRIGTTPPFSFSDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYEAAYDFEKAQEKV 660
 Db 592 TFRVGTTPPFSFSDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYEAAYDFEKAQEEV 651
 Qy 661 TALFTSTNPRGLKTDVXDHYHIDQVNSLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
 Db 652 TALFTSTNPRGLKTDVXDHYHIDQVNSLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 710

RESULT 5
 US-08-286-870A-4
 ; Sequence 4, Application US/08286870A
 ; Patent No. 6063605
 ; GENERAL INFORMATION:
 ; APPLICANT: ELY, S
 ; APPLICANT: TAILOR, RH
 ; APPLICANT: TIPPETT, JM
 ; APPLICANT: BLENK, RG
 ; TITLE OF INVENTION: BACTERIAL GENES
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; ADDRESSEE: Intellectual Property Group of
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/286,870A
 ; FILING DATE: 05-AUG-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/520228
 ; FILING DATE: 09-MAY-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 8910624.9
 ; FILING DATE: 09-MAY-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PAUL N. KOKULIS
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 70608/220720
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0944
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 648 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-286-870A-4

Query Match 84.4%; Score 3160; DB 3; Length 648;
 Best Local Similarity 92.3%; Pred. No. 1.8e-282;
 Matches 598; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKQNMNEDYLRMSHESIDPFVSASTI 60
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHNEHEDCLKMSSEVENVEPFVSASTI 60
 Qy 61 QTGIGTAGKIILGTGVFAGQIASLYSFTILGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
 Db 61 QTGIGTAGKIILGTGVFAGQVASLYSFTILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120

RESULT 6
 US-08-286-870A-6
 ; Sequence 6, Application US/08286870A
 ; Patent No. 6063605
 ; GENERAL INFORMATION:
 ; APPLICANT: ELY, S
 ; APPLICANT: TAILOR, RH
 ; APPLICANT: TIPPETT, JM
 ; APPLICANT: BLENK, RG
 ; TITLE OF INVENTION: BACTERIAL GENES
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; ADDRESSEE: Intellectual Property Group of
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/286,870A
 ; FILING DATE: 05-AUG-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/520228
 ; FILING DATE: 09-MAY-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 8910624.9
 ; FILING DATE: 09-MAY-1989

Qy 121 RNKALSRLGLDALAVYHESLESWVENNRNTRARSVVKNOYIALELMFVKQLPSFAVSG 180
 Db 121 RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
 Qy 181 EEVPLLPITYAQAANLHLLLRDASIFGKEMGLSASEISTFYNRQVTRDYSDHCHIKWYN 240
 Db 181 EEVPLLPITYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVTRDYSDHCHIKWYS 240
 Qy 241 TGLNLRGTNAKSWVRYNQFRKDMTLMVLVLPPIKTTTSOLTREVYTDI 300
 Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVLPPIKTTTAQLTREVYTDI 300
 Qy 301 GTVHPNQAFASWTWYNNAPSFSAIEAAVIRSPHLLDLEKVTIYSLLSWSNTQYMMNW 360
 Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEKVTIYSLLSWSNTQYMMNW 360
 Qy 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVTYTESLAGLNFLTQPVNGVPR 420
 Db 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNFLTQPVNGVPR 420
 Qy 421 VDFHWKFTPLIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
 Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
 Qy 481 ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAENLSGAAVVRGPGTGGDILRRTN 540
 Db 481 ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAENLSGAAVVRGPGTGGDILRRTN 540
 Qy 541 TGTGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
 Db 541 TGTGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDLDYK 600
 Qy 601 TFRIGTTPPFSFSDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYEAAYDFEKAQEKV 660
 Db 601 TFRVGTTPPFSFSDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYEAAYDFEKAQEEV 660


```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 68.8%; Score 2573; DB 3; Length 535;
Best Local Similarity 91.0%; Pred. No. 2e-228;
Matches 487; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGKSOWEIFMEHVEEIIINOKILTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120

QY 121 RNKALSDLRGLDALAVYHESLESVWENNRNTRARSVVKNOYIALELMFVKLPSPAVSG 180
Db 121 RNKALTDLKGDLALAVHDSLESVWGNRNTARSVVKSQYIALELMFVKLPSPAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRAGDYSDDHCWKYS 240

QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDI 300
Db 241 TGLNLRGTNAESWRYNQFRDRMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDI 300

QY 301 GTVHPNQAFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTOYNNMW 360
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTOYNNMW 360

QY 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTPLPIASDNFYLYGACVGTQLODSENELPPTTQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHKVAVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 481 ASHKVAVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

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;
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTIQT 62
Db 20 VSNSTQWNLSPDARI-----EDSLCVAEVNNDIDPFVSASTVQT 58

QY 63 GIGIAGKILGTGVPFAGQIASLYSFLGELWPKGKSOWEIFMEHVEEIIINOKILTYARN 122
Db 59 GINIAGRILGVLPFAGQIASLYSFLGELWPSGRDPWEIPLHVEQLIROQVNTNRN 118

QY 123 KALSDLRGLDALAVYHESLESVWENNRNTRARSVVKNOYIALELMFVKLPSPAVSGEE 182
Db 119 TAIARLEGLGRVRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

QY 183 VPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYNTG 242
Db 179 VPLLMVYAQAANLHLLLRDASLFGSEWGMASDVNOYQEQIIRYIEYSHCHVQWYNTG 238

QY 243 LNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTRVYTDI 302
Db 239 LNNLRGTNAESWRYNQFRDRDLTGLVLDLVALFPSYDTRTYPINTSAQLTRITDPIGR 298

QY 303 VHPNQAFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTOYNNMW 362
Db 299 TNAPSGFASTWYNNNAPSFAIEAAVIRSPHLLDFPEQVTIYSSASSRWSSSTQHMNVWVG 358

QY 363 HRLSRPIGGALNTSTOGST-NTSINPVTLOFTSRDYRTESLAGLNLFLTQPVNGVPRV 421
Db 359 HRLNFRPIGGTINTSTOGLTNTSINPVTLOFTSRDYRTESNAGTNILFTTPVNGVPUA 418

QY 422 DFHWKFTPLPIASDNFYLYG-----YAGVGTQLODSENELPPTTQPNYESYSHRLS 474
Db 419 RFNF-----INPQNIYERGATTYSQPYQGVGQLFDFSETELPPTTQPNYESYSHRLS 472

QY 475 HIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
Db 473 HIGLIIGNTLRAPVYSWTHRSADRTNTEPNSITQIPLVKALNLHSGVTVVGGPGFTGGD 532

QY 535 ILRRTNTGFGDIRVNIINPPFAQRYRVRIRYASTTDIQLFHTSINGKAINQGNFSATNRRG 594
Db 533 ILRRTNTGFGDIRLNLINVPVLSQRYRVRIRYASTTDIQLFHTINGITVNIIGNFSRTNRRG 592

QY 595 EDLDVKTFTTIGTTPFSFSDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDFE 654
Db 593 DNLEYRSPRTAGSTPFPNLAQSTFTLGAQSFSN-QEVYIDRVEFVPAEVTFEAEYDLE 651

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179 VPLLMVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEESNHCWQYNTG 238
243 LNNLFGTNAKSWRYNQPRKDMTLMVLDLVALFPSPYDVLVPIKTSQLTREYVYTDAGT 302
239 LNNLRGTNAESWLRYNQPRDLTLGVLDLVALFPSPYDTRTPINTSAQLTFEIIYDPIGR 298
303 VHPNOAFASITWYNNNAPSFAIEAAVIRSPLLDFLEKVTIYSLLSRWSNTQYMMWVG 362
299 TNAPSGFASTWNNNAPSFAIEAAIRPPHLLDFPEQLTIYSSASRWSSTQHMMYVWG 358
363 HRLSPPIGALNTSTQGST-NTSINPVTLOFTSRDYVYRTESLAGLNLFLTOPVANGVPRV 421
359 HRLNFRPIGGTLNTSTQGLTNTSINPVTLOFTSRDYVYRTESNAGTNILFTTPVNGVPMW 418
422 DFHWKFPPTLPASDNFYLG-----YAGVGTQLQDSENELPPTTGPQNYESYSHRLS 474
419 RENF-----INPQNIYERGATYSQPYQGVGIGLDFDSETELPPETTERPNYESYSHRLS 472
475 HGLISASHVKALVYSWTHRSADRNTIBPNSITQIPLVKAFNLSSGAADVVRGPGFTGGD 534
473 HGLIIGNTLRAPVYSWTHRSADRNTIGNRTIQIPLVKALNLHSGVTVVGPGFTGGD 532
535 ILRRTWTGFGDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRG 594
533 ILRRTWTGFGDIRLNLNINPLSQRYVRIRYASTTDLOFTRINGTNNIGNFSRTMNRG 592
595 ELDLYKTPRTIGFTTFFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPE 654
593 DNLEYSRFTAGFTSTPFENFLNAQSTFTLGAQSFN-QEYVIDRVEFVPAEVTFAEYDLE 651
655 KQAEKVTAFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIKVYAKOIH 714
652 RAQKAVNALFTSTNPRGLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEIKVYAKELS 711
715 IERNM 719
712 DERNL 716

RESULT 9
US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709

655 KQAEKVTAFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIKVYAKOIH 714
652 RAQKAVNALFTSTNPRGLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEIKVYAKELS 711
715 IERNM 719
712 DERNL 716

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-865-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

3 LKNPDKHQSLSNAKVDKIATSLKNETDIELKMNEDVLRMSHESIDPFVSASTIQT 62
20 VSNFSTQMNLSPDARI-----EDSLCVAEVNNIDPFVSASTVQT 58
63 GIGTAGKILGTGVFPFAGQIASYFSLGELWPKGSQWEIFMEHVEEIIQKILTYARN 122
59 GINTAGRIILGVLPFAGQIASYFSLGELWPKGSQWEIFMEHVEEIIQKILTYARN 118
123 KALSLRLGIGDALAVYHESLESWENNRNTRARSVKNQYIALELMFVKLPSFAVSGEE 182
119 TAIARLEGLGRGYRSYQQALETWLDNRDARSIIERYVALELDITTAIPLFIRNEE 178
183 VPLPIYAQAANLHLLLRDASIFGKENGWLSASEISTFYNRQVTRTRDSDHCIKWYNTG 242

FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-038-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPDKHQSLSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTIQT 62
DB 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNIDPFVSASTVQT 58

QY 63 GIGIAGKILGTGVPPFAGQIASLYSFLGELWPKGKQWEIEMHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVPPFAGQLASFYSFLVGELWPSGRDPWEIIFLEHVEQLIRQVNTN 118

QY 123 KALSDRLGLGDALAVYHESLESWVENNNTRARSVKKNQYIALELMFVQKLPFAVSGEE 182
DB 119 TAIARLEGLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVETRDYSDHCWKYNTG 242
DB 179 VPLLVMVYAQAANLHLLLRDASLFGSEGMASDVNQYQEIIRYTEYSNHCVCWYNTG 238

QY 243 LNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDTLVYPIKTTSQLTRVYDTAIGT 302
DB 239 LNNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSTYDTLVYPIKTTSQLTRVYDTPIGR 298

QY 303 VHPNQAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMWVG 362
DB 299 TNAPSGFASTWNNFNNAPSFAIEAIPRPHLLDFPEQLTIYSASRWSNSTQHMNVWVG 358

QY 363 HRLSERPIGALNTSTQGST-NTSINPVTLOFTSRDVRVETESLAGLNLFLTQPVNGVPRV 421
DB 359 HRLNFRPIGTLNTSTQGLTNTSINPVTLOFTSRDVRVETESNAGTNILFTTPVNGVPPWA 418

QY 422 DFHWKPTPLPIASDNFYILG-----YAGVGTQLQDSNELPPETTGQPNVESYSHRLS 474
DB 419 RFNF-----INPQNIYERGATTYSQYQGVGIGLFDSETELPPETTERPNVESYSHRLS 472

QY 475 HIGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
DB 473 HIGLIIGNTLRAPVSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGD 532

QY 535 ILRRNTGTGFDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATNRG 594
DB 533 ILRRNTGTGFDIRLNLINPVSQRVIRYASTTDLQFFTRINGTTWIGNFSRTNRG 592

QY 595 ELDLYKTRFTGFTTFFSDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVYTYEABYDFE 654
DB 593 DNLEYSRFTAGFTTFFNLNAQSTFTLGAQFSN-QEYVIDRVEFPVPAEFTFEABYDLE 651

QY 655 KAOEKVTALFTSTNPRGLKTDVKDYHIDOVSNLVSDESDEFYDKRELFELVKVYAKQIH 714
DB 652 RAOQAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDKRELFELVKVYAKRLS 711

QY 715 IERNM 719
DB 712 DERNL 716

US-08-779-046-4
Sequence 4, Application US/08779046
Patent No. 5854053
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yeping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-046-4

Query Match 65.7%; Score 2459; DB 2; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPDKHQSLSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTIQT 62
DB 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNIDPFVSASTVQT 58

QY 63 GIGIAGKILGTGVPPFAGQIASLYSFLGELWPKGKQWEIEMHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVPPFAGQLASFYSFLVGELWPSGRDPWEIIFLEHVEQLIRQVNTN 118

QY 123 KALSDRLGLGDALAVYHESLESWVENNNTRARSVKKNQYIALELMFVQKLPFAVSGEE 182
DB 119 TAIARLEGLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISFYNNQVETRDYSDHCWKYNTG 242
DB 179 VPLLVMVYAQAANLHLLLRDASLFGSEGMASDVNQYQEIIRYTEYSNHCVCWYNTG 238

QY 243 LNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDTLVYPIKTTSQLTRVYDTAIGT 302
DB 239 LNNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSTYDTLVYPIKTTSQLTRVYDTPIGR 298

QY 303 VHPNQAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMWVG 362
DB 299 TNAPSGFASTWNNFNNAPSFAIEAIPRPHLLDFPEQLTIYSASRWSNSTQHMNVWVG 358

QY 363 HRLSRPIGALNTSTOGST-NTSINPVTLQFTSRDVRVTESLAGLNLFLTQPVNGVPRV 421
Db 359 HRLNFRPIGTLNTSTOGLTNTSINPVTLQFTSRDVRVTESLAGLNLFLTQPVNGVPRV 418
QY 422 DFHWKFTPLPIASDNFYLG-----YAGVGTQLODSENELEPPETGQPNVYESYSHRLS 474
Db 419 RFNF-----INQNIYERGATTYSQPYQGVGIQLFSETELPETTERPNVYESYSHRLS 472
QY 475 HIGLISASHVKALVYSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
Db 473 HIGLIIGNTLRAPVYSWTHRSADRNTNTPNRIQIPLVKALNLHSGVTVVGGPGFTGGD 532
QY 535 ILRRTNTGTFGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRG 594
Db 533 ILRRTNTGTFGDIRVNIWNPFSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRG 592
QY 595 EDLDYKFTRTIGFTTFFSDVQSTFTTGAMNPFSSGNEVYIDRIEFVFPVEVYEAEDFE 654
Db 593 DNLEYSRFTAGFTFPENFLNAQSTFTLGAQSFNS-QEVYIDRVEFVPAEVTFEAEYDLE 651
QY 655 KAOEKVLTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQIH 714
Db 652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFELVVKYAKRLS 711
QY 715 IERNM 719
Db 712 DERNL 716

RESULT 11

US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-881-340-4
Query Match 65.7%; Score 2459; DB 2; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;
QY 3 LKNPDKHOSLSNAKVDKIATDSLKNETDIELKMNMDYLRMSHEHESIDPFVSASTIQT 62
Db 20 VSNPSTQMLSPDARI-----EDSLCAEVNNDIDFVSASTVQT 58
QY 63 GIGIACKILGTGVPPFAGQIASLYSFTLIGELWPKGKSOWEIPFMEHYVEEIIINQKILTYARN 122
Db 59 GINIAGRILGVLGVPPFAGQIASLYSFTLIGELWPKGKSOWEIPFMEHYVEEIIINQKILTYARN 118
QY 123 KALSDRLGIGDALAVYHESLESVENNRNTRARSVKNQYIALELMFVKQLPSFAVSGEE 182
Db 119 TAIARLEGLGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178
QY 183 VPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYNTG 242
Db 179 VPLLMVYQAANLHLLLRDASIFGSEMGMASSDVNQYIQEQIRYTEESNHCVMQYNTG 238
QY 243 LNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDVLVPIKTTTSOLITREVYTDAGT 302
Db 239 LNNLRGTNAESWLRYNQFRRLDTLGVLDLVALFPSTYDTRTYPIINTSAQLTREIYTDPIGR 298
QY 303 VHPNQAFSTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWVG 362
Db 299 TNAPSGFASTNWFNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWVG 358
QY 363 HRLSRPIGALNTSTOGST-NTSINPVTLQFTSRDVRVTESLAGLNLFLTQPVNGVPRV 421
Db 359 HRLNFRPIGTLNTSTOGLTNTSINPVTLQFTSRDVRVTESLAGLNLFLTQPVNGVPRV 418
QY 422 DFHWKFTPLPIASDNFYLG-----YAGVGTQLODSENELEPPETGQPNVYESYSHRLS 474
Db 419 RFNF-----INQNIYERGATTYSQPYQGVGIQLFSETELPETTERPNVYESYSHRLS 472
QY 475 HIGLISASHVKALVYSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
Db 473 HIGLIIGNTLRAPVYSWTHRSADRNTNTPNRIQIPLVKALNLHSGVTVVGGPGFTGGD 532
QY 535 ILRRTNTGTFGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRG 594
Db 533 ILRRTNTGTFGDIRVNIWNPFSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRG 592
QY 595 EDLDYKFTRTIGFTTFFSDVQSTFTTGAMNPFSSGNEVYIDRIEFVFPVEVYEAEDFE 654
Db 593 DNLEYSRFTAGFTFPENFLNAQSTFTLGAQSFNS-QEVYIDRVEFVPAEVTFEAEYDLE 651
QY 655 KAOEKVLTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQIH 714
Db 652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFELVVKYAKRLS 711
QY 715 IERNM 719
Db 712 DERNL 716

RESULT 12

US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Naini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.

REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-448A-7

Query Match 61.9%; Score 2314.5; DB 2; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSHESIDPFVSASTIQTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGKS 99
Db 10 EDSLCAEGNNIDPFVSASTVQTGINIAGRIILGVLGVFPFAGQLASFYSFLVGLWPRGRD 69

QY 100 QWEIFMEHVEEIIINQKILTYARNKALSDRLGLGDALAVYHESLESWVENNTRARSVVK 159
Db 70 QWEIFLEHVEQLNQITENARNALTARLQGLGDSFRAYQQSLEDWLENRDDARTSVLY 129

QY 160 NOYIALELMFVQKLPSPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEIST 219
Db 130 TQYIALELDFLNAMPLFAIRNQEVPLLMVYQAANLHLLLRDASIFGSEFGLTSEIQIR 189

QY 220 FYNQOVERTRDYSCHCIKWYNTGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYD 279
Db 190 YYERQVERTRDYSYCVWEYNTGLNSLRGTNAASWRYNQFRDLTLGLVLDLVALFPSPYD 249

QY 280 TLVPIKTSQLTREYVYDAIGVHPNCAFSTWYNNAPSFSAEAAVIRSPHLLDFL 339
Db 250 TRTYPINTSAQLTREYVYDAIGATGVN--MASMNWYNNAPSFSAEAAVIRSPHLLDFL 307

QY 340 EKVITYLSRWSNTQYNNMGGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDYY 399
Db 308 EQLTIFASRSRWSNTHMYWGHGTIOQRPIGGLNTSTHGATNTSINPVTLRFASRDYY 367

QY 400 RTESLAGLNL--LTQPVNGVRVDFHWKFP--TLPIASDNFYLYGYAGVGTQLQDSNEL 456
Db 368 RTESYAGVLLWGIIVLEPHGVPTVRFENFTNPONISDRGTANTYQPYESPGQLKDSDEL 427

QY 457 PPEITGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTTIPNSITQIPLVKAF 516
Db 428 PPEITERNPNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTTIGPNRITQIIPMKAS 487

QY 517 NLSSGAAVRGPFGTGGDILRRNTGTGDIRVNNINPPFAQRYRVRIRYASTTDLOFHTS 576
Db 488 ELPOGTVVRGPGFTGGDILRRNTGTGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVS 547

QY 577 INKAINQGNFSATWNRGDLDYKTFRTIGFTTTPFSDVQSTFTTIGAMNFSGNEVYID 636
Db 548 RGGTVNNFRFLRWNSGDELKYNFVRRAFTTFTTQIQDIIRTSIQIGLNGEVEYID 607

QY 637 RIEFVPEVVEYAEYDFAKAEKVYALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFY 696
Db 608 KIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDDEF 667

QY 697 LDEKRELFVYKAKIHIERNM 719
Db 668 LDEKRELEKVKYAKRLSDERNL 690

RESULT 14

US-08-459-595A-7
Sequence 7, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-595A-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSHESIDPFVSASTIQTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGKS 99
Db 10 EDSLCAEGNNIDPFVSASTVQTGINIAGRIILGVLGVFPFAGQLASFYSFLVGLWPRGRD 69

QY 100 QWEIFMEHVEEIIINQKILTYARNKALSDRLGLGDALAVYHESLESWVENNTRARSVVK 159
Db 70 QWEIFLEHVEQLNQITENARNALTARLQGLGDSFRAYQQSLEDWLENRDDARTSVLY 129

QY 160 NOYIALELMFVQKLPSPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEIST 219
Db 130 TQYIALELDFLNAMPLFAIRNQEVPLLMVYQAANLHLLLRDASIFGSEFGLTSEIQIR 189

QY 220 FYNQOVERTRDYSCHCIKWYNTGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYD 279
Db 220 FYNQOVERTRDYSCHCIKWYNTGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSPYD 279

Db 190 YERQVTRDYSYCVWYNTGLNSLRGTNAASWRYNQFRDLTLGLVLDLVALPFSYD 249
Qy 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFSTWYNNAPSAIAEAAVIRSPHLLDFL 339
Db 250 TRTYPINTSAQLTREVYTDAGTGVN--MASWYNNAPSAIAEAAVIRSPHLLDFL 307
Qy 340 EKVYISLLSRWSNTQYNNMGGHRLSPGIGALNTSTQGSNTSINPVTIQTSDRVY 399
Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTIRFASRDVY 367
Qy 400 RTESLAGLNL--LTQPVNGVPRVDFHWKFP--TLPIASDNFYVLGYAGVGTQLQDSNEL 456
Db 368 RTESYAGVLLWGIYLEPIHGVTFRFNTPNQISDRGTANYSPQYESPGLQKDSDEL 427
Qy 457 PPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIETPNSITQIPLVKAF 516
Db 428 PPETTERPNYESYSHRLSHIGLILQSRVNVVYSWTHRSADRTNTIGPNRITQIPMVKAS 487
Qy 517 NLSSGAUVVRGPGFTGGDILRRNTGTGDIRVNNPFPQAQRYRIRYASTTDLQFHTS 576
Db 488 ELPGQTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGPLTQYRIGRYASTVDFDFVS 547
Qy 577 INKAINQGNFSAATMNRGDLKYKTFRTIGTTPFSDVQSTFTIGAWNFSSGNEVYID 636
Db 548 RGGTTVNNFRFLRNMNSGDELKYGNFVRAFTPTFTTQIQDIIRTSIQGLSGNGEYID 607
Qy 637 RIEFVPEVYEAEDFEKAQKVTAFTSTNPRGLTKDVKDHYDQVSNLVESLSDEFY 696
Db 608 KIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLTKDVTDYHIDQVSNLVACLSDDEF 667
Qy 697 LDEKLEFEIVKYAKQIHIERNM 719
Db 668 LDEKLEKVKYAKRLSDERNL 690

RESULT 15

US-08-459-504B-7
; Sequence 7, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,504B

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-504B-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

Qy 40 EDYLRMSEHESIDPFVSASTIQTGIGIAGKILGTGVFPFAGQIASLVSFILGELWPKGKS 99
Db 10 EDSLCAEGNNIDPFVSASTVQTGINAGRIILGVLGVFPFAGQIASLVSFILGELWPKGRD 69
Qy 100 QWEIFMEHVEIINQKILTYARNKALSLRGLGDALAVYHESLESWENRNTRRSWVK 159
Db 70 QWEIFLEHVEQLNQIITENARNALAKLQGLGDSFRAYQQSLEDWLENRDDARTSVLY 129
Qy 160 NOYIALELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLDASIFGKEWGLSASISIT 219
Db 130 TQYIALELDFLNAFLFAIRNQEVPLLMVYAQAANLHLLLDASLFGSEGLTSQBIQR 189
Qy 220 FYNQVTRTRDYSCHIKWYNTGLNNLGTNAKSWRYNQFRKDMTLMVLVLPFSYD 279
Db 190 YERQVTRDYSYCVWYNTGLNSLRGTNAASWRYNQFRDLTLGLVLDLVALPFSYD 249
Qy 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFSTWYNNAPSAIAEAAVIRSPHLLDFL 339
Db 250 TRTYPINTSAQLTREVYTDAGTGVN--MASWYNNAPSAIAEAAVIRSPHLLDFL 307
Qy 340 EKVYISLLSRWSNTQYNNMGGHRLSPGIGALNTSTQGSNTSINPVTIQTSDRVY 399
Db 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTIRFASRDVY 367
Qy 400 RTESLAGLNL--LTQPVNGVPRVDFHWKFP--TLPIASDNFYVLGYAGVGTQLQDSNEL 456
Db 368 RTESYAGVLLWGIYLEPIHGVTFRFNTPNQISDRGTANYSPQYESPGLQKDSDEL 427
Qy 457 PPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIETPNSITQIPLVKAF 516
Db 428 PPETTERPNYESYSHRLSHIGLILQSRVNVVYSWTHRSADRTNTIGPNRITQIPMVKAS 487
Qy 517 NLSSGAUVVRGPGFTGGDILRRNTGTGDIRVNNPFPQAQRYRIRYASTTDLQFHTS 576
Db 488 ELPGQTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGPLTQYRIGRYASTVDFDFVS 547
Qy 577 INKAINQGNFSAATMNRGDLKYKTFRTIGTTPFSDVQSTFTIGAWNFSSGNEVYID 636
Db 548 RGGTTVNNFRFLRNMNSGDELKYGNFVRAFTPTFTTQIQDIIRTSIQGLSGNGEYID 607
Qy 637 RIEFVPEVYEAEDFEKAQKVTAFTSTNPRGLTKDVKDHYDQVSNLVESLSDEFY 696
Db 608 KIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLTKDVTDYHIDQVSNLVACLSDDEF 667

QY 697 LDEKRELFELVYAKQIHIERNM 719
Db 668 LDEKRELFELVYAKQIHIERNM 690

Search completed: March 9, 2005, 17:27:50
Job time : 25.1512 secs